

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 15, 2004, 13:55:24 ; Search time 97 Seconds

(without alignments)  
1842.208 Million cell updates/sec

Title: US-10-079-111-1

Perfect score: 1657  
Sequence: 1 MARCSVLVLLTSIWTTRLL.....NPESKSPKTVRCLEAEV 322

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 682709 segs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEX=7

Database : Issued Patents NA.\*

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- 2: /cgn2\_6/ptodata/2/ina/5B COMB.seq.\*
- 3: /cgn2\_6/ptodata/2/ina/6A COMB.seq.\*
- 4: /cgn2\_6/ptodata/2/ina/6B COMB.seq.\*
- 5: /cgn2\_6/ptodata/2/ina/PTUS COMB.seq.\*
- 6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1657	100.0	2029	4	US-09-232-160-13 m.m.c
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3	1657	100.0	2372	4	US-09-905-125A-200
4	1657	100.0	2372	4	US-09-902-775A-200
5	1657	100.0	2404	4	US-09-833-381-849
6	1657	100.0	2404	4	US-09-833-381-853
7	1651	99.6	2313	2	US-08-892-880-1
8	1103	66.6	1896	4	US-09-724-864-28
9	354	21.4	492	2	US-08-892-880-12
10	349	21.1	466	2	US-08-892-880-13
11	286.5	17.3	498	2	US-08-892-880-15
12	234.5	14.2	1537	6	5504194-1

13	224	13.5	3207	1	US-07-946-497-1	Sequence 1, Appli
14	224	13.5	3207	1	US-08-483-322-1	Sequence 1, Appli
15	224	13.5	3207	2	US-08-478-882-1	Sequence 1, Appli
16	213	12.9	1794	3	US-09-213-719-1	Sequence 1, Appli
17	210	12.7	1297	4	US-09-023-655-876	Sequence 876, App
18	199.5	12.0	4675	4	US-09-566-921-97	Sequence 97, Appl
19	145	8.8	1414	1	US-08-024-868-1	Sequence 1, Appli
20	145	8.8	1414	2	US-08-242-097-1	Sequence 1, Appli
21	145	8.8	1414	3	US-09-206-695-1	Sequence 1, Appli
22	145	8.8	1414	4	US-09-799-118-1	Sequence 63, Appl
23	133.5	8.1	1734	4	US-09-484-970B-63	Sequence 1, Appli
24	128.5	7.8	3259	5	PCT-US95-03747-1	Sequence 212, App
25	127.5	7.7	1985	4	US-09-907-794A-212	Sequence 212, App
26	127.5	7.7	1985	4	US-09-905-125A-212	Sequence 212, App
27	127.5	7.7	1985	4	US-09-902-775A-212	Sequence 19, Appl
28	121	7.3	1587	4	US-09-010-147B-19	Sequence 19, Appl
29	114.5	6.9	5191	1	US-08-340-428B-1	Sequence 1, Appli
30	114.5	6.9	5191	5	PCT-US93-07306-1	Sequence 1, Appli
31	113	6.8	8224	6	5180808-1	Patent No. 5180808
32	112	6.8	1190	1	US-08-310-370-1	Sequence 1, Appli
33	111	6.7	1720	4	US-09-148-545-53	Sequence 53, Appl
34	107	6.5	1400	2	US-08-001-078A-2	Sequence 2, Appli
35	107	6.5	1400	2	US-08-463-218-2	Sequence 2, Appli
36	107	6.5	1400	5	PCT-US94-00253-2	Sequence 1, Appli
37	107	6.5	1520	1	US-08-225-477B-1	Sequence 1, Appli
38	107	6.5	1520	5	PCT-US95-04353-3	Sequence 1, Appli
39	107	6.5	2589	1	US-08-325-267A-3	Sequence 3, Appli
40	107	6.5	2685	3	US-08-362-525-21	Sequence 21, Appl
41	107	6.5	4614	1	US-08-325-267A-1	Sequence 1, Appli
42	106.5	6.4	1482	4	US-09-016-434-230	Sequence 230, App
43	106.5	6.4	2455	3	US-09-103-429A-1	Sequence 1, Appli
44	106.5	6.4	2821	3	US-09-103-429A-2	Sequence 2, Appli
45	103	6.2	1519	1	US-08-225-477B-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-232-160-13  
; Sequence 13, Application US/09232160  
; Patent No. 6368794  
; GENERAL INFORMATION:  
; APPLICANT: Steve Daniel  
; APPLICANT: James Gilmore  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Laura Stuve  
; TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL  
; TITLE OF INVENTION: PROLIFERATION  
; FILE REFERENCE: PA-0003 US  
; CURRENT APPLICATION NUMBER: US/09/232.160  
; CURRENT FILING DATE: 1999-01-15  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PERL Program  
; SEQ ID NO 13  
; LENGTH: 2029  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: 3044710  
US-09-232-160-13

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Pred. No.:	1657.00	Matches:	322
Score:	100.00%	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	100.00%	Gaps:	0
DB:	4		

US-10-079-111-1 (1-322) x US-09-232-160-13 (1-2029)

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Qy 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40  
Db 243 GTCCAGGCTCTTCGCTGCAGAGAGCTTTCATCCAGGTGTCATGCAGATTATGGG 302  
Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
Db 303 ATCACCTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTCACAGAGCTTAAGAGGCC 362  
Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
Db 363 TGTAGGCTGCTGGGCTAAGTTTGGCGGCAAGGACCAAGTTGAACAGCTTGAAGCT 422  
Qy 81 SerPheGlnThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle 100  
Db 423 AGCTTTGAACTTCAGCTATGGCTTGGGTTCGAGATGGATTCGTGGTCTATCTAGGATT 482  
Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTyrLysValProVal 120  
Db 483 AGCCCAAAACCCCAAGTGTGGGAAATGGGGTGGGTGCTCTGATTTGGAGGTTCCAGTG 542  
Qy 121 SerArgGlnPheAlaIleTyrCysTyrAsnSerSerAspThrTyrThrAsnSerCysIle 140  
Db 543 AGCCGACAGTTTGAGCCTATTGTACAACTCATCTGATCTTGGACTTAACCTGCGATT 602  
Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
Db 603 CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCACTTGAACCTAATCTGCGATT 662  
Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
Db 663 GAATTTATTGTCACTGACAGTACTACTCGTGGCATCCCTTACTTCAATACCTGCC 722  
Qy 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgLysLysLeuIle 200  
Db 723 CCTACTACTCTCTCTCTCCAGCTTCCACTTCTATTCCAGGAGAAAAAATTGATT 782  
Qy 201 CysValThrGluValPheMetGluThrThrSerThrMetSerThrGluThrGluProPheVal 220  
Db 783 TGTGTACAGAAAGTTTATGGAACTAGACCATGTCTACAGAACTGAACCATTTGTT 842  
Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
Db 843 GAAATTAAGAGCAGCATTAAGAAATGAAGTGTGGTGGTGTGCCCGCCGCTCTG 902  
Qy 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
Db 903 CTAGTGCTTGCTCTCTCTCTCTTGTGTGCTGCACTGGTCTTGGATTGCTATGTCAAA 962  
Qy 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
Db 963 AGGTATGTGAAGGCTTCCCTTTTACAAACAGAAATCAGCAGAGGAATGATCGAAACC 1022  
Qy 281 LysValValLysGluLysAlaLeuAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
Db 1023 AAAGTAGTAAGAGGAGAGGAGGCAATGATAGCAACCTTAATGAGGAATCAAGAAACT 1082  
Qy 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
Db 1083 GATAAAACCCAGAGAGTCCAGAGTCCAGAGAACTTACCGTGCATGCGCTGGAAGCT 1142  
Qy 321 GluVal 322  
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## RESULT 2

US-09-907-794A-200  
; Sequence 200, Application US/09907794A  
; Patent No. 6635468  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi

## Alignment Scores:

Pred. No.: 5,92e-177 Length: 2372  
Score: 1657.00 Matches: 322  
Percent Similarity: 100.00% Conservative: 0

; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/907,794A  
; CURRENT FILING DATE: 2001-07-17  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 200  
; LENGTH: 2372  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-907-794A-200



Best Local Similarity: 100.00%		Mismatches: 0
Query Match: 100.00%		Indels: 0
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Qy	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db	220	GTCCAAGGCTCTTTGGCGTGAAGAGAGCTTTCCATCCAGGTGTCAATGAGAAATTTAGGG 279
Qy	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db	280	ATCACCCCTTGTGAGCAAAAGGCGAACCAAGCTGAATTTACAGAGAGCTAAGAGGCC 339
Qy	61	CysArgLeuLeuGlySerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db	340	TGTAGGCTGCTGGACTAAGTTTGGCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 399
Qy	81	SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle 100
Db	400	AGCTTTGAAACTTGCAGCTATGGCTGGGTGGGTGGGTGGTCTGATTTGGAAAGGTTCCAGTG 459
Qy	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleThrLysValProVal 120
Db	460	AGCCCAAAACCCAGTGTGGGAAATGGGTGGGTGGTCTGATTTGGAAAGGTTCCAGTG 519
Qy	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrThrAsnSerCysIle 140
Db	520	AGCCGACAGTTTGCAGCTATTGTTACAACTCATCTGATCTTGGACTTAACCTGTCGATT 579
Qy	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db	580	CCAGAAATATTATCACCAAGATCCCATATTACACTCAAACTCAAACTCAACAAACAA 639
Qy	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db	640	GAATTTATTGTGTCAGTACAGACTACTCGTGGCATCCCTTACTCTACAATACCTGCC 699
Qy	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db	700	CCTACTACTACT 759
Qy	201	CysValThrGluValPheMetGluThrThrSerThrMetSerThrGluThrGluProPheVal 220
Db	760	TGTGTACAGAAAGTTTATGGAAACTTAGCACCATGTCACAGAACTGAACTGATTTGTT 819
Qy	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db	820	GAATATTAAGCAGCAATCAAGATGAAGCTGCTGGGTGGAGGTGTCCTCCACGGCTCTG 879
Qy	241	LeuValLeuAlaLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db	880	CTAGTGTCT 939
Qy	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db	940	AGGTATGTGAAGGCT 999
Qy	281	LysValValLysGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db	1000	AAAGTAGTAAAGGAGGAGAGCCCAATGATAGCAACCTTATGAGGAATCAAGAAACT 1059
Qy	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db	1060	GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAACTACCGTCCGATGCTGGAAGCT 1119
Qy	321	GluVal 322
Db	1120	GAAATT 1125

RESULT 3  
US-09-905-125A-200  
; Sequence 200, Application US/09905125A  
; Patent No. 6664376  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary B.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US 09/905,125A  
; CURRENT FILING DATE: 2001-07-12  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 200  
; LENGTH: 2372

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-905-125A-200

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Alignment Scores:		
Pred. No.:	5.92e-177	Length: 2372
Score:	1657.00	Matches: 322
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	4	Gaps: 0

US-10-079-111-1 (1-322) x US-09-905-125A-200 (1-2372)

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QY	21	ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	220	GTCCAGAGCTCTTTCGGTGCAGAGAGCTTTCCATCAGAGTGTCTATCAGAAATATATGGG	279
QY	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	280	ATCACCCCTGTGAGCAAAAGCGCAACAGCAGCTGAATTTACAGAACTAAGGAGGCC	339
QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	340	TGTAGGCTGCTGGAGCTAAGTTTGGCGCGCAAGACCAAGTTCGAAACAGCCTTTGAAAGCT	399
QY	81	SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle	100
Db	400	AGCTTTGAAACTTCAGCTATGCTGGGTGGAGATGGATTCGTGGTCACTCTCTAGGATT	459
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
Db	460	AGCCCAAAACCCAGTGTGGGAAAAATGGGTGGTCTCTGATTTTGGAAGGTTCCAGTG	519
QY	121	SerArgGlnPheAlaLysTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	520	AGCGACAGTTTGCAGCGCTATTGTTACACTCACTGATCTATGGACTAACTCGTGCAAT	579
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	580	CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACAAACAACA	639
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	640	GAATTTATTGTCAGTGCACGACTCTACTCGGTGGCATCCCTTACTCTACAAATACCTGCC	699
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Db	700	CCTACTACTACTCTCTCTCGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	759
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	760	TGTGTCCACAGAGTTTTTATGGAACACTAGCACCATGTCTCAGAGAACTGAACCACTTTGTT	819
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	820	GAAAAATAAGCAGCATTTCAAGAAATGAAGCTGTGGGTTTGGAGGTGTCCCCCAGCGCTCTG	879
QY	241	LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	880	CTAGTGTCTTGCTCTCTCTTCTTGGTCTCGAGCTGCTTGGATTTTGTATGTCAAA	939
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	940	AGGTATGTGAAGGCCCTTCCCTTTTACAAACAGAAATCAGCAGAGGAAATGATCGAAACC	999
QY	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
Db	1000	AAAGTAGTAAAGGAGGAGGCCCAATGATAGCAACCTTAATGAGGAATCAAGAGAAACT	1059

Qy	301	AspLysAsnProGluSerLysSerProSerLysThrThrValA-gCysLeuGluAla	320
Db	1060	GATAAAACCCAGAAGAGTCCAAGAGTCCAAAGCAAAACTACCGTGCAGTGCCTGGAGCT	1119
Qy	321	GluVal	322
Db	1120	GAAGTT	1125

## RESULT 4

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US-09-902-775A-200
; Sequence 200, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; ACIDS ENCODING THE SAME
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,775A
; CURRENT FILING DATE: 2001-07-10
; PRIORITY APPLICATION NUMBER: PCT/US00/04414
; PRIORITY FILING DATE: 2000-02-22
; PRIORITY APPLICATION NUMBER: US 60/143,048
; PRIORITY FILING DATE: 1999-07-07
; PRIORITY APPLICATION NUMBER: US 60/145,698
; PRIORITY FILING DATE: 1999-07-26
; PRIORITY APPLICATION NUMBER: US 60/146,222
; PRIORITY FILING DATE: 1999-07-28
; PRIORITY APPLICATION NUMBER: PCT/US99/20594
; PRIORITY FILING DATE: 1999-09-08
; PRIORITY APPLICATION NUMBER: PCT/US99/20944
; PRIORITY FILING DATE: 1999-09-13
; PRIORITY APPLICATION NUMBER: PCT/US99/21090
; PRIORITY FILING DATE: 1999-09-15
; PRIORITY APPLICATION NUMBER: PCT/US99/21547
; PRIORITY FILING DATE: 1999-09-15
; PRIORITY APPLICATION NUMBER: PCT/US99/23089
; PRIORITY FILING DATE: 1999-10-05
; PRIORITY APPLICATION NUMBER: PCT/US99/28214
; PRIORITY FILING DATE: 1999-11-29
; PRIORITY APPLICATION NUMBER: PCT/US99/28313
; PRIORITY FILING DATE: 1999-11-30
; PRIORITY APPLICATION NUMBER: PCT/US99/28564
; PRIORITY FILING DATE: 1999-12-02
; PRIORITY APPLICATION NUMBER: PCT/US99/28565
; PRIORITY FILING DATE: 1999-12-02
; PRIORITY APPLICATION NUMBER: PCT/US99/30095
; PRIORITY FILING DATE: 1999-12-16
; PRIORITY APPLICATION NUMBER: PCT/US99/30911

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Thu Sep 16 09:09:48 2004

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; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-902-775A-200

Alignment Scores:
Pred. No.: 5,92e-177 Length: 2372
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-079-111-1 (1-322) x US-09-902-775A-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCCAGGTGCTTCACGCTGGTGTCTCTCACCTCCATCTGGACCCAGGCTCCTG 219

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAAGGCTCTTTGCGTGCAGAGAGCTTTCCATCCAGGTGTCTATCGAAATTTATGGG 279

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnIleuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCCCTTGTGACCAAAAAGCGCAACAGCAGCTGAATTTCCAGAAAGCTTAAGAGGCC 339

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGAGCTAAGTTTGGCCGCAAGGCCAAGTTGAACAGCCCTTGAAAGCT 399

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTCAGACTATGGCTGGGTTCGAGATGATGATTCGTGTCATCTCTAGGATT 459

QY 101 SerProAsnProLysCysGlyAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAAAACCCCAAGTGTGGGAAAAAATGGGTGGGTGCTCGATTGTGAAGGTTCCAGTG 519

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGATTTGACGCTATTTGTTACACTCACTGATCTTGACTTAACCTCGTGCAAT 579

QY 141 ProGluIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTTATCACCAACAAAGATCCCATATTCAACACTCAAACTGCCAACACAAACAACA 639

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAAATTTATTTGTCAGTGACAGTACTACTCGGTGGCATCCCCCTTACTCTCAATAATCCTGCC 699

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCTCTCTCTCTCCAGCTTCCATTTCTATTCCACGGAGAGAAAAAATTGATT 759

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTTCACAGAAGTTTATATGGAACATAGCACCATGTCTACAGAAACTGAACCATTTGTT 819

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db 820 GAAAAATAAAGCAGCATTTCAAGAAATGAAGCTGTCTGGGTTTTGGAGGTCTCCCCACGGCTCTG 879

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCCTGCTCTCTCTCTCTTTGTGTGTGTGAGCTGGTCTTGGAATTTGTATGTCAAA 939

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261 ArgTyrValIysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
|
|
|
940 AGCTATGTGAAGCCCTTCCTTTTACAAAACAGAAATCAGCAGAGAAGAAATGATCGAAACC 999
|
|
|
281 LysValValIysGluGluLysAlaAsnAspSerAsnProAsnGlnGluSerLysLysThr 300
|
|
|
1000 AAATAGTAGTAAGAGAGAGAGGCCCAATGATAGACACCTTAATGAGGATCAAGAAAAACT 1059
|
|
|
301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
|
|
|
1060 GATATAAAACCAGAGAGTCCAAAGAGTCCAAAGCAAAACTACCGTGGGATGCCTGGAAGCT 1119
|
|
|
321 GluVal 322
|
|
|
Db 1120 GAAGTT 1125

RESULT 5
US-09-833-381-849
; Sequence 849, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 849
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-849

Alignment Scores:
Pred. No.: 6, 05e-177 Length: 2404
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

09/833382
Diana
Restriction
us-10-079-111-1 (1-322) x US-09-833-381-849 (1-2404)

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US-10-079-111-1 (1-322) x US-09-833-381-849 (1-2404)

QY 1 MetAlaAqCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 190 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTCCATCTGCACACGAGGCTCTGT 249
QY 21 ValGInGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 250 GTCCAAAGGCTCTTCGTGTCAGAAAGAGCTTTCATCCAGGTGTCTATGCAGAAATTATGGGG 309
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 310 ATCACCCCTGTGAGCAAAAAGCGCAACGACAGCTGAATTTCCACAGAGCTTAGAGAGCC 369
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 370 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAGAGCT 429
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 430 AGCTTTGAAACTTGACAGCTATGGCTGGGTGGAGATGGATTTCGTGGTCACTCTAGGATT 489
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 490 AGCCCCAAAACCCCAAGTGGGGAAAATGGGGTGGGTGTCCTGATTGGGAAGGTTCCAGTG 549
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140

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09/833382

Diava

Restoration

Db 550 AGCCGACAGTTGGAGCCTATTGTTACAACTCATCTGATCTGGACTTAACCTCGTGCATT 609  
 QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
 Db 610 CCAGAAATATACCAACCAAGATCCCATATTTCAACACTCAAACTGCAACCAACA 669  
 QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
 Db 670 GAATTTATTGTGAGTACAGTACCTACTCGTGGCATCCCTTACTCTCAATACCTGCC 729  
 QY 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLeuIle 200  
 Db 730 CCTACTACT 789  
 QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
 Db 790 TGTGTACAGAGTTTATGGAACTTAGCCATGCTCAGAACTGAAACCAATTTGTT 849  
 QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
 Db 850 GAAATATAAGCAGCATTCAGAAATGAAGCTGCTGGTGGAGGTGCCCAACGCTCTG 909  
 QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
 Db 910 CTAGTGTCT 969  
 QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
 Db 970 AGGTATGTGAAGCCTTCCCTTTTACAAACAGAAATCAGCAGAGGAAATGATCGAAACC 1029  
 QY 281 LysValValLysGluLysLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
 Db 1030 AAAGTAGTAAAGAGGAGGAGGCAATGATAGCAACCTTAATGAGGAATCAAGAAACT 1089  
 QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
 Db 1090 GATATAAACCCAGAGAGTCCAAAGTCCAAAGCAAAACTACCGTGGAGCT 1149  
 QY 321 GluVal 322  
 Db 1150 GAAGTT 1155

RESULT 6

US-09-833-381-853  
 ; Sequence 853, Application US/09833381  
 ; Patent No. 6672186  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Robison, Keith E.  
 ; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs  
 ; FILE REFERENCE: 5800-119  
 ; CURRENT APPLICATION NUMBER: US/09/833,381  
 ; CURRENT FILING DATE: 2001-04-11  
 ; PRIOR APPLICATION NUMBER: 09/516,448  
 ; PRIOR FILING DATE: 2000-02-29  
 ; NUMBER OF SEQ ID NOS: 2050  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 853  
 ; LENGTH: 2404  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-833-381-853

Alignment Scores:  
 Pred. No.: 6,05e-177 Length: 2404  
 Score: 1657.00 Matches: 322  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 4 Gaps: 0

US-10-079-111-1 (1-322) x US-09-833-381-853 (1-2404)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleThrThrArgLeuLeu 20

Db 190 ATGGCCAGGTCTTCAGCCTGGTGTGTCTTCATCTCCATCGACACAGGCTCCTG 249  
 QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
 Db 250 GTCCAAAGGCTCTTTCGGTGCAGAGAGCTTTCATCCAGGTGTCTATGCAGAAATATGGG 309  
 QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
 Db 310 ATCACCTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTTTCAGAGCTTAAGAGGCC 369  
 QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
 Db 370 TGTAGGCTGTGGGACTTAAGTTTGGCCGCAAGCAAGTTGAAACAGCCTTGAAGCT 429  
 QY 81 SerPheGluThrCysSerTyrGlyTyrValGlyValGlyValLeuIleThrLysValProVal 120  
 Db 430 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCTGGTGCATCTCTAGGATT 489  
 QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleThrLysValProVal 120  
 Db 490 AGCCCAAAACCCAAAGTGTGGGAAAAATGGGGTGGTCTCTGATTTGGAAGTTCCAGTG 549  
 QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrThrThrAsnSerCysIle 140  
 Db 550 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTGATCTGGAATACTCGTGCATT 609  
 QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
 Db 610 CCAGAAATATACCAACCAAGATCCCATATTCAACACTCAACTCAAACTGCAACCAACA 669  
 QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
 Db 670 GAATTTATTGTGAGTACAGTACCTACTCGTGGCATCCCTTACTCTCAATACCTGCC 729  
 QY 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200  
 Db 730 CCTACTACT 789  
 QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
 Db 790 TGTGTACAGAAATTTTATGGAACTTAGCCATGCTCAGAACTGAAACCAATTTGTT 849  
 QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
 Db 850 GAAATATAAGCAGCATTCAGAAATGAAGCTGCTGGTGGAGGTGCCCAACGCTCTG 909  
 QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
 Db 910 CTAGTGTCT 969  
 QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
 Db 970 AGGTATGTGAAGCCTTCCCTTTTACAAACAGAAATCAGCAGAGGAAATGATCGAAACC 1029  
 QY 281 LysValValLysGluLysLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
 Db 1030 AAAGTAGTAAAGAGGAGGAGGCAATGATAGCAACCTTAATGAGGAATCAAGAAACT 1089  
 QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
 Db 1090 GATATAAACCCAGAGAGTCCAAAGTCCAAAGCAAAACTACCGTGGAGCT 1149  
 QY 321 GluVal 322  
 Db 1150 GAAGTT 1155

RESULT 7

US-08-892-880-1  
 ; Sequence 1, Application US/08892880  
 ; Patent No. 5942417  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NI, JIAN

102(e)

issued Aug 24, 1999

fd 7/15/97

Nil et al.

APPLICANT: GENTZ, REINER L.  
 APPLICANT: DILLON, PATRICK J.  
 TITLE OF INVENTION: CD44-LIKE PROTEIN  
 NUMBER OF SEQUENCES: 15  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 STREET: 1100 NEW YORK AVENUE, NW, SUITE 600  
 CITY: WASHINGTON  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005-3934

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/892,880  
 FILING DATE: HEREWITH  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/021,762  
 FILING DATE: 15-JUL-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: STEFFE, ERIC K  
 REGISTRATION NUMBER: 36,688  
 REFERENCE/DOCKET NUMBER: 1488.0490001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-371-2600  
 TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2313 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 91..1056  
 FEATURE:  
 NAME/KEY: mat\_peptide  
 LOCATION: 154..1056  
 FEATURE:  
 NAME/KEY: sig\_peptide  
 LOCATION: 91..153  
 US-08-892-880-1

Alignment Scores:  
 Pred. No.: 2,71e-176 Length: 2313  
 Score: 1651.00 Matches: 321  
 Percent Similarity: 99.69% Conservative: 0  
 Best Local Similarity: 99.69% Mismatches: 1  
 Query Match: 99.64% Indels: 0  
 DB: 2 Gaps: 0

US-10-079-111-1 (1-322) x US-08-892-880-1 (1-2313)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrrPThrArgLeuLeu 20  
 DB 91 ATGCCAGGCTCTTTCAGCTGGTGTCTTCTCATCTCCATCTGGACACAGAGCTCTG 150  
 QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40  
 DB 151 GTCCAGGCTCTTTCAGCTGGTGTCTTCTCATCTCCATCTGGACACAGAGCTCTG 210  
 QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
 DB 211 ATCACCTTGTGAGCAAAAGCGAACCCAGCAGCTGAATTTTCAGAGAGCTTAAGGAGCC 270  
 QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
 DB 271 TGTAGGCTGCTGGGACTAAGTTTGGCCCGGAGGACCAAGTTTGAACAGCCTTGANAGCT 330

QY 81 SerPheGluThrCysSerTyrGlyTrrPValGlyAspGlyPheValValIleSerArgIle 100  
 DB 331 AGCTTTGCACTTGCAGCTATGGCTGGGTGGGATGATTCGTGGTCTATCTTAGGATT 390  
 QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrrPValProVal 120  
 DB 391 AGCCCAACCCCAAGTGGGAAATGGGTGGTGTCTGATTGGAGGTTCCAGTG 450  
 QY 121 SerArgGlnPheAlaIaTyrCysTyrAsnSerSerAspThrTrrPThrAsnSerCysIle 140  
 DB 451 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTTGGACTTAACTCGTGCATT 510  
 QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
 DB 511 CCAGAAATTATCACCCCAAGATCCCATATTCACATCTCAACCTGCAACACAAACA 570  
 QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
 DB 571 GAATTTATGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTTACATACTGCTGC 630  
 QY 181 ProThrThrProAlaProAlaSerThrSerIleProAsnArgLysLysLeuIle 200  
 DB 631 CCTACTACTCTCTCTCCAGCTTCCACTTCTATTTCCACGGAGAAAAAATIGATT 690  
 QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
 DB 691 TGTGTACACAGAAAGTTTATGAAACTAGCACCATGTCTACAGAACTGAACCAATTTGTT 750  
 QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaIaGlyPheGlyGlyValProThrAlaLeu 240  
 DB 751 GAAATAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 810  
 QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaIaGlyLeuGlyPheCysTyrValLys 260  
 DB 811 CTAGTGTCT 870  
 QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
 DB 871 AGTATGTGAAGGCTTCCCTTTTCAACACAGAAATCAGCAGAGGAATGATCGAAACC 930  
 QY 281 LysValValLysGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
 DB 931 AAAGTAGTAAAGGAGGAGGAGGCAATGATAGCAACCTTAATGAGGAATCAAGAAAACT 990  
 QY 301 AspLysAsnProGluLysSerProSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
 DB 991 GATAAAACCCAGAGAGTCCAGAGTCCAGAGCAAAACTACCGTGCATGCTTGGAGCT 1050  
 QY 321 GluVal 322  
 DB 1051 GAAGTT 1056  
 RESULT 8  
 US-09-724-864-28  
 ; Sequence 28, Application US/09724864  
 ; Patent No. 6380362  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Watson, James D  
 ; APPLICANT: Murison, James G.  
 ; TITLE OF INVENTION: Polynucleotides, polypeptides expressed  
 ; TITLE OF INVENTION: by the polynucleotides and methods for their use.  
 ; FILE REFERENCE: 11000.105001  
 ; CURRENT APPLICATION NUMBER: US/09/724,864  
 ; CURRENT FILING DATE: 2000-11-28  
 ; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678  
 ; PRIOR FILING DATE: 1999-12-23  
 ; NUMBER OF SEQ ID NOS: 72  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 28  
 ; LENGTH: 1896  
 ; TYPE: DNA  
 ; ORGANISM: Mouse

US-09-724-864-28

## Alignment Scores:

Pred. No.: 1,62e-114 Length: 1896  
Score: 1103.00 Matches: 221  
Percent Similarity: 79.18% Conservative: 30  
Best Local Similarity: 69.72% Mismatches: 62  
Query Match: 66.57% Indels: 4  
DB: 4 Gaps: 3

US-10-079-111-1 (1-322) x US-09-724-864-28 (1-1896)

QY 6 SerLeuValLeuLeuLeuLeuLeuSerIleThrThrArgLeuLeuValGlnGlySerLeu 25  
DB 77 AGCGTGTGTACTCTCTCGCTCTATTGGACCACTAGGACCCAGTCCAGGTGGCGAC 136  
QY 26 ArgAlaGluLeuSerIleGlnValSerCysArgIleMetGlyIleThrValSer 45  
DB 137 CTGTCGCAAGACCTTCCATTCTCT---ACATGCAGAAATCATGGCGTTGCTGTGGC 193  
QY 46 LysLysAlaAsnGlnGlnLeuAsnPhleThrGluAlaLysGluAlaCysArgLeuLeuGly 65  
DB 194 AGAAACAAAACCCACAGATGAATTCACAGAGCCAAAGGCTGTAAAGATGCTGGGA 253  
QY 66 LeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAlaSerPheGluThrCys 85  
DB 254 CTGACTCTGCCAGCAGGAGCAGGTAGAGTCAGCGCAGAAATCTGGCTTTGAGACTTGC 313  
QY 86 SerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIleSerProAsnProLys 105  
DB 314 AGCTATGGATGGGTGGAGAACAGTCTCTGTCTATCTCTCGGATTTCTCAAAACCCGAG 373  
QY 106 CysGlyLysAsnGlyValGlyValLeuLeuLeuTrpLysValProValSerArgGlnPheAla 125  
DB 374 TGTGGGAAGATGGCAAGGTGTCCTGATTTGAATGCTCCCTCCAGCCAAAAGTTCAA 433  
QY 126 AlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIleProGluIleLeuThr 145  
DB 434 GCCTATTGTCACAACTCATCCGACACTGGTTAACTCTCTGCAATTCAGAAATCGTTACC 493  
QY 146 ThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThrGluPheIleValSer 165  
DB 494 ACATTTTACCCGTGTGGAGCACTCAA-----ACACCCGCAACAGAGTTTCTGTGAGC 547  
QY 166 AspSerThrTyrSerValAlaSerProTyrSerThrIleProAlaProThrThrThrPro 185  
DB 548 AGCAGCGCTACTTGGCTTTCCTCCCTGACTCCACACACCTGTTCTGCCACCCACC--- 604  
QY 186 ProAlaProAlaSerThrSerIleProArgLysLysLeuIleCysValThrGluVal 205  
DB 605 CGGGCTCCACCTTTGACCTCCATGGCAGCAAGACAAAAGATTTGTATCAGGAAATTT 664  
QY 206 PheMetGluThrSerThrMetSerThrGluThrGluProPheValGluAsnLysAlaLa 225  
DB 665 TATACAGAACCTATCACCATGCTACAGAAACAGAGACATTTGTTGCAAGTGGAGCAGCA 724  
QY 226 PheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeuValLeuAlaLeu 245  
DB 725 TTCAAGAACGAAGCAGCTGGGTTTGAGAGTGTCCCAACCGCCCTGCTGGTGTGCTCTC 784  
QY 246 LeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLysArgTyrValLysAla 265  
DB 785 CTCCTCTTGGTGTGGCGCTGTGCTGCTGTTTGTCTACGTGAAAGGTATGTGAAGGCC 844  
QY 266 PheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThrLysValValLysGlu 285  
DB 845 TTCCCTTTCAACCAACCAAGATCAACAGAGGAAATGATCGAAACCAAGTTGTAAAGGAA 904  
QY 286 GluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThrAspLysAsnProGlu 305  
DB 905 GAGAGAGGTGATGACGTCAACGCTAATGAAGAATCAAGAAACACCATTAATAAACCCAGAG 964  
QY 306 GluSerLysSerProSerLysThrThrValArgCysLeuGluAlaGluVal 322

DB 965 GAGGCCAAGAGTCCACCAAACTACGTCGCGCTTAGAAGCTGAAGTT 1015  
RESULT 9  
US-08-892-880-12  
; Sequence 12, Application US/08892880  
; Patent No. 5942417  
; GENERAL INFORMATION:  
; APPLICANT: NI, JIAN  
; APPLICANT: GENTZ, REINER L.  
; APPLICANT: DILLON, PATRICK J.  
; TITLE OF INVENTION: CD44-LIKE PROTEIN  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/892,880  
; FILING DATE: HEREWITH  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/021,762  
; FILING DATE: 15-JUL-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC K  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.04900001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 492 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-892-880-12

Alignment Scores:  
Pred. No.: 7.76e-31 Length: 492  
Score: 354.00 Matches: 83  
Percent Similarity: 77.39% Conservative: 6  
Best Local Similarity: 72.17% Mismatches: 12  
Query Match: 21.36% Indels: 16  
DB: 2 Gaps: 2

US-10-079-111-1 (1-322) x US-08-892-880-12 (1-492)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleThrThrArgLeuLeu 20  
DB 99 ATGGCCAGTCTTCCAGCTGGTGTGTTTCATCTTCATCTCCATCCAGGTGTCTATGAGGCTCTG 158  
QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40  
DB 159 GTCAAGGCTCTTTCGTCGTCAGAAAGCTTCCATCCAGGTGTCTATGAGGCTCTG 218  
QY 41 IleThrLeuValSerLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
DB 219 ATCACCTTGTGACAAAAGCGCAACAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 278  
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
DB 279 TGTAGTGTCTNGGACTAAGTTTGGCCGCAAGCCCAAGTTG---AACAGCTTGAAGT- 334

QY 81 SerPheGluThrCysSerTyrGlyTrpValGly----- 91  
 Db 335 AGCTTTGAAT-TGCAGTTGGCTTGGTGGATGTTGNGNCATTTAGTGTAGCCCAA 393  
 QY 92 -----AspGlyPheValIleSerArgIleSerPro 102  
 Db 394 CCCANTTTGGAANTGGGTGGNCCNATTGAGTCCCTTAGCCCN 438

RESULT 10  
 US-08-892-880-13  
 ; Sequence 13, Application US/08892880  
 ; Patent No. 5942417  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NI, JIAN  
 ; APPLICANT: GENTZ, REINER L.  
 ; APPLICANT: DILLON, PATRICK J.  
 ; TITLE OF INVENTION: CD44-LIKE PROTEIN  
 ; NUMBER OF SEQUENCES: 15  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 ; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600  
 ; CITY: WASHINGTON  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20005-3934  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/892,880  
 ; FILING DATE: HERewith  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 60/021,762  
 ; FILING DATE: 15-JUL-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: STEFFE, ERIC K  
 ; REGISTRATION NUMBER: 36,688  
 ; REFERENCE/DOCKET NUMBER: 1488.0490001  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-371-2540  
 ; TELEFAX: 202-371-2540  
 ; INFORMATION FOR SEQ ID NO: 13:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 466 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; US-08-892-880-13

Alignment Scores:  
 Pred. No.: 2.61e-30 Length: 466  
 Score: 349.00 Matches: 89  
 Percent Similarity: 83.33% Conservative: 1  
 Best Local Similarity: 82.41% Mismatches: 10  
 Query Match: 21.06% Indels: 8  
 Gaps: 2

US-10-079-111-1 (1-322) x US-08-892-880-13 (1-466)

QY 219 PheValGluAsnLysAlaPheLysAsnGluAlaGlyPheGlyValProThr 238  
 Db 15 TTTGTTGAAATAAAGCAGCAATTCAAGATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACG 74

QY 239 AlaLeuLeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyr 258  
 Db 75 GCTCTGCTAGTGTCTAT 134

QY 259 ValLysArgTyrVal-LysAlaPheProPheThrAsnLysAsnGlnGlnLys-GluMetI 278

Db 135 GTCAAAGTATGTGAAGGCTTCCCTTTTACAAACAAGATCNGCAGAGGAAATGA 194  
 QY 278 leGluThrLysValVal-LysGluGluLysAlaAsnAspSerAsnPro-AsnGluGluSe 297  
 Db 195 TCGAAACCAAGTAGTGTGAAGGAGGAGGAGGCAATGNTAGCAACCTGAATGAGGGATT 254  
 QY 297 rlys---LysThrAspLysAsnPro---GluGluSerLysSerProSerLysThr-ThrV 315  
 Db 255 CAAGGAAACCTGNTTAAACCCAGTAGNAGTTCAGAGAGTNCACAGCAAACTACCG 314  
 QY 315 al-ArgCysLeu 318  
 Db 315 TGTGATGCTG 326

RESULT 11  
 US-08-892-880-15  
 ; Sequence 15, Application US/08892880  
 ; Patent No. 5942417  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NI, JIAN  
 ; APPLICANT: GENTZ, REINER L.  
 ; APPLICANT: DILLON, PATRICK J.  
 ; TITLE OF INVENTION: CD44-LIKE PROTEIN  
 ; NUMBER OF SEQUENCES: 15  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 ; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600  
 ; CITY: WASHINGTON  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20005-3934  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/892,880  
 ; FILING DATE: HERewith  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 60/021,762  
 ; FILING DATE: 15-JUL-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: STEFFE, ERIC K  
 ; REGISTRATION NUMBER: 36,688  
 ; REFERENCE/DOCKET NUMBER: 1488.0490001  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-371-2600  
 ; TELEFAX: 202-371-2540  
 ; INFORMATION FOR SEQ ID NO: 15:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 498 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; US-08-892-880-15

Alignment Scores:  
 Pred. No.: 3.35e-23 Length: 498  
 Score: 286.50 Matches: 62  
 Percent Similarity: 90.00% Conservative: 1  
 Best Local Similarity: 88.57% Mismatches: 4  
 Query Match: 17.29% Indels: 3  
 Gaps: 1

US-10-079-111-1 (1-322) x US-08-892-880-15 (1-498)

QY 254 LeuGlyPheCysTyrValLysArgTyrValLysAlaPheProPheThrAsnLysAsnGln 273  
 Db 14 CTTGATTTTGCTATGTCAAAAGGTATGTNAAGCCTTCCTTTTACAAACAAGATCAG 73

QY 274 GlnLysGluMetIleGluThrLysValLysGluGluLysAlaAsnAsp-SerAsnPr 293  
 |||||  
 Db 74 CAGAAGGAATGATCGAAACCAAGTAGTAAGGAGGAGGAGGCAATAGCAACCC 133  
 |||||  
 QY 293 oAsnGluLysSerLysThrAspLysAsnProGlu-GluSerLysSerProSerLysT 313  
 |||||  
 Db 134 TAATGAGGAATCAAGAGAACTGATATAAAACCCAGTAGAGTCCAAGAGTCCAAGCAAA 193  
 |||||  
 QY 313 hr---ThrValArgCysLeuGluAla 320  
 |||||  
 Db 194 CTTACCGTNGCNGATGCTGGAAGCT 219  
 |||||

## RESULT 12

5504194-1  
 ; Patent No. 5504194  
 ; APPLICANT: ST. JOHN, THOMAS P.; GALLATIN, W. MICHAEL; IDZERDA, REJEAN  
 ; TITLE OF INVENTION: LYMPHOCYTE ADHESION RECEPTOR FOR HIGH  
 ; ENDOTHEL-UM, CD44  
 ; NUMBER OF SEQUENCES: 4  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/884,624  
 ; FILING DATE: 15-MAY-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 628,646  
 ; FILING DATE: 12-DEC-1990  
 ; APPLICATION NUMBER: 325,224  
 ; FILING DATE: 17-MAR-1989  
 ; SEQ ID NO.1:  
 ; LENGTH: 1537  
 5504194-1

## Alignment Scores:

Pred. No.: 1-55e-16 Length: 1537  
 Score: 234.50 Matches: 100  
 Percent Similarity: 38.66% Conservative: 38  
 Best Local Similarity: 28.01% Mismatches: 109  
 Query Match: 14.15% Indels: 111  
 DB: 6 Gaps: 16

US-10-079-111-1 (1-322) x 5504194-1 (1-1537)

QY 20 LeuValGlnGlySerLeuArgAlaGluLysLeuSerIleGlnValSerCysArgIleMet 39  
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 Db 161 CTCGTGACGTGAGCCTG-----GGCAGATCGATTGTAATATAACCTGTCCTTCGAA 214  
 |||||  
 QY 40 GlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGlu 59  
 |||||  
 Db 215 GGTATATACCGTGGAGAAAAATGGTCGTATAGCATCTCTGGACGGAGGCGAGCTGAC 274  
 |||||  
 QY 60 AlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLys 79  
 |||||  
 Db 275 CTCGCAAGCTTCAATAGCACCTTGCCCAATGGCCAGATGGAGAAAGCTCTGAGC 334  
 |||||  
 QY 80 AlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArg 99  
 |||||  
 Db 335 ATCGGGTTTGAGACCTGCGAGGTACGGTTCAATA--GAAGGCGACGTGGTGTCTCTCGG 391  
 |||||  
 QY 100 IleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValPro 119  
 |||||  
 Db 392 ATCCACCCCACTCCATCTGTGCGACGAAACACACAGGGGGTGATACATTCTCAGCTCCAAC 451  
 |||||  
 QY 120 ValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTyrThrAsnSerCys 139  
 |||||  
 Db 452 ACCTCC---CAGTATGACACATATTGCTTCATGTCTCAGCTCCACCTGGAGAAAGATTGT 508  
 |||||  
 QY 140 IleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThr 159  
 |||||  
 Db 509 -----ACATCATGTACAGACCTGCCCAATGCCCTTGTGATGGACCAATTACC 553  
 |||||  
 QY 160 ThrGluPheIleValSerAspSerThr---TyrSerValAlaSerProTyrSerThrIle 178  
 |||||

Db 554 ATAACATATTGTTAAACCGGACCGGACCCGGTATGTCAAGAAAGGGGAATACAGAACGAAT 613  
 |||||  
 QY 179 Pro-----AlaProThr----- 182  
 |||||  
 Db 614 CCTGAGGACATCAACCCGACGAGCCCTACTACGACGACGTAAGCAGCGGATCTCCAGT 673  
 |||||  
 QY 183 -----ThrThrProPro 186  
 |||||  
 Db 674 GAAAGGAGCAGCACCTTTAGGAGGTTACATCTTTTATAACCACTTTTCAACTTCACACCC 733  
 |||||  
 QY 187 AlaProAlaSerThrSerIleProArgArgLysLysLeuIleCysValThrGluValPhe 206  
 |||||  
 Db 734 ATCCCATGATGAGGAGGT----- 751  
 |||||  
 QY 207 MetGluThrSerThrMetSerThrGluThrGluProPheValGluAsnLysAlaAlaPhe 226  
 |||||  
 Db 752 ---CCCTGGATCACCGACAGACAGACAGACCCCTCTACCAGACCAAGGTGCATTC 808  
 |||||  
 QY 227 Lys-----AsnGluAlaAlaGlyPhe----- 233  
 |||||  
 Db 809 GACCCAGCGGGGCTCCCATACCACTCATGATGATCTGATCAGCTGCTGCTTACATGGG 868  
 |||||  
 QY 234 -----GlyGly-----ValProThr 238  
 |||||  
 Db 869 AGTCGAGAGGTGGGGCAACACACACTCCGTCCTTTAAGGACACCCCAATTCAGAA 928  
 |||||  
 QY 239 AlaLeuLeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPhe----- 256  
 |||||  
 Db 929 TGGTTGATCATCTTGGCATCCCTCTT-----GGCCTTGGCTTTGATCT 972  
 |||||  
 QY 257 CysTyrValLysArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGlu 276  
 |||||  
 Db 973 TGCAGTTTG-----CATTCAGTCAACAGTCGAAG 1002  
 |||||  
 QY 277 MetIleGluThrLysValLysGluLysAlaAsnAsp-SerAsnProAsn----- 294  
 |||||  
 Db 1003 -----AAGGTGGGCGAGAGAAAGCTTAGTGATCAACAATGGCAATGGAGC 1050  
 |||||  
 QY 295 ----GluGluSerLysThrAspLysAsnProGluGluSerLysSer 309  
 |||||  
 Db 1051 TGTGGAGGACAGAAAGTCAAGTGGACTCAACGAGGAGGCCAGCAAGTCT 1099  
 |||||

## RESULT 13

US-07-946-497-1  
 ; Sequence 1, Application US/07946497  
 ; Patent No. 5506119  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HERRLICH, Peter  
 ; APPLICANT: PONTA, Helmut  
 ; APPLICANT: GUENTHER, Ursula  
 ; APPLICANT: MATZKU, Siegfried  
 ; APPLICANT: WENZL, Achim  
 ; TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA  
 ; TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: 3000 K Street, N.W., Suite 500  
 ; CITY: Washington, D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20007-5109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/946,497  
 ; FILING DATE: 19921109  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BENT, Stephen A.



```

; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16915/145
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3207 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: p-Meta-1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 113..1624
US-07-946-497-1

Alignment Scores:
Pred. No.: 7.8e-15 Length: 3207
Score: 224.00 Matches: 87
Percent Similarity: 37.68% Conservative: 43
Best Local Similarity: 25.22% Mismatches: 171
Query Match: 13.52% Indels: 44
DB: 1 Gaps: 12

US-10-079-111-1 (1-322) x US-07-946-497-1 (1-3207)
QY 3 ArgCysPheSerLeuValLeuLeuLeuThr-----SerIleTrrpThr 16
Db 86 AGATCCTTGGTTTCATCTCGACATCGGACACAGCTTGGTGGACACAGCTGGGA 145
QY 17 ThrArgLeuValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCys 36
Db 146 CTACTTGGCTCTACAGTTGAGCTGGCAGCAGCAGATGATTTGAATATAACCTGC 205
QY 37 ArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGlu 56
Db 206 CGTTACGCGAGTGTATTCATGTTGGAGAAATATGGCGCTACAGTATCTCCAGGACTGAA 265
QY 57 AlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThr 76
Db 266 GCAGCTGACCTCTGCGAGGTTTCAACACCCTTGGCCACCATGCTCAGATGGAGTTA 325
QY 77 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrrpValGlyAspGlyPheValVal 96
Db 326 GCCTCGAGAAAGGGTTTGAACATGCAGGTATGGGTTTCATA--GAAGGACACGTGGTA 382
QY 97 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrrp 116
Db 383 ATCCCGAGGATCCACCCCAACGCTATCTGTGCGCCCAACACACAGGAGGTATATCCTC 442
QY 117 LysValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrrpThr 136
Db 443 CTGCGATCCACACCTCCCACTATGACACATATGCTTCATGCTCAGCTCCTCTTGAA 502
QY 137 AsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla 156
Db 503 GAAGACTGT-----ACATCAGTCACAGACCTACCCAATTCCTTCGATGGA 547
QY 157 ThrGlnThrThrGluPheIleValSerAspSerThr---TyrSerValAlaSerProTyr 175
Db 548 CCAGTTACCAATACTATTGTTCAACCGTGTGGCAGCCGCTACAGCAAGAGGGCGAGTAT 607
QY 176 SerThr-----IleProAlaProThr----- 182
Db 608 AGAACACACCAAGAACATCGATCGCTTCAACATTTATAGATGATGATGATGATGATGGA 667
QY 183 -----ThrThrProAla---ProAlaSerThrSerIleProArgArg 196
Db 668 TCCACCATTTGAGAGAGACACCCCAAGAGGCTACATTTTGGACACCGACCTTCCACACTCA 727

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QY 197 LysLysLeuIleCysValThrGluValPheMetGluThrSerThrMetSerThr---Glu 215
Db 728 CAGCCTACTGGAGACCGGATGACCCCTTCTTTATTGGGACACCCCTGGCCACCATTTGCA 787
QY 216 ThrGluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGly 235
Db 788 ACTACTCCATGGGTTTCTGCCACACAAAACAGAACAGGACGAGCCAGTGGAAACCG 847
QY 236 Val-----ProThrAlaLeuLeuValLeuAlaLeuLeuPhePheGlyAlaAla 252
Db 848 ATCCATTCAACCCCAAGAGTACTACTTCAGACCAACCCAGGATGACTGATATAGACAGA 907
QY 253 GlyLeuGlyPheCysTyrValLysArgTyrValLys-----AlaPheProPheThrAsn 270
Db 908 AACAGCACCAGTGTCTCATGGAGAAACTGGACCCAGGACACACAGCCTCTTCAATAAC 967
QY 271 LysAsnGlnGlnLysGluMetIleGluThrLysValValLysGluLysAlaAsnAsp 290
Db 968 CATGAGTATCAGGATGAAGAG--GAGACCCCATGCTTACAAGCACAACCTGGGCGAGAT 1024
QY 291 SerAsnProAsnGluSerLysLysThrAspLys-----AsnProGlu 305
Db 1025 CCTAATAGCACAAACAGAGAGCAGCTACCCAGAGGAGAGTGGTTTGAGATGAATGG 1084
QY 306 GluSerLysSerPro 310
Db 1085 CAGGGGAGAACCCA 1099

RESULT 14
US-08-483-322-1
; Sequence 1, Application US/08483322
; Patent No. 5760178
; GENERAL INFORMATION:
; APPLICANT: HERRLICH, Peter
; APPLICANT: PONTA, Helmut
; APPLICANT: GUENTHER, Ursula
; APPLICANT: MATZKU, Siegfried
; APPLICANT: WENZL, Achim
; TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
; TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
; TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,322
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/946,497
; FILING DATE: 09-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16915/145
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3207 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double

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DB: 2      Gaps: 12

US-10-079-111-1 (1-322) x US-08-478-882-1 (1-3207)

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DB 503 GAAGACTGT-----ACATCAGTCACAGACTACCCCAATTCCTTCGATGGA 547
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Job time : 120 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 15, 2004, 11:26:54 ; Search time 4676 Seconds  
(without alignments)  
2984.700 Million cell updates/sec

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Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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27: em.un.\*

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36: em.htg\_mam.\*  
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41: em.htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1657	100.0	1755	6	AX136227 Sequence
3	1657	100.0	1755	6	BD123566 Secretary
4	1657	100.0	1755	9	AK075443 Homo sapi
5	1657	100.0	2029	6	AR204700 Sequence
6	1657	100.0	2029	6	BD222718 Human sig
7	1657	100.0	2372	6	AR410761 Sequence
8	1657	100.0	2372	6	AX092274 Sequence
9	1657	100.0	2372	6	AX454446 Sequence
10	1657	100.0	2372	6	AX490924 Sequence
11	1657	100.0	2372	6	AX697609 Sequence
12	1657	100.0	2372	6	BD075532 Secretary
13	1657	100.0	2372	6	BD172392 Secreted
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16	1657	100.0	2372	6	BD173349 Secreted
17	1657	100.0	2372	6	BD175383 Secretary
18	1657	100.0	2372	9	AX358925 Homo sapi
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20	1638	98.9	2313	9	AF118108 Homo sapi
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23	1103	66.6	2027	10	BC038892 Mus muscu
24	1095	66.1	1516	10	AJ311501 Mus muscu
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26	803	48.5	716	6	BD123769 Secretary
27	755	45.6	165698	9	AC009532 Homo sapi
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31	389	23.5	239307	2	AC129402 Rattus no
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34	277	16.7	373	6	BD073800 5'EST of
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43	229	13.8	1932	10	BC061531 Rattus no
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ALIGNMENTS

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 LOCUS Homo sapiens hyaluronid acid receptor (HAR) mRNA, complete cds.  
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 AF127670.2 GI:10800121  
 Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 1 (bases 1 to 1285)  
 Winkelman, J.C., Basu, S., Ozdemir, E. and Blough, R.I.  
 HAR: a novel homolog of CD44 and putative hyaluronic acid receptor  
 encoded by a gene on human chromosome 11p15  
 Unpublished  
 2 (bases 1 to 1009)  
 Winkelman, J.C., Basu, S., Ozdemir, E. and Blough, R.I.  
 Direct Submission  
 Submitted (11-FEB-1999) Hematology-Oncology, University of  
 Cincinnati, 231 Bethesda Avenue, Cincinnati, Ohio 45267-0508, USA  
 3 (bases 1 to 1285)  
 Winkelman, J.C., Basu, S., Ozdemir, E. and Blough, R.I.  
 Direct Submission  
 Submitted (12-OCT-1999) Hematology-Oncology, University of  
 Cincinnati, 231 Bethesda Avenue, Cincinnati, Ohio 45267-0508, USA  
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 On Oct 13, 2000 this sequence version replaced gi:5732667.  
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## source

## gene

## CDS

## ORIGIN

## Alignment Scores:

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 Percent Similarity: 100.00% Conservative: 0  
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 DB: 9 Gaps: 0

US-10-079-111-1 (1-322) x AF127670 (1-1285)

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## RESULT 2

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 VERSION AX136227.1 GI:14272635  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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 Ota, T., Isogai, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and  
 Hayashi, K.  
 Secretory protein or membrane protein  
 Patent: EP 1067182-A 149 10-JAN-2001;  
 Helix Research Institute (JP)

[illegible]

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RESULT 4  
AK075443  
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DEFINITION  
Homo sapiens cDNA PSEC0135 fis, clone PLACE1004850, highly similar  
to Homo sapiens lymphatic endothelium-specific hyaluronan receptor  
LYVE-1 mRNA.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AK075443  
AK075443.1 GI:22761535  
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1  
Ota, T., Nishikawa, T., Suzuki, Y., Kawai-Hio, Y., Hayashi, K.,  
Ishii, S., Saito, K., Yamamoto, J., Wakamatsu, A., Nagai, T.,  
Nakamura, Y., Nagahari, K., Sugano, S. and Isogai, T.,  
HRI human cDNA sequencing project  
Unpublished  
2 (bases 1 to 1755)  
Isogai, T. and Yamamoto, J.  
Direct Submission  
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)  
HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass  
sequencing, clone selection and full insert sequencing; Helix  
Research Institute (supported by Japan Key Technology Center etc.);  
cDNA library construction; Institute of Medical Science, University  
of Tokyo, Laboratory of Genome Structure, Human Genome Center.

REFERENCE  
AUTHORS

TITLE  
JOURNAL

REFERENCE  
AUTHORS

TITLE  
JOURNAL

COMMENT

FEATURES  
source

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ORIGIN

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Query Match: 100.00% Indels: 0  
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US-10-079-111-1 (1-322) x AK075443 (1-1755)

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LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

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ORIGIN

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DB



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Goddard, A., Godowski, P.J., Grimaldi, C.J., Gurney, A.L., Hillan, K.J.,			
Kljasin, I.J., Mather, J.P., Pan, J., Paoni, N.F., Roy, M.A.,			
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Secreted and transmembrane polypeptides and nucleic acids encoding			
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Db	220	GTCCAGGCTCTTTGGTGTGAGAGAGCTTCCATCCAGTGTGATGAGAAATATGGG	279
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Db	580	CCAGAAATTTATCACCAACCAAGATCCCATATTCAACACTCAAACTCCAAACAACA	639
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	640	GAATTTATTGTCACTGACAGTACTCTCGTGGCATCCCTTACTCTACATACCTGCC	699
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REFERENCE  
AUTHORS  
TITLE

## JOURNAL

## COMMENT

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1 (bases 1 to 2372)
Wood,W.I., Gurney,A.L., Goddard,A., Penica,D., Chen,J. and Yuan,J.
Secretory and transmembrane polypeptide and nucleic acid encoding
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Patent: JP 2001516580-A 165 02-OCT-2001;
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## AUTHORS

Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and  
Yuan, J.

## TITLE

Secreted and transmembrane polypeptides and nucleic acids encoding  
the same

## JOURNAL

Patent: JP 2002223786-A 165 13-AUG-2002;

## COMMENT

GENENTECH INC  
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WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI  
JIAN ZHENG,  
PI JEAN YUAN  
PC C12N15/09, C07K14/47, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC  
C12N5/10,

PC C12P21/02//C12P21/08, (C12P21/02, C12R1:19), (C12P21/02, C12R1:91), PC  
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REFERENCE
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## AUTHORS

Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and Yuan, J.

## TITLE

Secreted and transmembrane polypeptides and nucleic acids encoding the same

## JOURNAL

Patent: JP 2002238586-A 165 27-AUG-2002;

## COMMENT

GENENTECH INC

OS Homo sapiens (human)

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PD 27-AUG-2002

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WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI

JIAN ZHENG,

PI JEAN YUAN

PC C12N15/09, C07K14/47, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC

C12N5/10,

PC C12P21/02//C12P21/08, (C12N1/19, C12R1:645), (C12N1/21, C12R1:19),

(C12N5/10, C12R1:91), (C12P21/02, C12R1:91), (C12P21/02, C12R1:645), PC

(C12P21/02, C12R1:19), (C12P21/08, C12R1:91), C12N15/00, C12N5/00, PC

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CC Secreted and transmembrane polypeptides and nucleic CC acids

encoding the same

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Location/Qualifiers

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GenCore version 5.1.6  
 Copyright (c) 1993 - 2004 CompuGen Ltd.

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 ; APPLICANT: Streeter, David G.  
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 ; FILE REFERENCE: PC-0053 CIP  
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 ; CURRENT FILING DATE: 2002-02-20  
 ; PRIOR APPLICATION NUMBER: 09/232,160  
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DB 580 CCAGAAATTTATCACCCAAAGATCCCATATTTCAACACTCAAACTGCAACAAACAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
DB 640 GAAATTTATTTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACTGCG 699
QY 181 ProThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
DB 700 CCTACTACTACTCCTCCTGCTCCAGCTTCCATCTTATTCCACGGAGAAAAAATGAT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
DB 760 TGTGTGCAGAGAGTTTATGAACTAGACCATGCTCTACAGAACTGAACCAATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
DB 820 GAAATATAAGCAGCAATTCAGAAATGAAGCTGCTGGGTTTTGGAGGTGTCCTCCACGGCTGTG 879
QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
DB 880 CTAGTCTTGTCTCTCTCTTCTTGTGCTGCAGCTGGTCTTGGAATTTTGTATGTCATAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
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; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-905-291A-200

Alignment Scores:
Pred. No.:      2,23e-188      Length:      2372
Score:          1657.00      Matches:      322
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:               9           Gaps:         0

US-10-079-111-1 (1-322) x US-09-905-291A-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTyrThrThrArgLeuLeu 20
Db 160 ATGGCCAGGTGCTTCAGCTGGTGTGTCTTCACCTTCATCTGCACCCAGGCTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluLeuLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAAGGCTCTTTCGTGCAGAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGG 279
QY 41 IleThrLeuValSerIlyslalalenGlnGlnLeuAsnPheThrGluAlalysGluAla 60
Db 280 ATCACCCCTGTGAGCAAAAAGCGAACCCAGCAGCTGAATTTCCAGAAAGCTAAGGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGlnThrAlaLeuLysAla 80
Db 340 TGTAGGCTCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGACAGTATGGCTGGTGGTGGAGATGGATTGGTGTCTATCTTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCCAAACCCCAAGTGTGGGAAAAATGGGTGGTGGTGGTCTGCTGATTTGGGAAGGTTCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTGCAGCCATTGTTTCAACTATCTGATGATCTTGGACTAATCTGTCGAT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTTATCACCAACCAAGATCCATATTCACACTCAAACTCAACACCAACAAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTTGTAGTGACAGTACTACTCGGTGGCATCCCTTACTCTCAATACATCTGCC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200

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Db 700 CCTACTACTACTCTCTCTCTCCAGCTTCCACTTCTATTTCACGCGAGAAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTACAGAGATTTTATGGAAACTAGCACCATTGCTACAGAAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATAAAGCAGCATTCAAGAACTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGTCTCTCTCTTCTTGGTCTGCAGCTGCTTGGATTTTGGCTATGCTCAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAAATCAGCAGAGAAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAGTAGTAAAGGAGGAGGAGGCCAATGATAGCAACCTTATGAGAAATCAAGAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCCAGAGAGCTCCAGAGAGTCCAAAGAACTACCGTCGATGCTCGAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAAGTT 1125

RESULT 5
US-09-902-853-200
; Sequence 200, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US/09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28

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; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-907-824-200

Alignment Scores:
Pred. No.: 2,238-188 Length: 2372
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-079-111-1 (1-322) x US-09-907-824-200 (1-2372)

Qy 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrArgLeuLeu 20
Db 160 ATGGCCAGGTGTTTCAGCTGGTGTGTTCTTCATCTTCATCTGCACACGAGGCTCTCG 219
Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAAGCTCTTTGGTGCAGACAGCTTTCCATCCAGGTGTCATGCAGATTATGGGG 279
Qy 41 IleThrLeuValSerIlyslsAlaGlnGlnLeuAsnPhetThrGluAlaLysGluAla 60
Db 280 ATCACCTTTGTGAGCAAAAAGGCGAACACAGCAGCTGAATTTTCACAGAAGCTAAGGAGGCC 339
Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGCTCTGGGACTTAAGTTTGGCCGCAAGGACCAAGTTGAACACGCTTGAAGCT 399
Qy 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAACACTGCAGCTATGGCTGGTGGAGATGGATTGGTGTCACTCTAGGATT 459

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Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuLeuTrpLysValProVal 120
Db 460 AGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCGATTGGAGAGGTTCCAGTG 519
Qy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCTATTGTTACAACCTCACTGATCTTGACATACTCGTGCAAT 579
Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAAACTGCAACCAACAACA 639
Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCAATCCCTTACTCTCAATACCTGCC 699
Qy 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCTCTCTCTCCAGCTTCCACTTCTATTCCACGAGAAAAAATTGATT 759
Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTACAGAAAGTTTTTATGGAACCTAGCACCATGCTACAGAAACTGAACCAATTTGTT 819
Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATAAAGCAGCAATCAAGATGAAGCTCTGGTTGGAGGTGTCCTCCACGGCTCTG 879
Qy 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGTCTCTCTCTCTTGGTGTCTGAGCTGCTGCTGTTGTTGTTGTTGTTGTT 939
Qy 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCTTCTCCCTTTTACAAACAAGAATCAGCAGAGGAAATGATCGAAACC 999
Qy 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1059
Qy 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCCCAAGAGAGTCCCAAGAGTCCCAAGAGTCCCAAGAGTCCCAAGAGTCCCAAG 1119
Qy 321 GluVal 322
Db 1120 GAAAGTT 1125

RESULT 7
US-09-907-841-200
; Sequence 200, Application US/09907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.

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Db	520	AGCCGACAGTTTGCAGCCTATTGTTTCAACACTCATCTGATACCTTGGACTAACTCGTGCATT	579
Qy	141	ProGluIlelleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	580	CCAGAAATATPACCCACCAAGATCCCATATTTCAACACTCAAACTGCAACACAAACA	639
Qy	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	640	GAATTTATTTGTCAGTGACGATCACTCTCGGTGCGATCCCCCTTACTCTTACAATACCTG	699
Qy	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Db	700	CCTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTCATT	759
Qy	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	760	TGTGTCTCAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	819
Qy	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	820	GAATAATTAAGCAGCATTCAGAAATGAAGCTGTGGGTTTGAGGTGCCCCACGGCTCTG	879
Qy	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	880	CTAGTGCTTGCTCTCTCTCTCTTTTGGTGCTGCAGCTGCTCTGGATTTTGTATGTCAA	939
Qy	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	940	AGGTATGTGAAGGCTTCCCTTTTACAAAAAAGAAATCAGCAGAGGAATGATCGAAACC	999
Qy	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
Db	1000	AAAGTAGTAAGGAGGAGGAGGCAATGATAGCAACCTTAATGAGGAATCAAGAAAACT	1059
Qy	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1060	GATAAAAAACCAGAGAGTCCAGAGTCCAAAGCAAACTACCGTGCATGCTGGAGCT	1119
Qy	321	GluVal 322	
Db	1120	GAAGTT 1125	

RESULT 8

US-09-904-011-200

; Sequence 200, Application US/09904011

; Publication No. US20030003530A1

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

1 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
460 AGCCCAAAACCCCAAGTGTGGGAAATGGGTGGGTGCTCGATTTGGAGGTTCCAGTG 519  
121 SerArgGlnPheAlaAlaIleCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
520 AGCCGACAGTTTTCAGCCCTATTGTTTACAACTCATCTGATCTTGGACTAACTCGTGATT 579  
141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
580 CCAGAAATTTATCACCAACCAAGATCCCATATTTCAACACTCAAACTGCAACCAACA 639  
161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
640 GAATTTATTGTCAGTCAGACAGTACCTACTCGGTGGCATCCCTTACTTACATATCTGCC 699  
181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200  
700 CCTACTACT 759  
201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
760 TGTGTACAGAAAGTTTATTTGAAATAGCACTAGCCATGTCTACAGAAACTGAACATTGTT 819  
221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
820 GAAATTAAGCAGCATTTCAAGATGAGCTGCTGGTTTGGAGGTGTCCTCCAGGCTCTG 879  
241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
880 CTAGTGCTTGTCT 939  
261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
940 AGGTATGTGAAGGCTTCT 999  
281 LysValValLysGluLysAlaAsnAspSerAsnProAsnGluLysSerLysLysThr 300  
1000 AAAGTAGTAAAGGAGGAGAGGCAATGATGACCACTTATGAGAAATCAAGAAACT 1059  
301 AspLysAsnProGluLysSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
1060 GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAACTACCGTCGATGCTCGAAGCT 1119  
321 GluVal 322  
1120 GAAATT 1125  
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US-09-906-742-200  
; Sequence 200, Application US/09906742  
; Publication No. US20030023054A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US 09/906,742  
CURRENT FILING DATE: 2001-07-16  
PRIOR APPLICATION NUMBER: 09/665,350  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 200  
LENGTH: 2372  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-09-906-742-200

Alignment Scores:  
Pred. No.: 2,23e-188 Length: 2372  
Score: 1657.00 Matches: 322  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-906-742-200 (1-2372)

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QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40

Db 220 GTCCAAAGGCTCTTGGCTGCAGAGAGCTTTCATCCAGGTGTATGCGAATATGGGG 279  
QY 41 IleThrLeuValSerIlyLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
Db 280 ATCACCCCTTGTGAGCAAAAAGCGAACACAGCAGCTGAATTTACAGAGCTAAGGAGGCC 339  
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
Db 340 TGTAGGCTGCTGGGCTAAGTTTGGCCGCAAGGCAAGTTGAAACACGCTTGAAGCT 399  
QY 81 SerPheGluThrCysSerTyrGlyTrrPValGlyAspGlyPheValValIleSerArgIle 100  
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QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrrPlysValProVal 120  
Db 460 AGCCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGTCTCTGATTGGAGGTTCCAGTG 519  
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrrPThrAsnSerCysIle 140  
Db 520 AGCCGACAGTTTGCAGCCTATTGTTTACAACTCATCTGACTTGGACTTAACCTCGTCATT 579  
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
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QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
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Db 700 CCTACTACTACTCTCTCTCCAGCTTCCACTTCTATTCCAGGAGAAAAAATTTGATT 759  
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
Db 760 TGTGTCCAGAGAGTTTATGGAACTAGCACCATGTCTACAGAACTGAACCATTTGTT 819  
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
Db 820 GAAAAATAAAGCAGCATTTCAAGAAATGAAGCTGTGGGTGGAGGTGTCCCCACGGCTCTG 879  
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
Db 880 CTAGTGCTTGTCTCTCTCTCTTGTGCTGAGCTGGTCTTGGATTGCTATGTCAAA 939  
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Db 940 AGGTATGTGAAGGCTTCCCTTTTACAAACAAAGATCAGCAGAGGAAATGATCGAAACC 999  
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Db 1000 AAAGTAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1059  
QY 301 AspLysAsnProGluLysSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
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QY 321 GluVal 322  
Db 1120 GAAAGTT 1125  
RESULT 10  
US-09-906-838-200  
; Sequence 200, Application US/09906838  
; Publication No. US20030027143A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.

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; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,838
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-906-838-200

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Alignment Scores:
Pred. No.: 2,23e-188 Length: 2372
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

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Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-10-079-111-1 (1-322) x US-09-906-838-200 (1-2372)
QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleThrThrArgLeuLeu 20
DB 160 ATGCCAGGTGCTTCAGCTGGTGTGTTCTCATTCCATCTGGACACACGAGGCTCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
DB 220 GTCCAAAGGCTCTTTCGTCGTCAGAGAGCTTTCCATCCAGGTGTCATGCAGATTATGGGG 279
QY 41 IleThrLeuValSerIleLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
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QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
DB 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
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QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleThrLysValProVal 120
DB 460 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCTGATTGGAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrThrThrAsnSerCysIle 140
DB 520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATCTTGGACTTAATCTGTGCATT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
DB 580 CCAGAAATATTACCACCAAGATCCCATATTCAACTCAAACTCAAACTCAAACTCAAACTCA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
DB 640 GAAATTTATTGTGAGTGACAGTACCTACTCGGTGGATCCCCCTTACTCTACATACTCTGCC 699
QY 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
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QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
DB 880 CTAGTGCTTGTCTCTCTCTTCTTGTGCTGCAGCTGGTCTTGGATTTTGTATGTCAA 939
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QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
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QY 321 GluVal 322
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## RESULT 11

US-09-907-613-200  
; Sequence 200, Application US/09907613  
; Publication No. US20030027145A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Steward, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/907,613  
; PRIORITY FILING DATE: 2001-07-17  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 200  
; LENGTH: 2372  
; TYPE: DNA

## ; ORGANISM: Homo sapiens

US-09-907-613-200

## Alignment Scores:

Pred. No.: 2,23e-188 Length: 2372  
Score: 1657.00 Matches: 322  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-907-613-200 (1-2372)

QY	1	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleThrThrThrThrArgLeuLeu	20
DB	160	ATGGCCAGGTGCTTCAGCCTGGTGTCTCTCACTTCATCTGGACCAAGAGGCTCTG	219
QY	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
DB	220	GTCCCAAGGCTCTTTGGTGCGAAGAGCTTTCATCCAGGTGTCTATGCAAAATTATGGGG	279
QY	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
DB	280	ATCACCTTGTGAGCAAAAGCGCAACAGCAGCTGAATTTCCAGAACTTAAGGAGGCC	339
QY	61	CysArgLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
DB	340	TGTAGGCTGCTGGGACTAAGTTTGGCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCT	399
QY	81	SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle	100
DB	400	AGCTTTGAAACTTGGAGCTATGGCTGGGTGGAGATGATTCGTGGTCACTCTAGGATT	459
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
DB	460	AGCCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTCTCTGATTTGGAAGGTTCCAGTG	519
QY	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrThrThrAsnSerCysIle	140
DB	520	AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTTGGACTTAACCTCGTCATT	579
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
DB	580	CCAGAAATTAATCCACCACCAAGATCCCATATTCACACTCAAACTGCAACACAAACA	639
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
DB	640	GAATTTATTGTCAAGTACCTACTCTCGTGGCATCCCTTACTCTACAAATACCTGCC	699
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
DB	700	CCTACTACT	759
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
DB	760	TGTGTCCAGAAATTTTATGGAATACTAGCACCATTGTCTACAGAACTGAACCATTTGTT	819
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
DB	820	GAATAATAAGCAGCATTCAGAAATGAAGCTGTGGGTGGAGGTGTCCCAACGGCTCTG	879
QY	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys	260
DB	880	CTAGTGCTGTCT	939
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
DB	940	AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAAATCAGCAGAGAAATGATCGAAACC	999
QY	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
DB	1000	AAAGTAGTAAAGGAGAGAGCCCAATGATAGCAACCCCTAATGAGGAATCAAGAAACT	1059

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QY 301 AspLysAsnProGluCysLeuSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCCAGAAAGTCCAAGAGTCCAGCAAAACTACCGTGGATGCTTGGAAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 12
US-09-907-942-200
; Sequence 200, Application US/09907942
; Publication No. US20030027146A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Fertara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,942
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
```

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; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-942-200

Alignment Scores:
Pred. No.: 2,23e-188 Length: 2372
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-907-942-200 (1-2372)
QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTriThrThrArgLeuLeu 20
Db 160 ATGGCCAGGTGCTTCAGCCTGGTGTCTTCTCACTTCCATCTGCACACAGGCTCCG 219
QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAAGCTCTTTGCGTCGAGAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTTATGGGG 279
QY 41 IleThrLeuValSerLysLysAlaAlaAsnGlnGlnLeuLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCTTTGTGAGCAAAAGGCGAACCCAGCTGAATTTCCAGAGCTTAAGGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGGTCTATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTriPlysValProVal 120
Db 460 AGCCCAAAACCCCAAGTGTGGGAAAATGGGTGGGTGCTCTGATTTGGAAGGTTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTriThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATCTTGGACTAACTCGTGCAATT 579
QY 141 ProGluIleIleThrThrIlysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTTATCACCAAAAGATCCCATATTCAACACTCAAACTCAAACTGCAACAAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAAATTTATTGTCAGTGACAGTACCTACTCTGGTGGGATCCCTTACTCTACAAATACTGCG 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCTCTCTCTCCAGCTTCCACTTCTATTCCACGGGAGAAAAAATTTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTGCACAGAAAGTTTTTATGGAATACTAGCACCATGCTCTACAGAAACTGAACATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATAAAGCAGCATTCAAGAAATGAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGTCTTGTCTCTCTCTTGTGTGCTGCAGCTGCTTGGATTTTGTATGTCAAA 939
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QY 261 ArgTyrValLysAlaPheProThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGCCCTTCCTTTTCAAAACAAGATCAGCAAGAGAAATGATCGAAACC 999
QY 281 LysValValLysGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGAGAGCCCAATGATAGCAACCCCTAATGAGGAATCAAGAAACT 1059
QY 301 AspLysAsnProGluLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATCGCTGGAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125

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RESULT 13
US-09-904-859-200
; Sequence 200, Application US/09904859
; Publication No. US20030036060A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.

```

```

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,859
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29

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; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-904-859-200

Alignment Scores:
Pred. No.: 2,23e-188 Length: 2372
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-904-859-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGGCCAGGTGCTTCAGCCTGGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAGAGGCTCTTTGCGTGCAGAGAGCTTTCCATCCAGTGTCTCATGCAAGATTTATGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCAGCCCTTGTGAGCAAAAGGCGAACAGCAGAGCTGAATTTTCACAGAGCTAAGGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGTGGGACTAAGTTTGGCGGCAAGGACCAAGTTTGAACACAGCCCTTGAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCTGTGTCTCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCTGATTTGGAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTGACTTAACCTCGTGCAAT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATATATACCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTTACAAATACCTGCC 699
QY 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220

```





Db	640	GAATTTATTGTTCAGTGACAGTACCTACTCGGTGGGATCCCTTACTCTTACAAATACCTGCC	699
Qy	181	ProThrThrThrProAlaProAlaSerThrSerIleProArgAlgLysLysLeuIle	200
Db	700	CCTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	759
Qy	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	760	TGTGTCAcAGAAGTTTTTATCGAAACTAGCACCATGTCTACAGAAACTGAACCACTTTGTT	819
Qy	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	820	GAAATAAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGAGGTGTCCCCACGGCTCTG	879
Qy	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	880	CTAGTGTCTGTGCTCTCTCTCTTTTGGTGTCTGAGCTGTGTGATTTTGTATGTCAAA	939
Qy	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	940	AGGTATGTGAAGGCTTCCCTTTTACAAAACAAGAAATCAGCAAGAGAAATGATCCAAACC	999
Qy	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
Db	1000	AAAGTAGTAAAGAGGAGGAGGCCCAATGATAGCAACCTAATAGGAATCAAGAAACT	1059
Qy	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1060	GATAAAACCCAGAAGAGTCCAGAGTCCAAAGCAAAACTACCGTGCATGCTCGGAAGCT	1119
Qy	321	GluVal	322
Db	1120	GAAGTT	1125

## RESULT 15

US-09-904-320-200

Sequence 200, Application US/09904820  
Publication No. US20030036094A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/904,820  
CURRENT FILING DATE: 2001-07-13  
PRIOR APPLICATION NUMBER: 09/665,350  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22

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; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-904-820-200

Alignment Scores:
Pred. No.: 2,23e+188      Length: 2372
Score: 1657,00           Matches: 322
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 10      Gaps: 0

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Alignment Scores:

Pred. No.:	2, 23e-188	Length:	2372
Score:	1657.00	Matches:	322
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-079-111-1 (1-322) x US-09-904-820-200 (1-2372)

Qy	1	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu	20
Db <td>160</td> <td>ATGCCCAGGTCTTCAGCCTGGTGTGTCTTCACCTCCATCTGCACACGAGGTCCTG</td> <td>219</td>	160	ATGCCCAGGTCTTCAGCCTGGTGTGTCTTCACCTCCATCTGCACACGAGGTCCTG	219
Qy <td>21</td> <td>ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly</td> <td>40</td>	21	ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db <td>220</td> <td>GTCCAGGCTCTTTGGCGTGCAAGAGAGCTTTCCATCCAGGTGTCATGCAGATTATGGG</td> <td>279</td>	220	GTCCAGGCTCTTTGGCGTGCAAGAGAGCTTTCCATCCAGGTGTCATGCAGATTATGGG	279
Qy <td>41</td> <td>IleThrLeuValSerLysLysAlaAsnGlnIleuAsnPheThrGluAlaLysGluAla</td> <td>60</td>	41	IleThrLeuValSerLysLysAlaAsnGlnIleuAsnPheThrGluAlaLysGluAla	60
Db <td>280</td> <td>ATCACCTTTGTGACAAAGGCGCAACAGCAGCTGAAATTTACACAGAAGCTTAAGAGGCC</td> <td>339</td>	280	ATCACCTTTGTGACAAAGGCGCAACAGCAGCTGAAATTTACACAGAAGCTTAAGAGGCC	339
Qy <td>61</td> <td>CysArgLeuLeuGlyLeuSerSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla</td> <td>80</td>	61	CysArgLeuLeuGlyLeuSerSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db <td>340</td> <td>TGTAGGCTGCTGGACTAAGTTTGGCGGCAAGGACCACAAAGTTGAAACAGCCCTTGAAGCT</td> <td>399</td>	340	TGTAGGCTGCTGGACTAAGTTTGGCGGCAAGGACCACAAAGTTGAAACAGCCCTTGAAGCT	399
Qy <td>81</td> <td>SerPheGluThrCysSerTyGlyTrpValGlyAspGlyPheValValIleSerArgIle</td> <td>100</td>	81	SerPheGluThrCysSerTyGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
Db <td>400</td> <td>AGCTTTGAAACTTCAGCTATGGCTGGGTTCGAGATGATTTCGTGGTCACTCTAGGATT</td> <td>459</td>	400	AGCTTTGAAACTTCAGCTATGGCTGGGTTCGAGATGATTTCGTGGTCACTCTAGGATT	459
Qy <td>101</td> <td>SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal</td> <td>120</td>	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
Db <td>460</td> <td>AGCCCAAAACCCCAAGTTGGGAAAAATGGGTGGGTGCTCTGATTGGAAGGTTCCAGTG</td> <td>519</td>	460	AGCCCAAAACCCCAAGTTGGGAAAAATGGGTGGGTGCTCTGATTGGAAGGTTCCAGTG	519

Qy	121	SerArgGlnPheAlaIaTyrCysTyrAsnSerSerAspThrThrTrpThrAsnSerCysIle	140
Db	520	AGCCGACAGTTTGCAGCTATTGTTACAACATCATCTGATCTGGACTTAACTCGTGCATT	579
Qy	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	580	CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCACACACAAACACA	639
Qy	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	640	GAATTTATTGTCACTGACAGTACCTACTCTCGGTGGCATCCCTTACTCTACAAATACCTGCC	699
Qy	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysIle	200
Db	700	CCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	759
Qy	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	760	TGTGTACAGAAAGTTTATGGAAACTAGACCATGTCTACAGAAACTGAACCATTTGTT	819
Qy	221	GluAsnLysAlaIaPheLysAsnGluAlaIaGlyPheGlyGlyValProThrAlaLeu	240
Db	820	GAATAATAAGCAGCATTCAAGAATGAAGCTGCTGGTTTGGAGGTGTCCTCCACGCTCTG	879
Qy	241	LeuValLeuAlaLeuLeuPhePheGlyAlaIaAlaGlyLeuGlyPheCysTyrValLys	260
Db	880	CTAGTGCTTGCTCTCTCTCTTTGGTGCTGAGCTGCTTGGATTGTGCTATGTCAAA	939
Qy	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	940	AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAATCAGCAGAGGAATGATCGAAACC	999
Qy	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
Db	1000	AAAGTAGTAAAGGAGGAGGAGGCAATGATAGCAACCTAATAGGAATCAAGAAAAACT	1059
Qy	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1060	GATAAAAAACCCAGAAAGATCCAAAGAGTCCAAAGAAACTACCGTCGATGCTTGAAGCT	1119
Qy	321	GluVal	322
Db	1120	GAAGTT	1125

Search completed: September 15, 2004, 21:23:14  
Job time : 593 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 15, 2004, 13:19:40 ; Search time 3066 Seconds  
(without alignments)  
3136.211 Million cell updates/sec

Title: US-10-079-111-1  
Perfect score: 1657  
Sequence: 1 MARCFSLVLLTSTWTRLL.....NPEESKSPKTTVRCLEAEV 322

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USPTO\_spool/US10079111/runat\_l3092004\_102135\_13568/app\_query.fasta\_1.519  
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-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45  
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-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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2: em\_esthum.\*  
3: em\_estin.\*  
4: em\_estmu.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_hic.\*  
9: gb\_est1.\*  
10: gb\_est2.\*  
11: gb\_hic.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estfun.\*  
16: em\_estom.\*  
17: em\_gss\_hum.\*  
18: em\_gss\_inv.\*  
19: em\_gss\_pln.\*  
20: em\_gss\_vrt.\*  
21: em\_gss\_fun.\*  
22: em\_gss\_mam.\*  
23: em\_gss\_mus.\*  
24: em\_gss\_pro.\*  
25: em\_gss\_rod.\*  
26: em\_gss\_phg.\*  
27: em\_gss\_vrl.\*  
28: gb\_gss1.\*

29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	1510.5	91.2	1201	9	AL550621	AL550621 AL550621
3	1480	89.3	1015	9	AL552299	AL552299 AL552299
4	1476.5	89.1	1201	9	AL546669	AL546669 AL546669
5	1439	86.8	1201	9	AL551020	AL551020 AL551020
6	1323.5	79.9	1014	9	AL553858	AL553858 AL553858
7	1316	79.4	913	13	EX459046	EX459046 BX459046
8	1283	77.4	1201	13	BX366718	BX366718 BX366718
9	1278	77.1	1172	9	AL550911	AL550911 AL550911
10	1275	76.9	972	9	AL549512	AL549512 AL549512
11	1264	76.3	911	9	AL543874	AL543874 AL543874
12	1262	76.2	1201	9	AL547774	AL547774 AL547774
13	1253	75.6	1172	9	AL552127	AL552127 AL552127
14	1243.5	75.0	1201	13	BX402505	BX402505 BX402505
15	1243	75.0	1201	9	AL544430	AL544430 AL544430
16	1235	74.5	1201	13	BX366589	BX366589 BX366589
17	1230	74.2	1116	9	AL552661	AL552661 AL552661
18	1225.5	74.0	1151	9	AL550829	AL550829 AL550829
19	1224	73.9	839	9	AL546217	AL546217 AL546217
20	1211	73.1	970	9	AL550615	AL550615 AL550615
21	1207.5	72.9	1201	9	AL546623	AL546623 AL546623
22	1168	70.5	1074	9	AL552777	AL552777 AL552777
23	1160	70.0	863	12	B1761420	B1761420 603044235
24	1142	68.9	864	9	AL545331	AL545331 AL545331
25	1103	66.6	2607	11	AK004726	AK004726 Mus muscu
26	1054.5	63.6	760	14	CB959809	CB959809 AGENCOURT
27	1019	61.5	746	14	CD238639	CD238639 FNBCH08
28	1005.5	60.7	990	13	BX418211	BX418211 BX418211
29	970	58.5	743	9	AL598709	AL598709 DKFp313B
30	936	56.5	1201	12	BG483354	AL553712 AL553712
31	935.5	56.5	801	12	BG483354	BG483354 602504223
32	926	55.9	794	12	BG566260	BG566260 602585128
33	922	55.6	1201	13	BX366791	BX366791 BX366791
34	905	54.6	1023	13	BY704927	BY704927 BY704927
35	901	54.4	596	9	AA046671	AA046671 z112d09.r
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ALIGNMENTS

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LOCUS AL550279 1154 bp mRNA linear EST 31-MAY-2003  
DEFINITION AL550279 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
clone CS0DI039YJ06 5-PRIME, mRNA sequence.  
ACCESSION AL550279  
VERSION AL550279.2 GI:31272096  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1154)

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT On Feb 15, 2001 this sequence version replaced gi:12887098.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 5952.r For  
 more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgi-bin/cluster.cgi?seq=CSODI039DE03QP1&cluster=5952.r. Contact :  
 Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CSODI039DE03QP1.  
 Location/Qualifiers  
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 /note="1st strand cDNA was primed with a NotI-oligo(dT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and cloned into the Not I and EcoR V  
 sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES  
 source

ORIGIN

Alignment Scores:  
 Pred. No.: 9,19e-143 Length: 1154  
 Score: 1657.00 Matches: 322  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-10-079-111-1 (1-322) x AL550279 (1-1154)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20  
 Db 122 ATGGCCAGGTGCTTCAGCGCTGTTGCTTCTCACCTTCATCTGCAGCACGAGGCTCTGT 181  
 QY 21 ValGlnGlySerLeuArgAlaGlnLeuSerIleGlnValSerCysArgIleMetGly 40  
 Db 182 GTCCAAAGCTCTTTCGCTGCAGAACAGCTTTCATCCAGGTGTCTATGCAGAAATTATGGGG 241  
 QY 41 IleThrLeuValSerLysLysAlaAsnGlnLeuAsnPheThrGluAlaLysGluAla 60  
 Db 242 ATCACCTTGTGAGCAAAAGCGACACGAGCTGAATTTACAGAACTTAAGAGGCC 301  
 QY 61 CysArgLeuLeuGlySerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
 Db 302 TGTAGGCTCTGGGACTAAGTTTGGCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 361  
 QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100  
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 QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
 Db 482 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTGGCACTAAGCTCGTGCATT 541  
 QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
 Db 542 CCAGAAATTATCACCAACCAAGATCCATATTCAACACTCAAACTCAACACCAACACCA 601  
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Db 602 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTTCTACATACCTGCG 561  
 QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgLysLysLeuLeu 200  
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 QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
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 QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
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 Db 962 AAGTAGTAAAGGAGAGAGAGCCCAATGATACCACTTATGAGGAATCAAGAAACT 1021  
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 clone CSODI058YNI4 5-PRIME, mRNA sequence.  
 ACCESSION AL550621  
 VERSION AL550621.2 GI:31272438  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 Full-length cDNA libraries and normalization  
 Unpublished (2001)  
 On Feb 15, 2001 this sequence version replaced gi:12887769.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 5952.r For  
 more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgi-bin/cluster.cgi?seq=CSODI058DG07QP1&cluster=5952.r. Contact :  
 Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CSODI058DG07QP1.  
 Location/Qualifiers  
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 /note="1st strand cDNA was primed with a NotI-oligo(dT)

FEATURES  
 source

primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

## Alignment Scores:

Pred. No.: 3,648-129 Length: 1201  
Score: 1510.50 Matches: 296  
Percent Similarity: 95.53% Conservative: 3  
Best Local Similarity: 94.57% Mismatches: 11  
Query Match: 91.16% Indels: 3  
DB: 9 Gaps: 1

US-10-079-111-1 (1-322) x AL550621 (1-1201)

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DB 158 ATGGCCAGGTGTTTCAGCTGGTGTGTCTTCTCACTTCATCTGCACACGAGGCTCTG 217  
QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40  
DB 218 GTCCAAAGGCTCTTCGGTGCAGAAAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGG 277  
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
DB 278 ATCACCTTGTGAGCAAAAGCGAACCAGCAGCTGAATTCACAGAGCTTAAGAGGCC 337  
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
DB 338 TGTAGGCTGTGGGACTAAGTTTGGCGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 397  
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100  
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QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrrThrAsnSerCysIle 140  
DB 518 AGCCGACAGTTTGCAGCTTATGTTTACAACTCATCTGATCTTGGACTTAACCTGTCATT 577  
QY 141 ProGluIleIleThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
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QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
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QY 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLeuIle 200  
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DB 998 MAAGTAGTAAAGGAGGAGCAATGATWASACCCYAAATGAGGATCAAGAAACT 1057  
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ACCESSION AL552299  
VERSION AL552299.2 GI:31274114  
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1015)  
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT On Feb 15, 2001 this sequence version replaced gi:12891068.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seq@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 5952.r For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CSODI069G01Q1P1&cluster=5952.r. Contact :  
Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CSODI069G01Q1P1.  
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primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."  
ORIGIN  
Alignment Scores:  
Pred. No.: 1,98-126 Length: 1015  
Score: 1480.00 Matches: 288  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 89.32% Indels: 0  
DB: 9 Gaps: 0  
US-10-079-111-1 (1-322) x AL552299 (1-1015)  
QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrrThrThrArgLeuLeu 20  
DB 144 ATGGCCAGGTGCTTCAGCTGGTGTGTCTTCTCACTTCATCTGCACACGAGGCTCTG 203  
QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40  
DB 204 GTCCAAAGGCTCTTTGGTGCAGAAAGAGCTTTTCATCCAGGTGTCATGCAGAAATTATGGG 263  
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
DB 264 ATCACCTTGTGAGCAAAAGCGAACCAGCAGCTGAATTTTCACAGAGCTTAAGAGGCC 323  
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80

Db 324 TGTAGGCTGCTGGAGTAAGTTTGGCCGCAAGGACCAAGTTGAACACAGCCTTGAAGACT 383

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100  
|||||

Db 384 AGCTTTGAACACTTGCAGCTATGCTGGTGGAGATGGATTGCTGGTCACTCTAGGATT 443

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValIleTrpLysValProVal 120  
|||||

Db 444 ACCCAAAACCCCAAGTGGGAAAATGGGTGGGTGCTCTGATTGGGAAGTTCCAGTG 503

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
|||||

Db 504 AGCCGACAGTTTGCAGCTATTGTTACAACTCATCTGATACCTGGACTAACTCGTGCAAT 563

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
|||||

Db 564 CCAGAAATATATACCAACCAAGATCCCATATTTCAACACTCAAACTGCAACACAAACA 623

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
|||||

Db 624 GAATTTATGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 683

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200  
|||||

Db 684 CCTACTACTCTCTCTCTCCAGCTCCACTTCTATTCCACGGAGAAAAAATTGATT 743

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluThrProPheVal 220  
|||||

Db 744 TGTGTACAGAAAGTTTATGAAACTAGCACCATGTCTACAGAACTGAACCATTTGTT 803

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
|||||

Db 804 GAAATATAAGCAGCATTCAGAAATGAGCTGTGGTTGGAGTGTCCCCACGGCTCG 863

QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
|||||

Db 864 CTAGTGTGCTCTCTCTCTTGTGTGTCAGCTGGTCTTGGATTGCTATGTCAAA 923

QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
|||||

Db 924 AGGTATGTGAAGCCCTTCCCTTTTCAAAACAGAAATCAGCAAGAAATGATCGAAACC 983

QY 281 LysValValLysGluGluLysAla 288  
|||||

Db 984 AAAGTAGTAAAGAGAGAGAGGCC 1007

## RESULT 4

AL546669

LOCUS

DEFINITION AL546669 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0D1029YJ09 5-PRIME, mRNA sequence.

ACCESSION

AL546669

VERSION

AL546669.2

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)

Li.W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:12880008.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segrefgenoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 5952.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0D1029CE05QPl&amp;cluster=5952.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CS0D1029CE05QPl.

## FEATURES

source

1..1201  
/location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0D1029YJ09"  
/tissue\_type="PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

Alignment Scores:  
Pred. No.: 5,13e-126 Length: 1201  
Score: 1476.50 Matches: 302  
Percent Similarity: 96.24% Conservative: 5  
Best Local Similarity: 94.67% Mismatches: 11  
Query Match: 89.11% Indels: 5  
DB: 9 Gaps: 1  
US-10-079-111-1 (1-322) x AL546669 (1-1201)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20  
|||||

Db 126 ATGGCCAGGTGGCTTCAGGCTGGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 185  
|||||

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
|||||

Db 186 GTCCAGAGCTCTTTGCGTGCAGAGAGCTTTCATCCAGGTGTCTGAGAAATTATGGGG 245  
|||||

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
|||||

Db 246 ATCACCCCTGTGAGCAAAAGGCAACAGCAGCTGAATTTTCCAGAAAGCTAAGGAGGCC 305  
|||||

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
|||||

Db 306 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTTGAACAGCCTTGAAGCT 365  
|||||

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100  
|||||

Db 366 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGATTCGTGGTCACTCTAGGATT 425  
|||||

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
|||||

Db 426 AGCCCAAAACCCCAAGTGGGAAAAATGGGTGGGTGCTCTGATTGGAAAGGTTCCAGTG 485  
|||||

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
|||||

Db 486 AGCCGACAGTTTGCAGCCTATTGTTTACAACTCATCTGATCTACTTGGACTTAACCTCGTGCA 545  
|||||

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
|||||

Db 546 CCAGAAATATATACCAACCAAGATCCCATATTTCAACACTCAAACTGCAACACAAACA 605  
|||||

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
|||||

Db 606 GAAATTTATGTCAGTGACAGTACCTACTCTCGGTGGCATCCCTTACTCTACAATACCTGCC 665  
|||||

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200  
|||||

Db 666 CCTACTACT 725  
|||||

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluThrProPheVal 220  
|||||

Db 726 TGTGTACAGAAAGTTTATGGAACACTAGCACCATGTCTACAGAACTGAACCAATTGTT 785  
|||||

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
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Db 786 GAAAAATAAGAGCAGCATTCAGAAATGAAGCTGTGGGTTTGGAGGTGTCCCCACGGCTCTG 845  
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Qy 241 LeuValLeuAlaLeuLeuPheGlyAlaalaLaGlyLeuGlyPheCysTyrVallys 260  
Db CTAGTGCTGTGTCFCCCTCTTTCTTTGGTGCAGCTGCTCTTGATTTTGCATGTCAA 905

Qy 261 ArgTyrVallysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
Db AGGTATGTGAAGGCCCTTCCCCTTTTACAAACAAGAATCAGCAAGGAAATGATCGAAACC 965

Qy 281 LysValVallysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
Db ACAGTAGTAAGGAGGR-GAGGGCAATGATAGCAM-CCTAATRGGATC-AAAGAAACT 1021

Qy 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGlu 319  
Db GATAAAAA-CCAGAAGAGTCAGAA--GTCACGCAAACTTMCGTGCGATGTCGGAG 1074

RESULT 5  
AL551020 1201 bp mRNA linear EST 31-MAY-2003  
DEFINITION AL551020 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODI066Yl13 5-PRIME, mRNA sequence.  
ACCESSION AL551020  
VERSION AL551020.2 GI:31272837  
KEYWORDS EST  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1201)  
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT On Feb 15, 2001 this sequence version replaced gi:12888564.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5952.r For more information about this cluster, see http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSODI066CF07QP1&cluster=5952.r. Contact : Feng Liang Email : flliang@lifetech.com URL : http://fulllength.invitrogen.com/ invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODI066CF07QP1.

FEATURES source  
1..1201  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clones="CSODI066Yl13"  
/tissue\_type="PLACENTA COT 25-NORMALIZED"  
/culture\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN  
Alignment Scores:  
Pred. No.: 1.53e-122 Length: 1201  
Score: 1439.00 Matches: 300  
Percent Similarity: 94.98% Conservative: 3  
Best Local Similarity: 94.04% Mismatches: 14  
Query Match: 86.84% Indels: 7  
DB: 9 Gaps: 2

US-10-079-111-1 (1-322) x AL551020 (1-1201)

Qy 1 MetaLargCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20  
Db 98 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCATCTCCATCTCGACACAGAGCTCGT 157





Db 692 GAATTTATTGTGTCAGTGACAGTACTACTCGGTGGCATCCCTTACTCTACATACCTGCC 751  
 QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuLeu 200  
 Db 752 CTTACTACTACTACTCTCTCTCCAGCTTCCACTTCTATTCCAGGAGAAAAAATGGATT 811  
 QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
 Db 812 TGTGTACAGAGAGTTTATGAACTAGACCATGCTACAGAAACTGAACCAITTTGTT 871  
 QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
 Db 872 GAAATAAAGCAGCATTAAGAAATKAAGCTGCTGGGTTTGG-AGKPKTCCCKGCTCTG 930  
 QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
 Db 931 CTAGTGTCTTCT 990  
 QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGln 274  
 Db 991 ADGTATGTGAAGMCAC-CCTTTTMCACMAGATCAGCAG 1031

RESULT 9  
 AL550911  
 LOCUS  
 DEFINITION 1172 bp mRNA linear EST 31-MAY-2003  
 clone CS0DI065YD17 5-PRIME, mRNA sequence.  
 ACCESSION AL550911  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 Full-length cDNA libraries and normalization  
 Unpublished (2001)  
 COMMENT On Feb 15, 2001 this sequence version replaced gi:12888352.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 5952.r For  
 more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgi-bin/cluster.cgi?seq=CS0DI065CB09QPl&cluster=5952.r. Contact :  
 Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CS0DI065CB09QPl.  
 Location/Qualifiers

## FEATURES

1..1172  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CS0DI065YD17"  
 /tissue\_type="PLACENTA COT 25-NORMALIZED"  
 /clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
 /note="1st strand cDNA was primed with a NotI-oligo(dT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and cloned into the Not I and EcoR V  
 sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

Alignment Scores:  
 Pred. No.: 1.21e-107 Length: 1172  
 Score: 1278.00 Matches: 277  
 Percent Similarity: 91.29% Conservative: 6  
 Best Local Similarity: 89.35% Mismatches: 24  
 Query Match: 77.13% Indels: 9  
 Db: Gaps: 2

RESULT 10  
 AL549512  
 LOCUS  
 DEFINITION 972 bp mRNA linear EST 31-MAY-2003  
 clone CS0DI044YN16 5-PRIME, mRNA sequence.  
 ACCESSION AL549512  
 VERSION

US-10-079-111-1 (1-322) x AL550911 (1-1172)  
 QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20  
 Db 154 ATGGCCAGGTGCTTACGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 213  
 QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
 Db 214 GTCCAAAGGCTCTTTCGTGCAAGAGCTTTCATCCAGGTGTCAATGAGAAATATAGGGG 273  
 QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
 Db 274 ATSAACCTTGTGACCAAAAGGSGAASCHAGAGCTGAATTTTSASAGAAGCTAAGGAGGCC 333  
 QY 61 CysArgLeuLeuGlyLysSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
 Db 334 TGTAGGTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 393  
 QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100  
 Db 394 AGCTTTGAACCTTGACGCTATGGSTGGTTGGAGATGGATTGGTGTCACTCTAGGATT 453  
 QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
 Db 454 AGSCCAAAACSCCAAGTGTGGGAAAATGGGTGGTGTCTGATTTTGAAGGTTCCAGTG 513  
 QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
 Db 514 AGCSGACAGTTTGCAGCCTATTGTTTACAACCTCATCTGATCTTGGACTTGAACCTCGTGCATT 573  
 QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
 Db 574 SSAGAAATATATGACCACCAAGATCCCATATTTCAACACTCAAACTGCAACACAAACA 633  
 QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAl 180  
 Db 634 GAAATTTATTGTGACGAGACGATACCTACTCGGTGGCATCCCCCTTACTCTACGAATACCTGS 693  
 QY 180 aProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeu 200  
 Db 694 SCTTACTACT 753  
 QY 200 eCysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVa 220  
 Db 754 TTGTTGSACAGAGTTTTTATGGAACCTAGCAACCATGTCTACAAAACCTGAACCATTTGT 813  
 QY 220 IgluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLe 240  
 Db 814 TGAATAATAAGCAGCATTCAGAAATGAAGCTGCTGGTTTGGAGGTGT-CCCACGCTCT 872  
 QY 240 uLeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrVally 260  
 Db 873 GCTAGTGTCT 932  
 QY 260 sArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
 Db 933 AAGGTATGTGAAGGCTTCCCTTTTACAAACAGRAT-CAGCAGAAGGA-ATGATCAAAAC 990  
 QY 280 rLysValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysTh 300  
 Db 991 CAAAGTA-GTAAAGGAGGAGAGGC--AATGATAGCAC-CCTAATGAGGAT---CAAGAAAC 1043  
 QY 300 rAspLysAsnProGluGluSerLysSer 309  
 Db 1044 TGACAAAWMC---MGAAAGRTCAAAARTCA 1068

**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
**REFERENCE** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**AUTHORS** 1 (bases 1 to 972)  
**TITLE** Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
**JOURNAL** Full-length cDNA libraries and normalization  
**COMMENT** Unpublished (2001)  
 On Feb 15, 2001 this sequence version replaced gi:12885569.  
**CONTACT** Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 5952.r For  
 more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgi-bin/cluster.cgi?seq=CSODI044DG08QP1&cluster=5952.r. Contact :  
 Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CSODI044DG08QP1.  
**FEATURES**  
 Location/Qualifiers  
 1..972  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CSODI044YN16"  
 /tissue\_type="PLACENTA COT 25-NORMALIZED"  
 /note="1st strand cDNA was primed with a NotI-oligo(dT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and cloned into the Not I and EcoR V  
 sites of the pCMVSPORT 6 vector. Library was normalized."  
**ORIGIN**  
 Alignment Scores:  
 Pred. No.: 1.74e-107 Length: 972  
 Score: 1275.00 Matches: 261  
 Percent Similarity: 96.36% Conservative: 4  
 Best Local Similarity: 94.91% Mismatches: 9  
 Query Match: 76.95% Indels: 4  
 DB: 9 Gaps: 1  
 US-10-079-111-1 (1-322) x AL549512 (1-972)  
 Qy 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTriPThrThrArgLeuLeu 20  
 Db 143 ATGGCCAGGTGCTTCAGCTGGTGTGTCTTCTCACTTCCATCTGCACGAGGCTCCTG 202  
 Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
 Db 203 GTCCAAAGGCTCTTTGCGTGCAGAAAGGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 262  
 Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
 Db 263 ATCACCTTGTGAGCAAAAGCGAAGCAGACGCTGAATTTACAGAGCTGAAGAGGCC 322  
 Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
 Db 323 TGTAGGCTGCTGGGACTTAAGTTTGGCCGCGAAGCAAGTTGAACGCTTGAAGCY 382  
 Qy 81 SerPheGluThrCysSerTyrGlyTriPValGlyAspGlyPheValIleSerArgIle 100  
 Db 383 AGCTTTGAACCTGACGCTATGCGTGGGTGGAGATGGATTCGTGCTCTCTAGGATT 442  
 Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTriPlysValProVal 120  
 Db 443 AGCCCAACCCCAAGTGTGGGAAAATGGGGGGGTGCTCTGATTTGGAGGTTCCAGTG 502  
 Qy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTriPThrAsnSerCysIle 140  
 Db 503 AGCCGACAGTTTGCAGCCCTATTGTTACAACTCATCTGATACTTGGACTAATCTGTCGATT 562

Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
 Db 563 CCAGAAATTTATCACCACCAAGATCCCATATTTCAACACTCAAACTGCAACCAACAACA 622  
 Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
 Db 623 GAATTTATGTGAGTGACAGTACCTACTCGGTGGATCCCTTACTTACAAATACCTGCC 682  
 Qy 181 ProThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200  
 Db 683 CCTACTACTCTCTCTCTCCAGTTCCTTCTATTCACCGAGAGAAAAAATTGATT 742  
 Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
 Db 743 TGTGTSACAGAAGTTTTTATGAAACTAGCACCATGTCTACAGAAACTGAACCACTTTGTT 802  
 Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
 Db 803 GAAATAAAGCAGCATTCAGAAATGAAGCTGCTGGTTTGAGGTGTCCTCCGCG-CTCTK 861  
 Qy 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260  
 Db 862 CTAGTGCTTCTCTCTCTCTCTTGGTGTGCG-GCTGCTCTGGATTTTGTCTATGT-AAA 919  
 Qy 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLys 275  
 Db 920 AGGTATGTAGGSCT---TCCTTTTTCAAAGAATAASAGAAGG 961  
**RESULT** 11  
 AL543874  
**LOCUS** AL543874 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
**DEFINITION** clone CSODI005YG13 5-PRIME, mRNA sequence.  
**ACCESSION** AL543874  
**VERSION** AL543874.2 GI:31265719  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
**REFERENCE** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**AUTHORS** 1 (bases 1 to 911)  
**TITLE** Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
**JOURNAL** Full-length cDNA libraries and normalization  
**COMMENT** Unpublished (2001)  
 On Feb 15, 2001 this sequence version replaced gi:12876353.  
**CONTACT** Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 5952.r For  
 more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgi-bin/cluster.cgi?seq=CSODI005AD07QP1&cluster=5952.r. Contact :  
 Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CSODI005AD07QP1.  
**FEATURES**  
 Location/Qualifiers  
 1..911  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CSODI005YG13"  
 /tissue\_type="PLACENTA COT 25-NORMALIZED"  
 /note="1st strand cDNA was primed with a NotI-oligo(dT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and cloned into the Not I and EcoR V  
 sites of the pCMVSPORT 6 vector. Library was normalized."  
**ORIGIN**  
 Alignment Scores:



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Qy 161 GluPheilleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 743 GAAATTTATGTGAGTGACAGTACTACCTGGTGGCATCCCTTACTCTACCAATACCTGCC 802

Qy 181 ProThrThrThrProProAlaProAlaSerThrSerIleProAlaArgLysLysLeuile 200
Db 803 CCTACTACTACTCTCTCTGCTCCAGTTCACCTTCTATTCACGGAGAAAAATTTGATT 862

Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 863 TGTGTCAAGAGAGTTTATGGAAGTACAGCACTAGTCTACAGAACTGAACCACTTTGTT 922

Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db 923 GAAATTAAGCAGCAGATTCAAGATGAAGCTGCTGGGTTTGAGGGTGTCCCGC-GCTCTG 981

Qy 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 982 CTAGTGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1039

Qy 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLys 275
Db 1040 RG-TATGTGAAGSCT---CCCTTTTACAAATAAATMRCAGAAG 1080

RESULT 13
AL552127 1172 bp mRNA linear EST 31-MAY-2003
LOCUS AL552127 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CSODI059YA12 5-PRIME, mRNA sequence.
ACCESSION AL552127
VERSION AL552127.2 GI:31273943
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1172)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12890728.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqreg@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI059BA06QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI059BA06QP1.
Location/Qualifiers
FEATURES
source
1. 1172
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI059YA12"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.: 2,51e-105 Length: 1172
Score: 1253.00 Matches: 258
Percent Similarity: 95.94% Conservative: 2
Best Local Similarity: 95.20% Mismatches: 10
Query Match: 75.62% Indels: 4

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DB: 9 Gaps: 1
US-10-079-111-1 (1-322) x AL552127 (1-1172)

Qy 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTyrThrArgLeuLeu 20
Db 242 ATGCCAGGTGCTTCAGCTGGTGTGCTTCTCTACTTCCATCGACCCAGAGGCTCCTG 301

Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 302 GTCCAAGGCTCTTTTCGCTGCAGAAAGAGCTTTCCATCCAGGTGTCTATGCAGAAATTATGGG 361

Qy 41 IleThrIleValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 362 ATCACCCTTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTTTCAGAAAGCTTAAGAGGCC 421

Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 422 TGTAGGCTGTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCCTTGAAGCT 481

Qy 81 SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle 100
Db 482 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCTGGTCTATCTTAGGATT 541

Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTyrLysValProVal 120
Db 542 AGCCCAAAACCCCAAGTGTGGGAAATGGGTGGGTGCTGATTTGGAAGGTTCCAGTG 601

Qy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTyrThrAsnSerCysIle 140
Db 602 AGCCGACAGTTTTCAGCCTATTGTTCAACTCATCTGATACTTGGACTTAACCTCGTGCAAT 661

Qy 141 ProGluIleThrThrLysAspProLlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 662 CCAGAAATTTATCAGCACCAAGATCCCATATTAACACTCAAACTGCAACCAACAAACA 721

Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 722 GAAATTTATGTGAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAAATACCTGCC 781

Qy 181 ProThrThrThrProProAlaProAlaSerThrSerIleProAlaArgLysLysLeuile 200
Db 782 CCTACTACTACTCTCTCTGCTCCAGTTCACCTTCTATTCACGGAGAAAAATTTGATT 841

Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 842 TGTGTCAAGAGTTTATGGAAGTACAGCACCCTGTCTACAGAACTGAACA-TTTGTT 900

Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db 901 GA-AATAAAGCAGCAGATTCAAGATGAAGCTGCTGGTTTGAGGGTGTCCCAAGGCTCTT 959

Qy 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 960 CTAGTGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1018

Qy 261 ArgTyrValLysAlaPheProPheThrAsnLys 271
Db 1019 RGTATTTTAAGG---CTTCCTTTTAYAAACAAA 1048

RESULT 14
BX402505 1201 bp mRNA linear EST 13-MAY-2003
LOCUS BX402505 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CSODI045YA10 5-PRIME, mRNA sequence.
ACCESSION BX402505
VERSION BX402505.1 GI:30630733
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)

```

AUTHORS Li.W.B., Gruber,C., Jessee,J. and Polayes,D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 5952.r For  
 more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgi-bin/cluster.cgi?seq=CSA1012ZA06QPl&cluster=5952.r. Contact :  
 Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CSA1012ZA06QPl.  
 FEATURES Location/Qualifiers  
 source  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CSOD1045YA10"  
 /tissue\_type="PLACENTA COT 25-NORMALIZED"  
 /clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
 /note="1st strand cDNA was primed with a NotI-oligo (dT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and cloned into the Not I and EcoR V  
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:  
 Pred. No.: 1,97e-104 Length: 1201  
 Score: 1243.50 Matches: 259  
 Percent Similarity: 97.74% Conservative: 0  
 Best Local Similarity: 97.74% Mismatches: 5  
 Query Match: 75.05% Indels: 5  
 DB: 13 Gaps: 0

US-10-079-111-1 (1-322) x BX402505 (1-1201)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20  
 Db 212 ATGGCCAGGTGCTTCCAGCTGGTGTGCTTCTCACTTCCATCTGACCAAGGCTCCTG 271  
 QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40  
 Db 272 GTCCAAAGCTCTTGGTGCAGAGCTTCCATCCAGGTGTCATGCAGAAATATGGGG 331  
 QY 41 IleThrLeuValSerIleValAlaGlnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
 Db 332 ATCACCTTGTGAGCAAAAGCGAACCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 391  
 QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
 Db 392 TGTAGGCTGCTGGAGTAAGTTTGGCCGCGCAGGACCAAGTTGAACAGCTTGAAGCT 451  
 QY 81 SerPheGluThrCysSerTyrrGlyTrpValGlyAspGlyPheValIleSerArgIle 100  
 Db 452 AGCTTTGAAACTTGCAGCTATGCTGGGTGGAGATGATTCGTGTCATCTCTAGGATT 511  
 QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
 Db 512 AGCCCAAAACCCCAAGTGTGGGAAAATGGGGTGGTGTCTCTGATTGGAAAGGTTCCAGTG 571  
 QY 121 SerArgGlnPheAlaAlaTyrrCysTyrrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
 Db 572 AGCCGACAGTTTGACGCTATTGTTACCACTCACTGATCTGACCTAATCTGTGCAATT 631  
 QY 141 ProGluIleIleThrThryLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
 Db 632 CCAGAAATATATCACCACCAAGATCCCATATATTCAACTCAACTGCAACCAACAACA 691  
 QY 161 GluPheIleValSerAspSerThrTyrrSerValAlaSerProTyrrSerThrIleProAla 180

692 GAATTTATTGTTCAGTGACAGTACCTACTCGTGGTGGCATCCCTTACTCTACAATACCTGCC 751  
 QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200  
 Db 752 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 811  
 QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
 Db 812 TGTGTGCACAGAAGTTTTATGGAACTAGCACCACTGTCTACAGAAACTGAAACATTGTT 871  
 QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
 Db 872 GAAATAAAGCAGCATTTCAAGATCAAGCTGCTGGTTTGGAGGTGT-CCCACGGCTCTG 930  
 QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrrValLys 260  
 Db 931 CTAGTGTCTGCTCT-CTCTTCTTGTGTGTGCAGY-GGTCTTGGATTGTS-TATTCAAA 987  
 QY 261 ArgTyrrValLysAla 265  
 Db 988 AG-TATGTGAAGCT 1001

RESULT 15  
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 LOCUS  
 DEFINITION AL544430 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA  
 clone CSOD1018YG12 5-PRIME, mRNA sequence.  
 ACCESSION AL544430  
 VERSION AL544430.2 GI:31266274  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 1201)  
 AUTHORS Li.W.B., Gruber,C., Jessee,J. and Polayes,D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT On Feb 15, 2001 this sequence version replaced gi:12876910.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 5952.r For  
 more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgi-bin/cluster.cgi?seq=CSOD1018BD06QPl&cluster=5952.r. Contact :  
 Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CSOD1018BD06QPl.  
 FEATURES Location/Qualifiers  
 source  
 1..1201  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CSOD1018YG12"  
 /tissue\_type="PLACENTA COT 25-NORMALIZED"  
 /clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
 /note="1st strand cDNA was primed with a NotI-oligo (dT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and cloned into the Not I and EcoR V  
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:  
 Pred. No.: 2,2e-104 Length: 1201  
 Score: 1243.00 Matches: 256  
 Percent Similarity: 95.90% Conservative: 1  
 Best Local Similarity: 95.52% Mismatches: 9  
 Query Match: 75.02% Indels: 5  
 DB: 9 Gaps: 2



US-10-079-111-1 (1-322) x AL544430 (1-1201)

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QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db |||||
239 ATGGCCAGGTGCTTCAGCGCTGGTGTGCTTCTCACTTCATCGACACGAGGCTCCTG 298
QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db |||||
299 GTCCCAAGGCTCTTCGCGTGCAAGAGCTTCCATCCAGGTGTCATGCAGAAATTAATGGG 358
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db |||||
359 ATCACCCCTGTGAGCAAAAGCGCAACCCAGCAGCTGAATTCACAGAAAGCTAAGGAGGCC 418
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db |||||
419 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 478
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db |||||
479 AGCTTTGAAACTTGAGCTATGGCTGGGTGGAGATGGATTCGTGGTCACTCTAGGATT 538
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db |||||
539 AGCCCAAAACCCCAAGCTGTGGGAAAAATGGGTGGGTGCTCTGATTGGAAAGGTTCCAGTG 598
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db |||||
599 AGCCGACAGATTTCAGCCTATTGTTTACAACTCATCTGATCTTGACTAACTCGTGCATT 658
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db |||||
659 CCAGAAATTTATCCACCAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 718
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db |||||
719 GAATTTATTGTGACGTGACAGTACTACTCGGTGGCATCCCTTTACTCTACAATACCTGCC 778
QY 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db |||||
779 CCTACTACTCTCTCTCTCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 838
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db |||||
839 TGTGTACACAGAGTTTTTATGGAAACTAGCACCATGTCTACAGAACTGAACCAATTGTT 898
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db |||||
899 GAAATAAAGCAGCATTCAAGAATCAAGCTGCTGGGTTGGAGGTGT-CCCACGGCTCTG 957
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db |||||
958 CTAGTGTGTCTCT-CTCTTCTTGGTGGCKSAGYGGTCT--TGGATTTGCTATGTCAA- 1012
QY 261 ArgTyrValLysAlaPheProPhe 268
Db |||||
1013 AGGTATGTRAGGCT-CCCTTT 1033
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Search completed: September 15, 2004, 16:29:37  
Job time : 3080 secs

B/ack

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 15, 2004, 11:24:09 ; Search time 493 Seconds  
(without alignments)  
2774.685 Million cell updates/sec

Title: US-10-079-111-1

Perfect score: 1657  
Sequence: 1 MARCFSLVLLTSTWTRLL.....NPERSKSPKTVRCLEAEV 322

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USPTO\_spool/US10079111/runat\_13092004\_102133\_13546/app\_query.fasta\_1.519  
-DB=N Geneseq 29Jan04 -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPEL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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-USER=US10079111@cgn 1.1 470 @runat\_13092004\_102133\_13546 -NCPU=6 -ICPU=3  
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOB=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N\_Geneseq\_29Jan04:\*  
1: Geneseqn1980s:\*  
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3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2003as:\*  
8: Geneseqn2003bs:\*  
9: Geneseqn2003cs:\*  
10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1657	100.0	1755	5 AAF93818	Aaf93818 Human cDN
2	1657	100.0	2027	10 ADE71449	Ade71449 Human cDN
3	1657	100.0	2029	3 AA298172	Aaz298172 Human sig
4	1657	100.0	2029	10 ADE71445	Ade71445 Human cDN
5	1657	100.0	2372	2 AA52250	Aax52250 Protein P
6	1657	100.0	2372	3 ADC78520	Adc78520 Human PRO
7	1657	100.0	2372	4 AAF72408	Aaf72408 Human PRO
8	1657	100.0	2372	4 AAF92060	Aaf92060 Human PRO

9	1657	100.0	2372	6 ABS74380	Abs74380 Human cDN
10	1657	100.0	2372	6 ABL88087	Ab188087 Human PRO
11	1657	100.0	2372	6 ABL95576	Ab195576 Human ang
12	1657	100.0	2372	7 ACA59060	Aca59060 Human PRO
13	1657	100.0	2372	7 ACA58457	Aca58457 cDNA enco
14	1657	100.0	2372	7 ACA60164	ACA60164 Human cDN
15	1657	100.0	2372	7 ACD07564	ACD07564 Novel hum
16	1657	100.0	2372	7 ACA91166	ACA91166 Novel hum
17	1657	100.0	2372	7 ACD81543	ACD81543 Human cDN
18	1657	100.0	2372	7 ACA60365	ACA60365 Novel hum
19	1657	100.0	2372	7 ABX71612	ABX71612 Human cDN
20	1657	100.0	2372	7 ACH06944	Ach06944 Human sec
21	1657	100.0	2372	7 ACA58812	ACA58812 cDNA enco
22	1657	100.0	2372	7 ACA63988	ACA63988 cDNA enco
23	1657	100.0	2372	7 ACA91252	ACA91252 cDNA enco
24	1657	100.0	2372	7 ACD45151	ACD45151 Human sec
25	1657	100.0	2372	7 ABX96181	ABx96181 Human sec
26	1657	100.0	2372	7 ACA05502	Aca05502 cDNA enco
27	1657	100.0	2372	7 ACA93699	Aca93699 Human cDN
28	1657	100.0	2372	7 ACD20169	ACD20169 Human sec
29	1657	100.0	2372	7 ACA67273	ACA67273 cDNA enco
30	1657	100.0	2372	7 ACH66246	ACH66246 Novel hum
31	1657	100.0	2372	7 ACD02300	ACD02300 Novel hum
32	1657	100.0	2372	7 ACA89291	Aca89291 Novel hum
33	1657	100.0	2372	7 ACA68928	ACA68928 Novel hum
34	1657	100.0	2372	7 ACA54972	ACA54972 Novel hum
35	1657	100.0	2372	7 ACA98450	ACA98450 Human PRO
36	1657	100.0	2372	8 ACA63375	ACA63375 cDNA enco
37	1657	100.0	2372	8 ACD19807	ACD19807 Human sec
38	1657	100.0	2372	8 ADB29405	ADB29405 Human sec
39	1657	100.0	2372	8 ADB17062	ADB17062 Human cDN
40	1657	100.0	2372	8 ACH03578	ACH03578 Human sec
41	1657	100.0	2372	8 ADA18261	Ada18261 Human sec
42	1657	100.0	2372	8 ACD66954	ACD66954 Human cDN
43	1657	100.0	2372	8 ADA19867	Ada19867 Novel hum
44	1657	100.0	2372	8 ADB17250	ADB17250 Human cDN
45	1657	100.0	2372	8 ACD83115	ACD83115 Human PRO

#### ALIGNMENTS

##### RESULT 1

AAF93818  
ID AAF93818 standard; cDNA; 1755 BP.

XX AAF93818;

XX 23-MAY-2001 (first entry)

XX Human cDNA encoding a membrane or secretory protein clone PSEC0135.

XX Human; secretory protein; membrane protein; vaccine; gene therapy;  
XX rheumatoid arthritis; diabetes; ss.

XX Homo sapiens.

XX EP1067182-A2.

XX 10-JAN-2001.

XX 07-JUL-2000; 2000EP-00114090.

XX 08-JUL-1999; 99JP-00194179.

XX 11-JAN-2000; 2000JP-00118775.

XX 02-MAY-2000; 2000JP-00183766.

XX (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayaashi K;

XX WPI; 2001-093989/11.

XX P-PSDB; AAB88391.

checked

PT Nucleic acids encoding secretory proteins/membrane proteins, useful in  
 PT gene therapy or as candidate target molecules in drug development.  
 XX

PS Claim 1; SEQ ID NO 149; 609pp + Sequence Listing; English.

XX This invention relates to nucleic acid sequences AAF93744 - AAF93916  
 CC which encode human secretory or membrane proteins represented by AAF88317  
 CC - AAF88419. Included in the invention are primers AAF93917 - AAF94295 and  
 CC AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the  
 CC invention. The invention also includes methods for the production of  
 CC antibodies directed against the proteins, and cDNA sequences, which can  
 CC be used in vaccines. The polynucleotide sequences can be used in gene  
 CC therapy. The polynucleotide sequences and the proteins they encode may be  
 CC used in the prevention, treatment and diagnosis of diseases associated  
 CC with inappropriate secretory protein/membrane protein expression. The  
 CC nucleic acids and complementary sequences may also be used as DNA probes  
 CC in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect  
 CC and quantitate the presence of similar nucleic acid sequences in samples.  
 CC They may also be used to study the expression and function of secretory  
 CC proteins/membrane polypeptides and their role in metabolism. The  
 CC polypeptides may be used as antigens in the production of antibodies  
 CC against them and in assays to identify modulators (agonists and  
 CC antagonists) of expression and activity. The antibodies and antagonists  
 CC may also be used as therapeutic agents to down regulate expression and  
 CC activity. The antibodies may also be used as diagnostic agents for  
 CC detecting the presence of the polypeptides in samples (e.g. by enzyme  
 CC linked immunosorbent assay (ELISA)). Examples of diseases which may be  
 CC treated include rheumatoid arthritis and diabetes

XX Sequence 1755 BP; 502 A; 422 C; 406 G; 425 T; 0 U; 0 Other;

# Alignment Scores:

Pred. No.: 2,66e-146 Length: 1755  
 Score: 1857.00 Matches: 322  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 5 Gaps: 0

US-10-079-111-1 (1-322) x AAF93818 (1-1755)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuLeuSerIleTrrPThrThrArgLeuLeu 20  
 Db ATGGCCAGGTCTTCAGCGTGGTGTGCTTCTTCTCCTTCCATCTGGACACGAGGCTCTCG 260  
 QY 21 ValGlnGlySerLeuArgIleGluLeuSerIleGlnValSerCysArgIleMetGly 40  
 Db GTCCCAAGGCTCTTTCGTCGACAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGGG 320  
 QY 41 IleThrLeuValSerIleValAlaAlaGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
 Db ATCCACCTTGTGAGCAAAAGGCGAACCGAGCTGAATTCACAGAGCTAAGAGGCC 380  
 QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
 Db TGTAGGCTGCTGGAGCTAAGTTTGGCCGAGGACCAAGTTGAAACAGCCCTTGAAGCT 440  
 QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100  
 Db AGCTTTGAACACTTGACGATGCTGGGTGGGTGGAGATGGATTCGTGTCATCTCTAGGATT 500  
 QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
 Db AGCCCAACCCCAAGTGTGGGAAATGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 560  
 QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrrPThrAsnSerCysIle 140  
 Db AGCCACACAGTTTGCAGCTATTGTTTACAACTCATCTGATCTGACTTAACCTCGTGCATT 620  
 QY 141 ProGluIleIleThrThrIleAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
 Db CCAGAAATATTACCAACCAAGATCCCATATTTCACAACTCAAACTCAAACTCAAACTCAAA 680

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
 Db GAATTTATTGTGAGTGACAGTACTACTCGGTGGCATCCCTTACTCTCAATACCTGCC 740  
 QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200  
 Db CTCTACTACTACT 800  
 QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
 Db TGTGTACACAGAAAGTTTATGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 860  
 QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
 Db GAAATAAAGCAGCATTCAGAAATGAAGCTGTGGGTGTTGGAGGTGTCCCCACGGCTCTG 920  
 QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
 Db CTAGTGTCTGCT 980  
 QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
 Db AGGTATGTGAGGCTTCCCTTTTACAAACAAGAATCAGCAGAGGAAATGATCGAAACC 1040  
 QY 281 LysValValLysGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
 Db AAAGTAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1100  
 QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
 Db GATAAAACCCAGAGAGTCCAAAGAGTCCAAAGAGTCCAAAGAGTCCAAAGAGTCCAAAG 1160  
 QY 321 GluVal 322  
 Db 1161 GAAGTT 1166

RESULT 2  
 ADE71449  
 ID ADE71449 standard; cDNA; 2027 BP.  
 XX  
 AC ADE71449;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human cDNA encoding PDEBC #2.  
 XX  
 KW breast cancer; PDEBC; metastatic; human; ss; gene.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003124543-A1.  
 XX  
 PD 03-JUL-2003.  
 XX  
 PF 20-FEB-2002; 2002US-00079111.  
 XX  
 PR 15-JAN-1999; 99US-00232160.  
 XX  
 PA (STUA/) STUART S G.  
 PA (STRE/) STREETER D G.  
 XX  
 PI Stuart SG, Streeter DG;  
 XX  
 DR WPI; 2004-009141/01.  
 DR P-PSDB; ADE71444.  
 XX  
 PT A new cDNA encoding a protein differentially expressed in breast cancer  
 PT designated PDEBC is useful to stage, treat, and monitor progression or  
 PT treatment of breast cancer, particularly an invasive, metastatic stage of  
 PT the disease.  
 XX  
 XX Claim 2; Fig 1; 31pp; English.  
 XX

CC The invention relates to an isolated cDNA encoding a protein that is  
 CC differentially expressed in breast cancer, designated PDBEC. The  
 CC invention is useful to diagnose breast cancer. The invention is also  
 CC useful to stage, treat, and monitor progression or treatment of breast  
 CC cancer, particularly an invasive, metastatic stage of the disease. The  
 CC present sequence represents cDNA encoding human PDBEC Incyte 3044710CBI.  
 CC Note: There are two sequences that have been assigned SEQ ID 2 in the  
 CC specification, the present sequence represents the sequence given in  
 CC figure 1.

XX SQ Sequence 2027 BP; 612 A; 461 C; 445 G; 509 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.:	3,25e-146	Length:	2027
Score:	1657.00	Matches:	322
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-079-111-1 (1-322) x ADE71449 (1-2027)

QY	1	MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrrThrThrArgLeuLeu	20
Db	181	ATGGCCAGGTGCTTCAGCTGGTGTGTCTTCTCACTTCCATCTGGACCGAGGCTCTCG	240
QY	21	ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	241	GTCCAAAGGCTCTTTCGTCGTCGACAGAGCTTTCATCCAGGTGTCTATGCAGAAATTATGGG	300
QY	41	IleThrLeuValSerLysLysAlaAsnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	301	ATCACCTTGTGAGCAAAAGCGCAACCCAGCAGCTGGAATTTACAGAGCTTAAGAGGCC	360
QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	361	TGTAGGCTGTGGACTAAGTTTGGCGGCAAGCAAGTTGAAACGCTTGAAGCT	420
QY	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
Db	421	AGCTTTGAAACTTGACAGCTATGGCTGGGTGGAGATGGATTCGTGCTCTCTAGGATT	480
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrrLysValProVal	120
Db	481	AGCCCAAAACCCCAAGTGGGAAAAATGGGTGGGTGCTCTGATTGGAAGGTTCCAGTG	540
QY	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrrThrAsnSerCysIle	140
Db	541	AGCCGACAGTTTGCAGCTATGTGTACAACTCATCTGATACCTTGGACTTAACCTCGTGCA	600
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	601	CCAGAAATTTATCACCAACCAAGATCCCATATTTCACACTCAAACTGCAACACAAACA	660
QY	161	GluPheIleValSerAspSerThrTrrThrSerValAlaSerProTyrSerThrIleProAla	180
Db	661	GAATTTATGTGAGTACAGTACCTACTCGGTGGCATCCCTTACTTACAAATCCTGCC	720
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgLysLysLeuIle	200
Db	721	CCTACTACTCTCTCTCTCTCCAGCTTCCACTTCTATTCACCGGAGAAAAAATTGATT	780
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	781	TGTGTTCACAGAAAGTTTATGAGAACTAGCACCATGTCTACAGAAACTGAACCAATTGTT	840
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	841	GAATAAAGACGACATTCAAGATTAAGCTGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT	900
QY	241	LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	901	CTAGTGTCT	960

QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	961	AGGTATGTGAAGGGCTTCCCTTTTACAAACAAGAAATCAGCAGAGAAATGATCGAAACC	1020
QY	281	LysValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
Db	1021	AAAGTAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1080
QY	301	AspLysAsnProGluGluSerLysSerProSerLysThrValArgCysLeuGluAla	320
Db	1081	GATAAAACCCAGAGAGTCCCAAGAGTCCAAAGCAAACTACCGTCGATGCTGGAAGCT	1140
QY	321	GluVal 322	
Db	1141	GAAGTT 1146	
RESULT 3			
AAZ98172			
ID	AAZ98172	standard; cDNA; 2029 BP.	
XX	XX		
AC	AAZ98172;		
DT	XX		
XX	11-MAY-2000 (first entry)		
DE	Human signal peptide containing protein HSP-64 cDNA SEQ ID NO:198.		
KW	Human; signal peptide-containing protein; HSP; diagnosis; cancer;		
KW	inflammation; cardiovascular disease; anticancer; anti-inflammatory;		
KW	antimicrobial; neurotropic; neuroprotective; cardiovascular; hepatotropic;		
KW	antiasthmatic; gene therapy; cell proliferation; neurological disorder;		
KW	reproductive disorder; developmental disorder; arteriosclerosis;		
KW	asthma; Crohn's disease; acquired immune deficiency syndrome; anaemia;		
KW	Parkinson's disease; Huntington's diseases; ovulatory defect;		
KW	muscular dystrophy; ss.		
XX	XX		
OS	Homo sapiens.		
XX	XX		
PN	WO200000610-A2.		
PD	06-JAN-2000.		
XX	XX		
PF	25-JUN-1999; 99WO-US014484.		
XX	XX		
PR	26-JUN-1998; 98US-0090762P.		
PR	31-JUL-1998; 98US-0094983P.		
PR	01-OCT-1998; 98US-0102686P.		
PR	11-DEC-1998; 98US-0112129P.		
XX	XX		
PA	(INCY-) INCYTE PHARM INC.		
XX	XX		
PI	Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;		
PI	Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;		
PI	Bandman O;		
XX	XX		
DR	WPI; 2000-160673/14.		
DR	P-PSDB; AAY87287.		
XX	XX		
PT	New human signal peptide-containing proteins useful in treatment,		
PT	prevention and diagnosis of e.g. cancer, inflammation and cardiovascular		
PT	disease.		
XX	XX		
PS	Claim 9; Page 288-289; 327pp; English.		
XX	XX		
CC	AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the		
CC	human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have		
CC	anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,		
CC	neuroprotective, cardiovascular and antiasthmatic activities, and can be		
CC	used in gene therapy. HSPs can be used to treat or prevent disorders		
CC	associated with decreased activity or function of HSP. Antagonists of		
CC	HSP are used to treat or prevent disorders associated with increased		
CC	activity or function of HSP. Such diseases include cell proliferation		



Qy	1	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu	20
Db	183	ATGCCCAGGCTCTTCAGCCTGGTGTGTTCTCACTTCATCTGCACACAGGCTCTCG	242
Qy	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	243	GTCCAAGGCTCTTGGCGTGCAAGAGCTTCCATCCAGGTGTCATGCAGAAATTATGGG	302
Qy	41	IleThrLeuValSerLysIysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	303	ATCACCCCTTGTGAGCAAAAGCGCAACGACGAGCTGAATTTACACAGAAGCTAAGGAGGCC	362
Qy	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	363	TGTAGGCTGTGGGACTAAGTTTGGCCGGCAGGACCAAGTTGAACAGCCTTGAAGCT	422
Qy	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle	100
Db	423	AGCTTTGAAACTTGACGATATGGCTGGGTGGAGATGGATTCTGGTCACTCTAGGATT	482
Qy	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
Db	483	AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCTGATTTGGGAAGGTTCCAGTG	542
Qy	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	543	AGCCGACAGTTTGGACGCTATTGTTTACAACTCATCTGATACCTTGGACTAACTCGTGCAAT	602
Qy	141	ProGluIleIleThrThryLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	603	CCAGAAATATCACACCACCAAGATCCCATATTCAACACTCAAACTGCAACACACACAAACA	662
Qy	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	663	GAATTTATTGTTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC	722
Qy	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Db	723	CCTACTACTCTCCCTCGCTCCAGCTTCCATCTTATTCCACGGAGAAAAAATTGAT	782
Qy	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	783	TGTGTACAGAGATTTTATGGAACTAGCACCATGTCTACAGAACTGAACCAATTGT	842
Qy	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	843	GAATAATAAGCAGCATTCGAAGATGAAGCTGTGGGTTTTGGAGGTGTCCCCACGGCTCG	902
Qy	241	LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	903	CTAGTGCTTGCTCTCTCTTGTGTGCTGCAGCTGGTCTTGGATTTTGTCTATGTCAAA	962
Qy	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	963	AGGTATGTGAAGGCCTTCCCTTTTACAAACAGAATCAGCAGNAGGAATGATCGAAACC	102
Qy	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysThr	300

PR 03-NOV-1997; 97US-0064248P.  
 PR 07-NOV-1997; 97US-0064809P.  
 PR 12-NOV-1997; 97US-0065186P.  
 PR 17-NOV-1997; 97US-0065846P.  
 PR 18-NOV-1997; 97US-0065693P.  
 PR 21-NOV-1997; 97US-0066120P.  
 PR 21-NOV-1997; 97US-0066364P.  
 PR 24-NOV-1997; 97US-0066453P.  
 PR 24-NOV-1997; 97US-0066466P.  
 PR 24-NOV-1997; 97US-0068511P.  
 PR 24-NOV-1997; 97US-0066770P.  
 PR 24-NOV-1997; 97US-0066772P.  
 PR 25-NOV-1997; 97US-0066840P.  
 PA (GETH ) GENENTECH INC.  
 XX  
 XX Wood WL, Gurney AL, Goddard A, Pennica D, Chen J, Yuan J;  
 XX WPI; 1999-229533/19.  
 DR P-PSDB; AAY13379.  
 XX  
 PT New isolated human genes and polypeptides used in, e.g. treatment of  
 PT gastrointestinal ulceration.  
 XX  
 PS Claim 2; Fig 73; 320pp; English.  
 XX  
 CC AAX52213-74 encode secreted and transmembrane human proteins, and are  
 CC obtained from cDNA libraries, prepared from fetal lung, fetal kidney,  
 CC fetal brain, fetal liver and fetal retina. The encoded polypeptides have  
 CC specific uses based on their homology to known polypeptides, e.g. PRO211  
 CC and PRO217 can be used for disorders associated with the preservation and  
 CC maintenance of gastrointestinal mucosa and the repair of acute and  
 CC chronic mucosal lesions (e.g. enterocolitis, Zollinger-Ellison syndrome,  
 CC gastrointestinal ulceration and congenital microvillus atrophy), skin  
 CC diseases associated with abnormal keratinocyte differentiation (e.g.  
 CC psoriasis, epithelial cancers such as lung squamous cell carcinoma of the  
 CC vulva and gliomas), potent effects on cell growth and development,  
 CC diseases related to growth or survival of nerve cells including  
 CC Parkinson's disease, Alzheimer's disease, ALS, neuropathies or cancer.  
 CC PRO265 can be used as for fibromodulin, e.g. for reducing dermal  
 CC scarring. PRO264 can be used as a target for anti-tumor drugs. PRO333 may  
 CC be used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can  
 CC be used as an anti-thrombotic agent; PRO287 polypeptides and portions may  
 CC have therapeutic applications in wound healing and tissue repair; PRO317  
 CC can be used for treating problems of the kidney, uterus, endometrium,  
 CC blood vessels, or related tissue, e.g. in the heart of genital tract  
 XX  
 SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 4.04e-146 Length: 2372  
 Score: 1657.00 Matches: 322  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 2 Gaps: 0

US-10-079-111-1 (1-322) x AAX52250 (1-2372)

QY 1 MetalaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrrPThrArgLeuLeu 20  
 DB 160 ATGCCAGGCTTTGCGTGCAGAGAGAGCTTTCATCCAGGTGTATGAGAAATATGGG 219  
 QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
 DB 220 GTCCAGGCTTTGCGTGCAGAGAGAGCTTTCATCCAGGTGTATGAGAAATATGGG 279  
 QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
 DB 280 ATCAACCTTGTGAGCAAAAGCGCAACAGCAGAGCTGAATTTACAGAGAGCTAAGAGGCC 339  
 QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80

Db 340 TGTAGGCTGCTGGACTAAGTTTGGCCGCAAGGACCAAGTTGAACACAGCCTTGAAGCT 399  
 QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100  
 Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTTCAGATGGATTCTGTGTCATCTCTAGGATT 459  
 QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
 Db 460 AGCCCAAAACCCCAAGTGTGGGAAATGGGGTGGTCTCTGATTGGAGGTTCAGGTG 519  
 QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
 Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACATCATCTGATACTTGGACTTAACCTGTCATT 579  
 QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
 Db 580 CCAGAAATATATCACCACCAAGATCCCATATTTCAACACTCAAACTGCAACACAAACA 639  
 QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
 Db 640 GNAATTTATGTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTTACAATACCTGCC 699  
 QY 181 ProThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200  
 Db 700 CCTACTACTCTCTCTCTCCAGCTTCCACTTCTATTCCACGAGAGAAAATTTGATT 759  
 QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
 Db 760 TGTGTGCACAGAGATTTTATGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819  
 QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
 Db 820 GAAATAAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGGAGGTGTCACACGGCTCG 879  
 QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
 Db 880 CTAGTGCTTGTCTCTCTCTCTTGTGCTGCAGCTGCTTGGATTGCTATGTCAAA 939  
 QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
 Db 940 AGGTATGTGAAGGCCCTTCCCTTTTCAAAACAAGAAATCAGCAGAGAAATGATCGAAAC 999  
 QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
 Db 1000 AAGTAGTAAAGGAGGAGAGAGCCATGATAGCAACCTTAATGAGAAATCAAGAAACT 1059  
 QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
 Db 1060 GATAAAACCCAGAGAGTCCAGAGTCCAAAGCAAAACTACCGTGGATGCTGGAAGCT 1119  
 QY 321 GluVal 322  
 Db 1120 GAAGTT 1125  
 RESULT 6  
 ADCT78520  
 ID ADCT78520 standard; cDNA; 2372 BP.  
 XX  
 AC ADCT78520;  
 XX  
 DT 01-JAN-2004 (first entry)  
 XX  
 DE Human PRO263 cDNA.  
 KW antiinflammatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian;  
 KW neurotropic; neuroprotective; vasotropic; chemotactic; angiogenic;  
 KW neurotrophic; osteopathic; antiasthmatic; antiarthritic; antineumatic;  
 KW antiarteriosclerotic; cardiant; antidiabetic; cerebroprotective;  
 KW thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome;  
 KW gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease;  
 KW Alzheimer's; ALS; neuropathy; dermal scarring; wound healing;  
 KW nerve repair; thrombosis; bone; cartilage formation; angiogenesis;  
 KW asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder;



KW atherosclerosis; cardiac injury; infertility; premature aging; AIDS;  
 KW diabetes; stroke; gene therapy; transgenic; PRO; human; ss; gene.  
 XX Homo sapiens.  
 OS WO200015796-A2.  
 PN 23-MAR-2000.  
 PD 15-SEP-1999; 99WO-US021090.  
 XX 16-SEP-1998; 98WO-US019330.  
 PF (GETH ) GENENTECH INC.  
 PR Chen J, Goddard A, Gurney AL, Hillan K, Pennica D, Wood WI;  
 XX Yuan J;  
 PI WPI; 2000-271434/23.  
 DR P-PSDB; ADC78521.  
 XX  
 PT Novel nucleic acids encoding secreted and transmembrane polypeptides with  
 PT homology, e.g. to growth and cancer-associated antigens.  
 XX  
 PS Claim 2; SEQ ID NO 200; 355pp; English.  
 XX  
 CC The invention relates to a novel nucleic acid encoding a PRO polypeptide.  
 CC The polypeptides and polynucleotides of the invention may be useful as  
 CC research tools and as therapeutics for treating enterocolitis, Zollinger-  
 CC Ellison syndrome, gastrointestinal ulceration, psoriasis, cancer,  
 CC Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal  
 CC scarring and wound healing, nerve repair, thrombosis, bone and/or  
 CC cartilage formation, angiogenesis, asthma, rheumatoid arthritis, multiple  
 CC sclerosis, inflammatory disorders, atherosclerosis, cardiac injury,  
 CC infertility, premature aging, AIDS, diabetes complications and stroke.  
 CC The molecules may also be utilised during gene therapy procedures and  
 CC transgenic animal production. The current sequence is that of the human  
 CC PRO cDNA of the invention.  
 XX  
 SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 4, 04e-146 Length: 2372  
 Score: 1657.00 Matches: 322  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 3 Gaps: 0

US-10-079-111-1 (1-322) x ADC78520 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 20  
 Db 160 ATGGCCAGGTGCTTCAGCCCTGGTGTGCTCTCTCACTTCCATCTGGACACGAGGCTCCTG 219  
 QY 21 ValGlnGlySerLeuArgLagLuuLeuSerLleGlnValSerCysArgileMetGly 40  
 Db 220 GTCCAGGCTCTTTGGCTGCAGAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279  
 QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPherThrGluAlalysGluAla 60  
 Db 280 ATCCACCTTGTAGCMAAAGGCGAACACGACGAGCTGAATTCACAGAACTAAGAGGCC 339  
 QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
 Db 340 TGTAGGCTCTGGACTAAGTTTGGCGCGCAGGACCAAGTTGAAACAGCCCTTGAAGCT 399  
 QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100  
 Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTCGTGTCATCTCTAGGATT 459  
 QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120

Db 460 AGCCCAAAACCCCAAGTGTGGGAAAAAATGGGTGGGTGTCTGATTGGGAAGGTTCCAGTG 519  
 QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
 Db 520 AGCCGACAGTTTGCAGCCTATTGTGTACAACTCATCTGATACCTTGGACTAATCGTGCATT 579  
 QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
 Db 580 CCAGAAATTATCACCCCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 639  
 QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
 Db 640 GAAITTTATGTGTCAGTGACAGTACTACTCGGTGGCATCCCTTACTCTACAATACTGCTGC 699  
 QY 181 ProThrThrThrProAlaProAlaSerThrSerIleProAlaSerProArgLysLysLeuIle 200  
 Db 700 CCTACTACT 759  
 QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
 Db 760 TGTGTACAGAGATTTTATGGAACACTAGCACCATGCTACAGAAACTGAAACCATTTGTT 819  
 QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
 Db 820 GAAATAAAGCAGCATTCAAGAACTGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 879  
 QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
 Db 880 CTAGTGTCTGTCT 939  
 QY 261 ArgTyrValLysAlaPhePhePheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
 Db 940 AGTATGTGAGGCCCTTCCCTTTTCAACAACAAGATCAGCAGAGAGAAATGATCGAACCC 999  
 QY 281 LysValValLysGluGluLysAlaAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
 Db 1000 AAAGTAGTAAAGGAGGAGGAGGCAATGATAGCAACCTTAATGAGGAATCAAGAGAACT 1059  
 QY 301 AspLysAsnProGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
 Db 1060 GATAAAAAACCCAGAGAGTCCAAAGAGTCCAAAGAACTACCGTCGATGCTCGGAAGCT 1119  
 QY 321 GluVal 322  
 Db 1120 GAAGTT 1125  
 RESULT 7  
 AAF72408  
 ID AAF72408 standard; cDNA; 2372 BP.  
 XX AAF72408;  
 AC AAF72408;  
 XX  
 DT 24-APR-2001 (first entry)  
 XX  
 DE Human PRO263 cDNA.  
 XX  
 KW Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;  
 KW antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant;  
 KW antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;  
 KW antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes;  
 KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;  
 KW ischaemia; inflammation; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200104311-A1.  
 XX  
 PD 18-JAN-2001.  
 XX  
 PF 22-FEB-2000; 2000WO-US004414.  
 XX  
 PR 07-JUL-1999; 99US-0143048P.  
 PR 26-JUL-1999; 99US-0145698P.

PR 28-JUL-1999; 99US-0146222P.  
 PR 08-SEP-1999; 99WO-US020594.  
 PR 13-SEP-1999; 99WO-US020944.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 15-SEP-1999; 99WO-US021547.  
 PR 05-OCT-1999; 99WO-US023089.  
 PR 29-NOV-1999; 99WO-US028214.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 02-DEC-1999; 99WO-US028564.  
 PR 02-DEC-1999; 99WO-US028565.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 20-DEC-1999; 99WO-US030911.  
 PR 20-DEC-1999; 99WO-US030999.  
 PR 05-JAN-2000; 2000WO-US000219.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;  
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;  
 PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kijavini LJ;  
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;  
 PI Williams PM, Wood WI;  
 XX  
 XX WPI; 2001-081051/09.  
 DR P-PSDB; AAB80247.  
 XX  
 PT Sixty one nucleic acids encoding PRO polypeptides which are useful in the  
 PT treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous  
 PT cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's  
 PT disease).  
 XX  
 PS Claim 2; Fig 73; 393pp; English.  
 XX  
 CC The present sequence is one of sixty one nucleic acids encoding novel  
 CC secreted and transmembrane PRO polypeptides. The PRO polypeptides are  
 CC useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung  
 CC squamous cell carcinoma), gastrointestinal disorders (e.g.  
 CC enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,  
 CC Parkinson's disease), wound repair, cardiovascular disorders (e.g.  
 CC endometrial bleeding angiogenesis, ischaemias such as coronary ischaemia,  
 CC atherosclerosis), inflammatory disorders (e.g. asthma, rheumatoid  
 CC arthritis, multiple sclerosis), infertility, AIDS and diabetes and  
 CC retinal disorders such as retinitis pigmentosum. The PRO nucleic acids  
 CC have applications in molecular biology, including use as hybridization  
 CC probes, and in chromosome and gene mapping  
 XX  
 SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 4,04e-146 Length: 2372  
 Score: 1657.00 Matches: 322  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 4 Gaps: 0

US-10-079-111-1 (1-322) x AAF72408 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTyrThrArgLeuLeu 20  
 Db 160 ATGGCCAGGTGCTTACAGCTGGTGTGTTCTTCTCACTTCATCTGACCAACGAGGCTCCTG 219  
 QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
 Db 220 GTCCAGGCTCTTTCGTCGACAGAGGCTTTCATCCAGGTGTCTAGCAATATGAGGG 279  
 QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
 Db 280 ATCACCCCTGTGAGCAAAAGCGCAACCCAGCAGCTGAATTCACAGAAAGCTAAGGAGGCC 339  
 QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
 Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAACAGCCTTGAAGCT 399

QY 81 SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle 100  
 Db 400 AGCTTTTGAACACTTGCAGCTATGCTGGTGGAGATGGATTCGTGCTCATCTCTAGGATT 459  
 QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleThrLysValProVal 120  
 Db 460 AGCCCAAAACCCAGTGTGGGAAATGGGGTGGGTCTCTGATTTGGAGGTTCCAGTG 519  
 QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTyrThrAsnSerCysIle 140  
 Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTTGGACTTAACCTCGTCATT 579  
 QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
 Db 580 CCAGAAATTTATCACCACCAAGATCCCATATTTCAACACTCAAACTGCAACACAAACA 639  
 QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
 Db 640 GAATTTATGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTTACAAATACCTGCC 699  
 QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200  
 Db 700 CCTACTACTACTCTCTCTCCAGCTTCCACTTCTATTCCACGAGAGAAAAAATTGATT 759  
 QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
 Db 760 TGTGTGCACAGAGATTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819  
 QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
 Db 820 GAAATATAAGCAGCATTTCAAGATGAGCTGCTGGTGTGGAGGTGTCCTCCACGGCTCTG 879  
 QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
 Db 880 CTAGTGCTTGCT 939  
 QY 261 ArgTyrValLysAlaPhePhePheThrAsnLysAsnGlnLysGluMetIleGluThr 280  
 Db 940 AGGTATGTGAAGGCTTCCCTTTTACAAACAGAAATCAGCAGAGAAATGATCGAAACC 999  
 QY 281 LysValValLysGluGluLysAlaAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
 Db 1000 AAAGTAGTAAAGGAGGAGAGGCCCAATGATAGCAACCTTATAGAGGAATCAAGAAACT 1059  
 QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
 Db 1060 GATAAAACCCAGAGAGTCCAGAGAGTCCAGCAAAACTACCGTCCGATGCTCGAAGCT 1119  
 QY 321 GluVal 322  
 Db 1120 GAAGTT 1125  
 RESULT 8  
 AAF92060  
 ID AAF92060 standard; cdna; 2372 BP.  
 XX  
 AC AAF92060;  
 XX  
 DT 15-MAY-2001 (first entry)  
 XX  
 DE Human PRO263 cdna.  
 XX  
 KW Human; PRO protein; mapping; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200116318-A2.  
 XX  
 PD 08-MAR-2001.  
 XX  
 PF 24-AUG-2000; 2000WO-US023328.  
 XX

PR 01-SEP-1999; 99WO-US020111.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 07-DEC-1999; 99US-0169495P.  
 PR 09-DEC-1999; 99US-0170262P.  
 PR 11-JAN-2000; 2000US-0175481P.  
 PR 18-FEB-2000; 2000WO-US004341.  
 PR 18-FEB-2000; 2000WO-US004342.  
 PR 22-FEB-2000; 2000WO-US004414.  
 PR 01-MAR-2000; 2000WO-US005601.  
 PR 03-MAR-2000; 2000US-0187202P.  
 PR 21-MAR-2000; 2000US-0191007P.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 25-APR-2000; 2000US-0199397P.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 05-JUN-2000; 2000US-0209832P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;  
 XX  
 DR WPI; 2001-183260/18.  
 DR P-PSDB; AAB87528.  
 XX  
 PT Eighty four nucleic acids encoding PRO polypeptides, useful in molecular  
 PT biology, including use as hybridization probes, and in chromosome and  
 PT gene mapping.  
 XX  
 PS Claim 2; Fig 5; 278pp; English.  
 XX  
 CC The present sequence is the coding sequence for a human PRO polypeptide  
 CC (secreted and transmembrane). The PRO protein, and PRO agonists, PRO  
 CC antagonists or anti-PRO antibodies are useful for preparation of a  
 CC medicament useful in the treatment of a condition which is responsive to  
 CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO  
 CC protein may also be employed as molecular weight markers for protein  
 CC electrophoresis. The PRO coding sequence has applications in molecular  
 CC biology, including use as hybridisation probes, and in chromosome and  
 CC gene mapping  
 XX  
 SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 4,04e-146 Length: 2372  
 Score: 1657.00 Matches: 322  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 4 Gaps: 0

US-10-079-111-1 (1-322) x AAF92060 (1-2372)

QY	1	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu	20
Db	160	ATGGCCAGGTGCTTCAGCCCTGGTGTCTTCTCCTCCATCTGGACCAAGGCTCTCTG	219
QY	21	ValGlnGlySerLeuArgLaGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	220	GTCCCAAGGCTCTTGGCGTCAGAGAGCTTCCATCCAGGTGTCATGCAGAAATTATGGG	279
QY	41	IleThrLeuValSerIleLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	280	ATCACCTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTCACAGAACTAAGGAGGCC	339
QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	340	TGTAGCTCTGGACTAAGTTTGGCCGCGAGGACCAAGTTGAACACCTTGAAGCT	399
QY	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
Db	400	AGCTTTGAAACTTGACGCTATGGCTGGGTGGAGATGGATTCGTGTCATCTCTAGGATT	459
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120

Db	460	AGCCCAAAACCCAGGTGGGAAATAATGGGTGGGTGCTCTGATTGGAGAGTTCAGTG	519
QY	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	520	AGCCGACAGTTTGGAGCCTATTGTTTACAACCTCATCTGATCTTGACTAACTCGTGCA	579
QY	141	ProGluIleIleThrThrIleAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	580	CCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACAACAACA	639
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	640	GAATTTATTGTCAGTGACAGTACCTACTCGGTGGATCCCTTACTCTACATACCTGCC	699
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Db	700	CCTACTACT	759
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	760	TGTGTACAGAAAGTTTATGGAAACTAGCAACCATGTCTACAGAACTGAACCATTTGTT	819
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	820	GAAATAAAGCAGCATTCAGNATGAGCTGCTGGTTTGGAGGTGTCCTCCACGGCTCTG	879
QY	241	LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	880	CTAGTGCTTGCT	939
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	940	AGGTATGTGAAGGCT	999
QY	281	LysValValLysGluGluLysAlaAlaAsnAspSerAsnProAsnGluGluSerLysLys	300
Db	1000	AAAGTAGTAAAGGAGGAGAGGCCANTATGACCACTTATGAGCAATCAANGAAACT	1059
QY	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1060	GATAAAACCCAGAGAGTCCAAGAGTCCAAGAAACTACCGTGGATGCTCGGAAGCT	1119
QY	321	GluVal 322	
Db	1120	GAAGTT 1125	
RESULT 9			
ID	ABS74380		
XX	ABS74380 standard; cDNA; 2372 BP.		
AC	ABS74380;		
XX			
DT	10-DEC-2002 (first entry)		
XX			
DE	Human cDNA encoding secreted/transmembrane protein PRO263.		
XX			
KW	Human; ss; gene; secreted protein; transmembrane protein; antirheumatic;		
KW	antiarthritic; osteopathic; sports-related joint problem;		
KW	articular cartilage defect; osteoarthritis; rheumatoid arthritis.		
OS	Homo sapiens.		
XX			
PN	US2002119130-A1.		
XX			
PD	29-AUG-2002.		
XX			
PF	06-DEC-2001; 2001US-00006867.		
XX			
PR	29-OCT-1997; 97US-0063435P.		
PR	29-OCT-1997; 97US-0064215P.		
PR	22-APR-1998; 98US-0082797P.		
PR	29-APR-1998; 98US-0083495P.		

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PR 15-MAY-1998; 98US-0085579P.
PR 02-JUN-1998; 98US-0087759P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088029P.
PR 10-JUN-1998; 98US-0088030P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 11-JUN-1998; 98US-0088863P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089653P.
PR 19-JUN-1998; 98US-0089552P.
PR 22-JUN-1998; 98US-0090246P.
PR 24-JUN-1998; 98US-0090444P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 02-JUL-1998; 98US-0091628P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097979P.
PR 01-SEP-1998; 98US-0098749P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100930P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101475P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101916P.
PR 30-SEP-1998; 98US-0102570P.
PR 06-OCT-1998; 98US-0103449P.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021194.
PR 22-DEC-1999; 99WO-US030720.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032378.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.

XX (GETH ) GENENTECH INC.
PA Raton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX WPI; 2002-731348/79.
DR P-PSDB; ABG95853.
XX
PT New isolated secreted and transmembrane PRO polypeptide useful for
PT modulating biological activity of a cell, or for treating sports-related
PT joint problems, osteoarthritis or rheumatoid arthritis.
XX Claim 2; Fig 5; 399pp; English.
XX
CC The invention relates to an isolated secreted and transmembrane PRO
CC polypeptide having 80 % sequence identity to a sequence appearing as
CC ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
CC extracellular domain of the proteins with their associated signal peptide
CC or lacking its associated signal peptide. Also included are the nucleic
CC acids encoding the proteins, vectors, host cells, fusion proteins and
CC antibodies which specifically bind to the proteins. The proteins are
CC useful for detecting a polypeptide designated as A, B, C or D in a sample
CC suspected of containing an A, B, C or D polypeptide, by contacting the
CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
CC and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide
CC conjugate in the sample, where the formation of the conjugate is
CC indicative of the presence of an A, B, C or D polypeptide in the sample,
CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
CC H or I polypeptide is labeled with a detectable label or is attached to a
CC solid support. The proteins are useful for linking a bioactive molecule
CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
CC or I, or antibodies against them are useful for modulating a biological
CC activity of a cell expressing a polypeptide designated as A, B, C or D or
CC E, F, G, H, or I. The cell is killed. The proteins are useful for
CC identifying agonists or antagonists, for the preparation of a medicament
CC useful in the treatment of a condition which is responsive to the
CC proteins, as molecular weight markers for protein electrophoresis
CC purposes, and as therapeutic agents for treating sports-related joint
CC problems, articular cartilage defects, osteoarthritis or rheumatoid
CC arthritis. Nucleic acids encoding the proteins are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of anti-sense RNA and DNA, for the preparation of the proteins, to
CC generate transgenic or knockout animals which are useful in the
CC development and screening of therapeutic useful reagents, for chromosome
CC identification, and in gene therapy. The antibody is useful as a
CC therapeutic agent, in a diagnostic assay and for affinity purification of
CC the protein from recombinant cell culture natural sources. The present
CC sequence encodes a novel secreted or transmembrane protein of the
CC invention.
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4,04e-146 Length: 2372
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-079-111-1 (1-322) x ABS74380 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
DB 160 ATGGCCAGGTGCTTCAGCGCTGGTGTGTCTTCTCACTTCATCGGACCAAGGGTCTCTG 219
```

```
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db |||||
QY 220 GTCCAGGCTCTTTGGTGAGAAAGCTTTCCATCCAGTGTCAGCAATATGGGG 279
Db |||||
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db |||||
QY 280 ATCACCTTGTGAGAAAAGGCGAACAGCAGCTGAATTCACAGAAGCTAAGGAGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db |||||
QY 340 TGTAGGCTGTGGGACTAAGTTTGGCGCGCAAGACCAAGTTTCAAAACAGCCTTGAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle 100
Db |||||
QY 400 AGCTTTGAACCTTGCAGCTATGCTGGTGGAGATGGATTCGTGTCACTCTAGGAT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db |||||
QY 460 AGCCCAAAACCCCAAGTGTGGAAAAATGGGTGGTGCTCTGATTTGGAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaIalalCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db |||||
QY 520 AGCCGACAGTTTGCAGCCTATTGTTCAACTCATCTGATCTTGGACTAACTCGTGCAAT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db |||||
QY 580 CCAGAAATATACACCAAGATCCATATTCACACTCAAACTGCAACACAAACAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db |||||
QY 640 GAATTTATTGTCACTGACAGTCACTACTCGTGGCATCCCTTCTTCTACAAATACCTGCC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db |||||
QY 700 CCTACTACTACTCTCTCTCTCCAGCTTCCACTTCTATTCACGAGAGAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db |||||
QY 760 TGTGTACAGAAGTTTATGGAACCTAGCACCATGCTACAGAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db |||||
QY 820 GAAATATAAGCAGCATTCAAGATGAAGCTGCTGGGTTTGGAGGTGCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db |||||
QY 880 CTAGTCCTTGTCTCTCTCTCTTGTGGTGCAGCTGGTCTTGGATTTTGTATGTCAAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db |||||
QY 940 AGGTATGTGAAGCCCTTCCCTTTTCAACAAGAAATCAGCAGGAAGGAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db |||||
QY 1000 AAAGTAGTAAAGGAGAGAGGCAATGATAGCAACCTAATCAGGAATCAAGAAAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db |||||
QY 1060 GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCCTGCGTGAAGCT 1119
QY 321 GluVal 322
Db |||||
QY 1120 GAAGTT 1125
```

## RESULT 10

ABL88087

ID ABL88087 standard; cDNA; 2372 BP.

XX

AC ABL88087;

XX

DT 16-MAY-2002 (first entry)

XX

DE Human PRO263 cDNA sequence SEQ ID NO:31.

Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerability; arteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; arteriosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; rheumatoid arthritis; myocardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping; gene; ss.

XX Homo sapiens.

WO200200690-A2.

PD 03-JAN-2002.

XX 20-JUN-2001; 2001WO-US019692.

XX 23-JUN-2000; 2000US-0211637P.

PR 20-JUL-2000; 2000US-0219556P.

PR 25-JUL-2000; 2000US-0220624P.

PR 25-JUL-2000; 2000US-0220664P.

PR 28-JUL-2000; 2000WO-US020710.

PR 02-AUG-2000; 2000US-0222695P.

PR 17-AUG-2000; 2000US-00643657.

PR 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.

PR 07-SEP-2000; 2000US-0230978P.

PR 18-SEP-2000; 2000US-00664610.

PR 18-SEP-2000; 2000US-00665350.

PR 24-OCT-2000; 2000US-0242922P.

PR 08-NOV-2000; 2000US-00709238.

PR 08-NOV-2000; 2000WO-US030952.

PR 10-NOV-2000; 2000WO-US030873.

PR 01-DEC-2000; 2000WO-US032678.

PR 20-DEC-2000; 2000US-00747259.

PR 20-DEC-2000; 2000WO-US034956.

PR 22-JAN-2001; 2001US-00767609.

PR 28-FEB-2001; 2001US-00796498.

PR 28-FEB-2001; 2001WO-US006520.

PR 01-MAR-2001; 2001WO-US006666.

PR 09-MAR-2001; 2001US-00802706.

PR 14-MAR-2001; 2001US-00808689.

PR 22-MAR-2001; 2001US-00816744.

PR 05-APR-2001; 2001US-00828366.

PR 10-MAY-2001; 2001US-00854208.

PR 10-MAY-2001; 2001US-00854280.

PR 25-MAY-2001; 2001US-00866028.

PR 25-MAY-2001; 2001US-00866034.

PR 25-MAY-2001; 2001WO-US017092.

PR 30-MAY-2001; 2001US-00870574.

PR 30-MAY-2001; 2001WO-US017443.

PR 01-JUN-2001; 2001WO-US017800.

(GETH ) GENENTECH INC.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;

PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;

PI Stephan JF, Williams CK, Williams PM, Wood WI, Ye W;

XX WPI; 2002-090516/12.

DR P-PSDB; ABB84832.

XX

PT One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.

XX Claim 2; Fig 31; 565pp; English.

CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to

CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,

CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic

CC activities, and can be used in gene therapy. The PRO polynucleotides,



PR 30-MAY-2001; 2001WO-US017443.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 20-JUN-2001; 2001WO-US019692.  
 XX (GETH ) GENENTECH INC.  
 PA (BAKE ) BAKER K P.  
 PA (FERR ) FERRARA N.  
 PA (GERR ) GERBER H.  
 PA (GERR ) GERRITSEN M E.  
 PA (GODD ) GODDARD A.  
 PA (GODO ) GODOWSKI P J.  
 PA (GURN ) GURNEY A L.  
 PA (HILL ) HILLAN K J.  
 PA (MARS ) MARSTERS S A.  
 PA (PANJ ) PAN J.  
 PA (PAON ) PAONI N F.  
 PA (STEP ) STEPHAN J F.  
 PA (WATA ) WATANABE C K.  
 PA (WILL ) WILLIAMS P M.  
 PA (WOOD ) WOOD W I.  
 XX  
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
 XX  
 DR WPI; 2002-171999/22.  
 DR P-PSDB; ABB95438.  
 XX  
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal.  
 XX  
 PS Claim 1; Fig 31; 567pp; English.  
 XX  
 CC The present invention provides the protein and coding sequences of human  
 CC PRO proteins. These are useful for treating or diagnosing a  
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
 CC hypertrophy, trauma, cancer, age-related macular degeneration,  
 CC atherosclerosis, hypertension, arterial stenosis, rheumatoid arthritis,  
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
 CC healing. The present sequence is a coding sequence of the invention  
 XX  
 SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 4,04e-146 Length: 2372  
 Score: 1657.00 Matches: 322  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-10-079-111-1 (1-322) x ABL95576 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrrPThrArgLeuLeu 20  
 DB 160 ATGCCAGGTGCTTCAGCTGGTGGTCTCTCACTTCCATCTCGACACGAGGCTCTG 219  
 QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40  
 DB 220 GTCCAAAGCTCTTTGGTGGCAGAAAGAGCTTCCATCAGGTGTCATGCAGAAATATGGGG 279  
 QY 41 IleThrLeuValSerLysLysAlaAsnGlnLeuAsnPheThrGluAlaLysGluAla 60  
 DB 280 ATCACCTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTTCCACAGAGCTAAGGAGGCC 339  
 QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
 DB 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 399  
 QY 81 SerPheGluThrCysSerTyrGlyTrrPValGlyAspGlyPheValValIleSerArgIle 100

Db 400 AGCTTTGAACCTTGACGCTATCGCTGGTGGAGATGGATTGGTGTCTCTAGGATT 459  
 QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrrPlysValProVal 120  
 Db 460 AGCCCAAAACCCCAAGTGTGGGAAAATGGGTGGGTGTCTGATTGGGAAGGTTCCAGTG 519  
 QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrrPThrAsnSerCysIle 140  
 Db 520 AGCCGACAGTGTTCAGCCCTATTGTTACAACTCATCTGATACCTTGGACTAACTCGTCAT 579  
 QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
 Db 580 CAGAAATTTATCACCAAAAGATCCCATATTCACACTCAAACTGCACACAAACAA 639  
 QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
 Db 640 GAATTTATTGTTCAGTGACAGTACCTACTCGTGGCATCCCTTACTCTACAAATACCTGCC 699  
 QY 181 ProThrThrThrProProAlaSerThrSerIleProArgArgLysLysLeuIle 200  
 Db 700 CCTACTACTACT 759  
 QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
 Db 760 TGTGTACAGAAAGTTTTATGGAACTAGACCAATGTCTACAGAACTGAACCATTTGTT 819  
 QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
 Db 820 GAAATAAAGCAGCATTTCAAGATGAAGCTGTGGGTTTGGAGGTGCCCCACGGCTCTG 879  
 QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
 Db 880 CTAGTGTCT 939  
 QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280  
 Db 940 AGGTATGTGAAGGCTTCCCTTTTACAAACAGAAATCAGCAGAGGAATATCGAAACC 999  
 QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
 Db 1000 AAAGTAGTAAAGGAGGAGGAGGCAATGATAGCACTTAATGAGGAATCAAAGAAACT 1059  
 QY 301 AspLysAsnProGluLysSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
 Db 1060 GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCTCTGGAAGCT 1119  
 QY 321 GluVal 322  
 Db 1120 GAAGTT 1125  
 RESULT 12  
 ACAS9060  
 ID ACAS9060 standard; cDNA; 2372 BP.  
 XX ACAS9060;  
 AC ACAS9060;  
 XX  
 DT 16-JUN-2003 (first entry)  
 XX  
 DE Human PRO polynucleotide #36.  
 XX  
 KW Human; PRO; gene; ss; secreted polypeptide; transmembrane polypeptide;  
 KW pathological disorder; cardiac insufficiency disorder; protein secretion;  
 KW pancreas; diabetes; gastrointestinal mucosa; mucosal lesion; psoriasis;  
 KW skin disease; keratinocyte differentiation; epithelial cancer; tumour;  
 KW lung squamous cell carcinoma; epidermoid carcinoma; vulva; glioma;  
 KW cytostatic; cardiac; endocrine; antidiabetic; gastrointestinal;  
 KW antiulcer; dermatological; vulnary.  
 XX Homo sapiens.  
 OS  
 XX US2002146709-A1.  
 PN  
 XX 10-OCT-2002.  
 PD





```
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
DB 460 AGCCCCAAACCCCAAGTGTGGGAAAATGGGGTGGGTCTCTGATTGGGAAGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
DB 520 ASCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACCTTGAGCTAACTCGTGCAAT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
DB 580 CCAGAAATATTACCAACCAAGATCCATATTCAACACTCAAACTGCAACACAAACAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
DB 640 GAATTATTATTGTCAGTGACAGTACTACTCGGTGGCATCCCTTACTCTCAATACCTGTC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
DB 700 CTTACTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
DB 760 TGTGTACACAGAAGTTTTTATGGAACCTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
DB 820 GAAATTAAGCAGCATTCAAGATGAAGCTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
DB 880 CTAGTGCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
DB 940 AGGTATGTGAAGGCTCTCCCTTTTACAAACAAGATCAGCAGAGGAAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
DB 1000 AAAGTAGTAGAGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1059
QY 301 AspLysAsnProGluLysSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
DB 1060 GATATAAACCCAGAGAGTCCAGAGTCCAGCAAAACTACCGTGGCATGCTGGAGCT 1119
QY 321 GluVal 322
DB 1120 GAAGTT 1125
RESULT 13
ACAS8457
ID ACAS8457 standard; cDNA; 2372 BP.
XX AC
AC ACAS8457;
DT AC
XX 10-JUN-2003 (first entry)
DE cDNA encoding human PRO polypeptide #36.
KW Human; secreted and transmembrane protein; PRO polypeptide; cancer;
KW Alzheimer's disease; ischaemia; cytosstatic; nootropic; vasotropic;
KW neuroprotective; gene; ss.
XX OS
XX Homo sapiens.
XX PN
XX US2002192659-A1.
XX PD
XX 19-DEC-2002.
XX PF
XX 10-JUL-2001; 2001US-00902853.
XX PR
XX 17-SEP-1997; 97US-0059113P.
XX PR
XX 17-SEP-1997; 97US-0059115P.
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PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 01-DEC-1998; 98WO-US025108.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
```

PR 02-JUN-2000; 2000WO-US015264.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 18-SEP-2000; 2000US-00665350.

XX (GETH ) GENENTECH INC.

XX Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;  
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;  
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;  
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;  
 PI Williams PM, Wood WI;  
 XX WPI; 2003-361832/34.  
 DR P-PSDB; ABU71480.

XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or  
 PT PRO1868, useful in molecular biology, chromosome and gene mapping, in  
 PT generating antisense RNA and DNA, and in gene therapy.

XX Claim 2; Fig 73; 474pp; English.

XX The present invention relates to the isolation of novel human secreted  
 CC and transmembrane proteins (PRO polypeptides), and the polynucleotide  
 CC sequences encoding them. The polynucleotide sequences are useful in  
 CC molecular biology, as hybridisation probes, in chromosome and gene  
 CC mapping, in generating antisense RNA and DNA, and in gene therapy. The  
 CC polynucleotide sequences may also be used in preparing PRO polypeptides  
 CC by recombinant techniques, and in generating either transgenic animals or  
 CC knock-out animals which, in turn, are useful in the development and  
 CC screening of therapeutically useful reagents. The PRO polypeptides or  
 CC their antibodies are useful in preparing a medicament for treating a  
 CC condition responsive to the polypeptide or antibody, such as cancer,  
 CC Alzheimer's disease or ischaemia, and in various diagnostic assays. The  
 CC present sequence encodes a human PRO polypeptide of the invention

SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 4,04e-146 Length: 2372  
 Score: 1657.00 Matches: 322  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 7 Gaps: 0

US-10-079-111-1 (1-322) x ACA58457 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20  
 Db 160 ATGGCCAGGTGCTTCAGCCTGGTGTTCCTTCCTCCTCCATTCCTGACACGAGGCTCCTG 219  
 QY 21 ValGlnGlySerLeuArgAlaGluLeuLeuSerIleGlnValSerCysArgIleMetGly 40  
 Db 220 GTCCAAAGGCTCTTTCGCTGCAGAAAGAGCTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279  
 QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
 Db 280 ATCAACCTTGAGCAAAAGCGACACGAGCTGAAATTCACAGAACTAAGGAGGCC 339  
 QY 61 CysArgLeuLeuGlySerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
 Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 399  
 QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100  
 Db 400 AGCTTTGAAACTTGACGCTATCGCTGGGTGGAGATGGATTCGTGGTCACTCTAGGAT 459  
 QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
 Db 460 AGCCCCAAACCCCAAGTGTGGHAAATGGGTGGGTGCTCTGATTTGGAAGGTTCCAGTG 519  
 QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140

Db 520 AGCCGACAGTTTGCAGCCCTATTGTTACAACCTCATCTGATCTTGGACTTAACCTCGTGATT 579  
 QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
 Db 580 CCAGAAATTTATCACCAACCAAGATCCCATATTCAACACTCAAACTCAACACACAAACA 639  
 QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
 Db 640 GAAATTTATTGTTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTCAATACCTGCC 699  
 QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200  
 Db 700 CCTACTACTACT 759  
 QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
 Db 760 TGTGTTCACAGAAAGTTTTATGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819  
 QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
 Db 820 GAAATTAAGAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879  
 QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
 Db 880 CTAGTGTCTGCT 939  
 QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
 Db 940 AGGTATGTGAAGCCTTCCCTTTTACAAACAAGAAATCAGCAGAGGAAATGATCGAAACC 999  
 QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluLysSerLysLys 300  
 Db 1000 AAAGTAGTAAAGAGGAGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAGAAACT 1059  
 QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
 Db 1060 GATAAAACCCAGAGAGTCCAGAGTCCAGCAAAACTACCGTGCATGCTGGAGCT 1119  
 QY 321 GluVal 322  
 Db 1120 GAAGTT 1125  
 RESULT 14  
 ACA60164  
 ID ACA60164 standard; cDNA; 2372 BP.  
 XX ACA60164;  
 AC ACA60164;  
 DT 12-JUN-2003 (first entry)  
 XX  
 DE Human cDNA for secreted/transmembrane protein PRO263.  
 XX  
 KW Human; ss; gene; secreted protein; transmembrane protein; PRO;  
 KW gene therapy; chromosome identification; chromosome marker.  
 XX Homo sapiens.  
 OS  
 XX  
 XX US2003003530-A1.  
 PN  
 XX  
 XX 02-JAN-2003.  
 PD  
 XX  
 PF 11-JUL-2001; 2001US-00904011.  
 XX  
 PR 17-SEP-1997; 97US-0059113P.  
 PR 17-SEP-1997; 97US-0059115P.  
 PR 17-SEP-1997; 97US-0059117P.  
 PR 17-SEP-1997; 97US-0059119P.  
 PR 17-SEP-1997; 97US-0059121P.  
 PR 17-SEP-1997; 97US-0059122P.  
 PR 17-SEP-1997; 97US-0059124P.  
 PR 18-SEP-1997; 97US-0059263P.  
 PR 18-SEP-1997; 97US-0059266P.

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PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063970P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 01-DEC-1998; 98WO-US025108.
PR 08-SEP-1999; 98WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 05-SEP-1999; 99WO-US021547.
PR 29-NOV-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX
XX
( GETH ) GENENTECH INC.

```

PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;  
 PI Filwaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;  
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin LJ;  
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;  
 PI Williams PM, Wood WI;  
 XX WPI: 2003-329602/31.  
 DR P-PSDB; ABU71926.  
 XX  
 PT New transmembrane polypeptides and nucleic acids encoding the  
 PT polypeptides, useful in gene therapy, in chromosome identification, as  
 PT chromosome markers, in generating probes and in tissue typing.  
 XX  
 PS Claim 2; Fig 73; 484pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid with at least 80%  
 CC nucleic acid sequence identity to a nucleotide sequence encoding one of  
 CC 61 secreted/transmembrane polypeptides, or PRO polypeptides or encoding a  
 CC PRO protein extracellular domain. Also included are a vector comprising a  
 CC the PRO nucleic acid, a host cell comprising the vector, producing a PRO  
 CC polypeptide (by culturing the host cell for the expression of the PRO  
 CC polypeptide, and recovering the PRO polypeptide from the cell culture),  
 CC an isolated PRO polypeptide (having at least 80% sequence identity to:  
 CC a) an amino acid sequence selected from the 61 PRO proteins; (b) an amino  
 CC acid sequence encoded by a nucleic acid molecule deposited with an ATCC  
 CC number (detailed in the specification); or (c) an extracellular domain of  
 CC a PRO polypeptide or to a PRO polypeptide lacking its associated signal  
 CC peptide), a chimeric molecule comprising a PRO polypeptide of fused to a  
 CC heterologous amino acid sequence, an anti-PRO antibody, detecting a  
 CC linking a bioactive molecule to a cell expressing the polypeptide, and  
 CC modulating at least one biological activity of a cell expressing a PRO245 or  
 CC or PRO1868. Nucleic acids which encode PRO can be used to generate either  
 CC transgenic animals or knock-out animals which may be used in the  
 CC development and screening of therapeutically useful reagents. The nucleic  
 CC acids may also be used in gene therapy, in chromosome identification, as  
 CC useful as molecular markers for protein electrophoresis, and the isolated  
 CC nucleic acids may be used for recombinantly expressing those markers. The  
 CC PRO polypeptides and nucleic acids may also be used in tissue typing.  
 CC Anti-PRO antibodies are useful in diagnostic assays for PRO, and in  
 CC affinity purification of PRO from recombinant cell culture or natural  
 CC sources. The present sequence encodes a PRO protein  
 XX  
 SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 4,04e-146 Length: 2372  
 Score: 1657.00 Matches: 322  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 7 Gaps: 0

US-10-079-111-1 (1-322) x ACA60164 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20  
 |||||  
 Db 160 ATGGCCAGGTGCTTCAGGCTGGTGTGTTCTTCTCACTCCATCTGCACGAGGCTCCTG 219  
 |||||

QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40  
 |||||  
 Db 220 GTCCAAGGCTCTTTTCGTGCAGAAAGAGCTTTCCATCCAGGTGTCTATGACAGATTATGGGG 279  
 |||||

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
 |||||  
 Db 280 ATCACCCCTGTGAGCAAAAAGCGACGAGCTGTAATTTTCACAGAGCTTAAGAGGCC 339  
 |||||

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
 |||||  
 Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGCAAGTTGAAACAGCCTTGAAGCT 399  
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QY 81 SerPheGluThrCysSerTyGlyTrpValGlyAspGlyPheValValIleSerArgIle 100

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Db 400 ACCTTTGAACTTGACGATATGCTGGGTGGAGATGGATTCGTGTCATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAAAACCCCAAGTGTGGGAAAATGGGTGGGTGCTCTGATTTGGAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaIatYrCysTyrAsnSerSerAspThrThrAsnSerCysIle 140
Db 520 AGCCGACAGTTGACGCCATTGTTACAACTCATCTGATCTTGGACTTAACCTCGTGCAAT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTTATCACCACCAAGATCCATATTCACACACTCAAACTGCAACACAAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTCAATACCTGCC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CTTACTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTCACAGAGAGTTTTTATGGAACCTAGCACCATGCTACAGAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATTAAGACAGCAATCAAGATGAAGCTGCTGGGTTTGGAGGTGCTCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCTTCCTCTTTTACAAACAGAAATCAGCAGAAAGAAATGATCGAAAC 999
QY 281 LysValValLysGluLysAlaAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAGAGAGAGAGGCAATAGTAGCAACCTTAATGAGGAATCAAGAAAACT 1059
QY 301 AspLysAsnProGluLysSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAATCCAGAGAGTCCAAAGAGTCCAGCAAAACTTACCGTGCATGCCCTGGAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 15
ACD07564
ID ACD07564 standard; cDNA; 2372 BP.
XX
AC ACD07564;
XX
DT 07-AUG-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO263 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; pharmaceutical;
KW diagnostic; biosensor; bioreactor; Parkinson's disease;
KW Alzheimer's disease; inflammation; nephritis; wound healing;
KW nerve repair; collateral blood vessel formation; cancer;
KW colorectal cancer; haemorrhage; rheumatoid arthritis; diabetes;
KW cirrhosis; fibrosis; restenosis; dermal fibrotic condition; keloid;
KW scarring; ischaemia; stroke; hypertension; heart attack; atherosclerosis;
KW infertility; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN US2002197671-A1.
```

PR 11-FEB-2000; 2000WO-US003565.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005941.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 24-AUG-2000; 2000WO-US023228.  
PR 18-SEP-2000; 2000US-00665350.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;  
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;  
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Klijavin IJ;  
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;  
PI Williams PM, Wood WI;  
XX  
WPI: 2003-370793/35.  
DR P-PSDB; ABO01809.  
XX  
XX New genes and secreted and transmembrane polypeptides (e.g. PRO245 or  
PT PRO335), useful for treating or diagnosing e.g. Alzheimer's disease,  
PT cancers, hemorrhage, rheumatoid arthritis, diabetes, cirrhosis, ischemia  
PT or strokes.  
XX  
XX Claim 2; Fig 73; 482pp; English.

XX The invention describes a new isolated nucleic acid molecule comprising  
CC the full length coding sequence of the DNA deposited with the American  
CC Type Culture Collection (e.g. ATCC Deposit No. 209258), or a sequence  
CC with at least 80% identity to a DNA encoding a PRO polypeptide comprising  
CC any of 61 sequences having 164-1119 amino acids fully defined in the  
CC specification. The PRO polypeptides or polynucleotides are useful as  
CC pharmaceuticals, diagnostics, biosensors or bioreactors. These are  
CC particularly useful for detecting or treating e.g. Parkinson's disease,  
CC Alzheimer's disease, inflammations, nephritis, wound healing, nerve  
CC repair, collateral blood vessel formation, cancers (e.g. colorectal  
CC cancer), hemorrhage (or reduce risk for haemorrhage), rheumatoid  
CC arthritis, diabetes, cirrhosis of the liver, fibrosis of the lungs,  
CC ischaemia, strokes, hypertension, heart attacks, atherosclerosis, or  
CC infertility in mammals (e.g. humans, dogs, cats, cattle, horses, sheep,  
CC pigs, goats, or rabbits) The PRO polypeptides are useful as targets for  
CC therapeutic intervention in these diseases, and diagnostic determination  
CC of the presence of these diseases. The PRO polypeptides are also useful  
CC as molecular weight markers, or for chromosome identification. The PRO  
CC genes are useful as hybridisation probes, or for screening libraries of  
CC human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene  
CC therapy, particularly for replacing a defective gene. This sequence  
CC encodes a novel human secreted and transmembrane PRO polypeptide  
XX

SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	4,04e-146	Length:	2372
Score:	1657.00	Matches:	322
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	7	Gaps:	0

US-10-079-111-1 (1-322) x ACD07564 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20  
Db 160 ATGGCCAGGTGCTTCAGCTGGTGTGCTTCTCACTTCCATCTGGACACGAGGCTCCCTG 219  
QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40  
Db 220 GTCCAAGGCTCTTTCGGTGCAGAGAGCTTTCATCCAGGTGTCATGCAGATTATGGGG 279

QY	41	IleThrLeuValSerIleLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	280	ATCACCCCTTGTGAGCAAAAAGGCGAACACAGCAGCTGAATTTCAAGAGCTTAAGAGGCC	339
QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGlnThrAlaLeuLysAla	80
Db	340	TGTAGGCTGCTGGGACTAAGTTTGGCCGCGCAAGGCAAGTGTGAACACAGCCTTTGAAAGCT	399
QY	81	SerPheGluThrCysSerTrpValGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
Db	400	AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTCGTGGTCACTCTCAGGATT	459
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
Db	460	AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGTGGTCTGATTTGGAAAGTTCCAGTG	519
QY	121	SerArgGlnPheAlaAlaIleCysTrpAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	520	AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTTGGACTAATCTCGTCATT	579
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	580	CCAGAAATTTATCACCAACCAAGATCCATATTTCAACACTCAACTGCACACAAACAACA	639
QY	161	GluPheIleValSerAspSerThrTrpSerValAlaSerProTrpSerThrIleProAla	180
Db	640	GAATTTATTGTGAGTGACAGTACTACTCGTGGCATCCCTTACTCTCAATAATACCTGCC	699
QY	181	ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Db	700	CTTACTACTACT	759
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	760	TGTGTGCACAGAAGTTTATGGAACCTAGCACCATGTCTACAGAACTGAAACCATTTGTT	819
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	820	GAATAATAAGCAGCATTTCAAGAAATGAAGTGTGGTGGTGGTGGTGGTGGTGGTGGT	879
QY	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTrpValLys	260
Db	880	CTAGTGTCTTCT	939
QY	261	ArgTrpValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	940	AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCACAGAGGAATGATCGAAACC	999
QY	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
Db	1000	AAAGTAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1059
QY	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1060	GATAAAACCCCAAGAGAGTCCAAGAGTCCAAGAGTCCAAGAGTCCAAGAGTCCAAGAGT	1119
QY	321	GluVal 322	
Db	1120	GAAAGTT 1125	

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Job time : 515 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 15, 2004, 21:04:16 ; Search time 3065 Seconds  
(without alignments)  
3137.234 Million cell updates/sec

Title: US-10-079-111-1  
Perfect score: 322  
Sequence: 1 MARCSVLVLLTSIWTRLL.....NPESKSPKTTVRCLEAEV 322

Scoring table: OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Word size: 12

Total number of hits satisfying chosen parameters: 101

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

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-NORM=ext -HAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10079111@cgn\_1\_13437@runat\_13092004\_102225\_13998 -NCPU=6 -ICPU=3  
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Database :

EST:\*

1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pin:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mas:\*  
25: em\_gss\_pro:\*  
26: em\_gss\_rod:\*  
27: em\_gss\_pbg:\*  
28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	322	100.0	1154	9	AL550279	AL550279 AL550279
2	288	89.4	1015	9	AL552299	AL552299 AL552299
3	280	87.0	1201	9	AL546669	AL546669 AL546669
4	285	82.3	1201	9	AL551020	AL551020 AL551020
5	237	73.6	911	9	AL546217	AL546217 AL546217
6	237	73.6	911	9	AL543874	AL543874 AL543874
7	237	73.6	913	13	AX459046	AX459046 BX459046
8	237	73.6	1014	9	AL553858	AL553858 AL553858
9	237	73.6	1201	9	AL544430	AL544430 AL544430
10	237	73.6	1201	9	AL547774	AL547774 AL547774
11	237	73.6	1201	13	AX402505	AX402505 BX402505
12	227	70.5	970	9	AL550615	AL550615 AL550615
13	225	69.9	1201	13	AX366718	AX366718 BX366718
14	221	68.6	1201	9	AL546623	AL546623 AL546623
15	219	68.0	1151	9	AL550829	AL550829 AL550829
16	217	67.4	1172	9	AL552127	AL552127 AL552127
17	191	59.3	972	9	AL549512	AL549512 AL549512
18	181	56.2	863	12	BI761420	BI761420 603044235
19	168	52.2	1201	9	AL550621	AL550621 AL550621
20	155	48.1	760	14	CB959809	CB959809 AGENCOURT
21	153	47.5	864	9	AL545331	AL545331 AL545331
22	136	42.2	802	14	CB994314	CB994314 AGENCOURT
23	131	40.7	1116	9	AL552661	AL552661 AL552661
24	125	38.8	596	9	AA046671	AA046671 zF12409.r
25	119	37.0	974	14	CB988195	CB988195 AGENCOURT
26	116	36.0	1074	9	AL552777	AL552777 AL552777
27	114	35.4	465	14	H69328	H69328 yu19a09.r1
28	113	35.1	368	10	BG012717	BG012717 IL5-GN023
29	112	34.8	872	12	BG541447	BG541447 602570880
30	107	33.2	801	12	BG483354	BG483354 602504223
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33	101	31.4	437	14	CA406980	CA406980 1003129.H
34	97	30.1	746	14	CD238639	CD238639 FNPBCH08
35	95	29.5	473	14	CB269023	CB269023 1007930.H
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38	89	27.6	877	12	BI763579	BI763579 603050140
39	89	27.6	1143	9	AL574194	AL574194 AL574194
40	88	27.3	865	14	CD106276	CD106276 AGENCOURT
41	86	26.7	757	14	CB229605	CB229605 AGENCOURT
42	84	26.1	1201	9	AL546565	AL546565 AL546565
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47	70	21.7	990	13	BX418211	BX418211 BX418211
48	58	18.0	790	29	AY411058	AY411058 Pan trogl
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52	54	16.8	1201	9	AL553712	AL553712 AL553712
53	53	16.5	1073	9	AL552625	AL552625 AL552625
54	51	15.8	960	9	AL553920	AL553920 AL553920
55	50	15.5	1201	9	AL571871	AL571871 AL571871
56	47	14.6	390	14	H78909	H78909 yu11d03.r1
57	46	14.3	318	14	R71437	R71437 Y151e04.r1
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59	43	13.4	380	9	AA081350	AA081350 zn33h09.r
60	42	13.0	1157	9	AL575514	AL575514 AL575514
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68	32	9.9	1298	14	CF110966	68	9.9	1298	14	CF110966	Shultzomi	/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
69	30	9.3	1201	9	AL546590	69	9.3	1201	9	AL546590	AL546590	/notes="1st strand cDNA was primed with a NotI-oligo(dT)
70	29	9.0	499	10	BE198670	70	9.0	499	10	BE198670	u81c01.y	primer. Five prime end cloned, double-strand cDNA was
71	29	9.0	579	9	AI391129	71	9.0	579	9	AI391129	mc02a12.y	digested with Not I and cloned into the Not I and EcoR V
72	29	9.0	2607	11	AK004726	72	9.0	2607	11	AK004726	Mus muscu	sites of the pCMVSPORT 6 vector. Library was normalized."
73	28	8.7	227	9	AA029420	73	8.7	227	9	AA029420	ze96c11.r	
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75	27	8.4	1070	14	CB989089	75	8.4	1070	14	CB989089	AGENCOURT	
76	27	8.4	1201	9	AL570563	76	8.4	1201	9	AL570563	AL570563	Alignment Scores:
77	26	8.1	420	10	BE767810	77	8.1	420	10	BE767810	CM3-GN004	Pred. No.: 7.84e-289
78	26	8.1	540	12	BM253102	78	8.1	540	12	BM253102	BM253102	Score: 322.00
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82	24	7.5	229	9	AA347305	82	7.5	229	9	AA347305	EST53585	Mismatches: 0
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86	22	6.8	1048	13	BX378468	86	6.8	1048	13	BX378468	BX378468	QY 1 MetAlaArgCysPheSerLeuValLeuLeuThr-SerIleTrpThrThrArgLeuLeu 20
87	21	6.5	973	9	AL574433	87	6.5	973	9	AL574433	AL574433	Db 122 ATGCCAGGTGCTTCAGCCTGGTGTCTCTCATTCCATCTGGACCCAGAGGCTCTG 181
88	20	6.2	456	14	H93850	88	6.2	456	14	H93850	YV08a03.r1	QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
89	19	5.9	607	10	AW956729	89	5.9	607	10	AW956729	EST368799	Db 182 GTCACAGGCTCTTGGCTGCAGAGAGCTTCCATCCAGGTGTCATGCAGATATATGGGG 241
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93	18	5.6	800	29	AY411059	93	5.6	800	29	AY411059	Mus muscu	Db 302 TGTAGGCTGCTGGGACTAAGTTTGGCGGCAAGGACCAAGTTGAACAGCCTTGAAGCT 361
94	16	5.0	556	12	BM935573	94	5.0	556	12	BM935573	UI-M-BH3-	QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgile 100
95	16	5.0	1023	13	HY704927	95	5.0	1023	13	HY704927	HY704927	Db 362 AGCTTTGAAACTTGCAGCTATGCTGGTGGAGATGGATTCTGCTCATCTCTAGGATT 421
96	14	4.3	371	10	BE684197	96	4.3	371	10	BE684197	BE684197	QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValIleLeuIleTrpLysValProVal 120
97	14	4.3	449	10	BF041814	97	4.3	449	10	BF041814	BP250014B	Db 422 AGCCCAACCCCAAGTGTGGGAAAATGGGGTGGTCTCTGATTTGGAGAGTTCCAGTG 481
98	14	4.3	790	29	CC490282	98	4.3	790	29	CC490282	CH240_323	QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
99	14	4.3	824	29	CC551496	99	4.3	824	29	CC551496	CH240_436	Db 482 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTTGGACTTAACCTGTCATT 541
100	13	4.0	642	14	CB442342	100	4.0	642	14	CB442342	692918 MA	QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160

ALIGNMENTS

AL550279 Homo sapiens mRNA linear EST 31-MAY-2003

clone CS0DI039YJ06 5-PRIME, mRNA sequence.

AL550279

AL550279.2 GI:31272096

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1154)

Li, W.B., Gruber, C., Jesse, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:12887098.

Contact: Genoscope

Genoscope - Centre National de Sequencage

Bp 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5952.r For more information about this cluster, see http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DI039DE03QP1&cluster=5952.r. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DI039DE03QP1.

Location/Qualifiers

1. .1154

FEATURES	Source
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LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	



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QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 902 AGGTATGTGAAGGCTTCCTCTTTTAAACACAGAAATCAGCAGAGAAATGTCGAACC 961

QY 281 LysValValLysGluLysAlaAsnAspSerAsnProAsnGluLysSerLysLysThr 300
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QY 301 AspLysAsnProGluLysSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1022 GATAAAAACCCAGAGAGTCCAGAGTCCAGCAAAACTACCGTGGATGCTGGAGACT 1081

QY 321 GluVal 322
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RESULT 2
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DEFINITION
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clone CSODI069YN02 5-PRIME, mRNA sequence.
ACCESSION
AL552299
VERSION
AL552299.2 GI:31274114
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1015)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12891069.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI069DG01QPI&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI069DG01QPI.
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="CSODI069YN02"
/tissue type="PLACENTA COT 25-NORMALIZED"
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/notes="1st strand cDNA was primed with a NotI-oligo(dT)
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FEATURES
source
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ALIGNMENT SCORES:
Pred. No.: 3,03e-257 Length: 1015
Score: 288.00 Matches: 288
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 89.44% Indels: 0
DB: 9 Gaps: 0

US-10-079-111-1 (1-322) x AL552299 (1-1015)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrArgLeuLeu 20
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QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
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QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 264 ATCACCTTTGTGAGCAAAAGGCAACAGCAGCTGAATTTACAGAGACTAAGGAGGCC 323

QY 61 CysArgLeuLeuGlyLysSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
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QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
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QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerSerThrTrpThrAsnSerCysIle 140
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QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
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QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 804 GAAATTAAGCAGCAGCATTCAGAAATGAGCTGCTGGTTGGAGGTGTCCTCCACGGCTCTG 863

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 864 CTAGTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 923

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Db 924 AGGTATGTGAAGGCTTCCTCTTTTCAAAACAAGAAATCAGCAGAGAAATGATCGAAACC 983

QY 281 LysValValLysGluLysAla 288
Db 984 AAAGTAGTAAAGAGAGAGAGGCC 1007

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clone CSODI029YJ09 5-PRIME, mRNA sequence.
ACCESSION
AL546669
VERSION
AL546669.2 GI:31268502
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
JOURNAL

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Qy 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrrThrThrArgLeuLeu 20
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Db 158 GTCCAGGCTCTTTCGCTGCAGAGAGCTTTCATCCAGGTGTCTATGCGAGATTTATGGG 217
Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 218 ATCACCCCTGTGAGCAAAAGGCAACACGAGCTGAATTTTACACAGAAGCTTAAGAGGCC 277
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Db 278 TGTAGGCTGCTGGGACTAAGTTTGGCCGCGAAGGACCAAGTTGAACAGCCTTGAAGACT 337
Qy 81 SerPheGluThrCysSerTyrGlyTrrValGlyAspGlyPheValValIleSerArgIle 100
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Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrrLysValProVal 120
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Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
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Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
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Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 758 GAAAAATAAAGCAGCATTCAGAAATGAAGCTGCTGGGTGTTGGAGGTGTCCCAACGCTCTG 817
Qy 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLysPheCysTyrValLys 260
Db 818 CTAGTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 877
Qy 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
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Qy 281 Lys 281
Db 937 AAG 939

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RESULT 5  
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 LOCUS  
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 VERSION AL546217.2 GI:31268051  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 839)

AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT On Feb 15, 2001 this sequence version replaced gi:12879120.  
 CONTACT: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 5952.r For  
 more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgi-bin/cluster.cgi?seq=CS0D1025DH08QPI&cluster=5952.r. Contact :  
 Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CS0D1025DH08QPI.

# FEATURES

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 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and cloned into the Not I and EcoR V  
 sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

Alignment Scores:  
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 Query Match: 73.60% Indels: 0  
 DB: 9 Gaps: 0  
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 Db 125 ATGCCAGGCTCTTTCAGGCTGGTGTCTTCTCACTTCATCTGGACACGAGGCTCCTG 184  
 Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
 Db 185 GTCCAGGCTCTTTCGCTGCAGAGAGCTTTCATCCAGGTGTCTATGCGAGATTTATGGG 244  
 Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
 Db 245 ATCACCCCTGTGAGCAAAAGGCAACACGAGCTGAATTTTACACAGAAGCTTAAGAGGCC 304  
 Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
 Db 305 TGTAGGCTGCTGGGACTAAGTTTGGCCGCGAAGGACCAAGTTTGAACAGCCTTGAAGCT 364  
 Qy 81 SerPheGluThrCysSerTyrGlyTrrValGlyAspGlyPheValValIleSerArgIle 100  
 Db 365 AGCTTTGAACCTTGAGCTATGGCTGGGTGGAGATGGATTCGTGCTATCTCTAGGATT 424  
 Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrrLysValProVal 120  
 Db 425 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCTGATTTGGAAGCTTCCAGTG 484  
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 Db 485 AGCCGACAGTTTGCAGCCTATTGTTTACAACTCATCTGATACTTGGACTTAACTCGTGCATT 544  
 Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
 Db 545 CCAGAAATATACACCAAGATCCATATTCACACTCAAACTGCAACACAAACA 604  
 Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180

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Db      605 GAATTTATTGTCAGTGACAGTACTACTCGTGGCATCCCTTACTCTCAATACCTGCC 664
QY      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeulle 200
Db      665 CCTACTACTACTCCTCCTGCTCCAGCTTCACACTTCTATTCCAGCGAGAAAAAATTGATT 724
QY      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db      725 TGTGTACAGAGAGTTTTATGGAACTAGCACCATGCTTACAGAAACTGAACATTGTTT 784
QY      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValPro 237
Db      785 GAAATAAAGCAGCAATCAAGATGAAGCTGCTGGGTGGAGGTGCCA 835

RESULT 6
AL543874
LOCUS
DEFINITION
AL543874 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI005YGL3 5-PRIME, mRNA sequence.
ACCESSION
AL543874
VERSION
AL543874.2 GI:31265719
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 911)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12876353.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI005AD07QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue Genoscope sequence ID : CS0DI005AD07QP1.
Location/Qualifiers
1. .911
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI005YGL3"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.: 7,92e-210 Length: 911
Score: 237.00 Matches: 251
Percent Similarity: 99.60% Conservative: 0
Best Local Similarity: 99.60% Mismatches: 1
Query Match: 73.60% Indels: 1
Dbs: 9 Gaps: 0

US-10-079-111-1 (1-322) x AL543874 (1-911)

QY      1 MetAlaArgCysPheSerIleuValLeuLeuThrSerIleThrThrArgLeuLeu 20
Db      155 ATGGCCAGTGCTTCAGCTGGTGTGCTTCTCACTTCATCTGACACAGAGGCTCTG 214
QY      21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40

```

```

Db      215 GTCCAAGGCTCTTTGGTGCAGAAAGAGCTTTCCATCCAGGTGCATGCAGAAATTATGGG 274
QY      41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db      275 ATCACCTTGTGAGCAAAAGGCAACAGCAGCTGAATTTACAGAAAGTAAGGAGGCC 334
QY      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db      335 TGTAGGCTGCTGGGACTAAGTTTGGCGCGCAAGGCCAAGTTGAAACAGCCTTGAAAGCT 394
QY      81 SerPheGluThrCysSerTyrGlyTropValGlyAspGlyPheValValIleSerArgIle 100
Db      395 AGCTTTTGAACCTTCGACGCTATGGCTGGGTGGAGATGGATTCTGTGTCATCTCTAGGATT 454
QY      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeulleThrLysValProVal 120
Db      455 AGCCCCAAACCCCAAGTGTGGGAAATGGGTGGGTGCTCTGATTTGGAAAGGTTCCAGTG 514
QY      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db      515 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTTGGACTTAACCTGTCGATT 574
QY      141 ProGluLeulleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db      575 CCAGAAATTTATCCACCACCAAGATCCCATATTCAACACTCAAACTCAACACAAACAACA 634
QY      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db      635 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTCAATACCTGCC 694
QY      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeulle 200
Db      695 CCTACTACTACTCCTCCTGCTCCAGCTTCACCTTCTATTCCACGGAGAAAAAATTGATT 754
QY      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db      755 TGTGTCCACAGAGTTTTTATGGAACTAGCACCACTGTCTACAGAACTGAACCAATTGTT 814
QY      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db      815 GAAATAAAGCAGCAATCAAGATGAAGCTGCTGGGTGGAGGTGT-CCCACGCTCTG 873
QY      241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAla 252
Db      874 CTAGTGTCTGCTCTCTCTTCTTGTGCTGCAGCT 909

RESULT 7
BX459046
LOCUS
DEFINITION
BX459046 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE011YN20
5-PRIME, mRNA sequence.
ACCESSION
BX459046
VERSION
BX459046.1 GI:31021086
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 913)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DE011DG10QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :

```



```

Db      282 ATCACCTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGCC 341
QY      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db      342 TGTAGGCTGCTGGACTAAGTTTGGCGCGGCAAGGACCAAGTTGAAACAGCTTTGAAAGCT 401
QY      81 SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle 100
Db      402 AGCTTTGAAACTTGCAGCTATGCTGGTTGGAGATGGATCTGTGTCATCTCTAGANT 451
QY      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTyrLysValProVal 120
Db      462 AGCCCAAAACCCCAAGTGTGGGAAATATGGCGTGGTCTCGATTTGGAAGGTTCCAGTG 521
QY      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTyrPheAsnSerCysIle 140
Db      522 AGCCGACAGTTTGCAGCCTATTGTTTAACTCATCTGATCTTGGACTAATCTCGTCATT 591
QY      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db      582 CCAGAAATTTATCACCAACCAAGATCCATATTCACACCTCAAACTGCACACAAACACA 641
QY      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db      642 GAAATTTATTTGTCAGTGACAGTACTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 701
QY      181 ProThrThrThrProAlaProAlaSerThrSerIleProArgLysLysLeuIle 200
Db      702 CTACTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 761
QY      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db      762 TGTGTCACAGAGTTTATGGAACCTAGCACCATCTCTACAGAACTGAAACCATTTGTT 821
QY      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db      822 GAAATATAAGCAGCATTCAAGATGAAGCTGTGCTGGTGTGGAGTGT-CCCACGGCTCTG 880
QY      241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db      881 CTAGTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 940

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## RESULT 9

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AL544430
LOCUS      1201 bp mRNA linear EST 31-MAY-2003
DEFINITION Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1018YG12 5-PRIME, mRNA sequence.

```

```

ACCESSION AL544430
VERSION    2
KEYWORDS   EST.
SOURCE     Homo sapiens (human)

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## ORGANISM

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

## REFERENCE

```

1. (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)

```

## COMMENT

```

On Feb 15, 2001 this sequence version replaced gi:12876910.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D1018BD06QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0D1018BD06QPI.
Location/Qualifiers
1. .1201

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## FEATURES

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source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1018YG12"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

```

## ORIGIN

```

Alignment Scores:
Pred. No.: 1,05e-209 Length: 1201
Score: 237.00 Matches: 237
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 73.60% Indels: 0
DB: Gaps: 0
US-10-079-111-1 (1-322) x AL544430 (1-1201)

```

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QY      1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTyrThrThrArgLeuLeu 20
Db      239 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCATCTGGACACGAGGCTCCTG 238
QY      21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db      299 GTCCAAGGCTCTTTGGTGCAGAAGAGCTTCCATCCAGGTGTCATGCAGAAATATTGGGG 358
QY      41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db      359 ATCACCTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTTACAGAACTAAGGAGGCC 418
QY      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db      419 TGTAGGCTCTGGACTAAGTTTGGCGCGCAGGACCAAGTTGAAACAGCTTTGAAAGCT 478
QY      81 SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle 100
Db      479 AGCTTTGAAACTTGCAGCTATGCTGGTGGTGGAGATGGATTCGTGTCATCTCTAGANT 538
QY      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTyrLysValProVal 120
Db      539 AGCCCAAAACCCCAAGTGTGGGAAATATGGGTGGTGGTCTCTGATTTGGAAGGTTCCAGTG 598
QY      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTyrPheAsnSerCysIle 140
Db      599 AGCCGACAGTTTGCAGCCTATTGTTTAACTCATCTGATCTTGGACTAATCTCGTCATT 658
QY      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db      659 CCAGAAATTTATCACCAACCAAGATCCATATTCACACCTCAAACTGCACACAAACACA 718
QY      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db      719 GAAATTTATGTCAGTGACAGTACTCTCGGTGGCATCCCTTACTCTTACAAATACCTGCC 778
QY      181 ProThrThrThrProAlaProAlaSerThrSerIleProArgLysLysLeuIle 200
Db      779 CCTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 838
QY      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db      839 TGTGTCACAGAGTTTATGGAACCTAGCACCATGCTCTACAGAACTGAAACCATTTGTT 898
QY      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValPro 237
Db      899 GAAATATAAGCAGCATTCAAGAAAGAGAGCTGCTGGGTTTGGAGGTGCTCCCA 949

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## RESULT 10

```

AL547774
LOCUS

```

```

AL547774      1201 bp mRNA linear EST 31-MAY-2003

```

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DEFINITION AL547774 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI033YD11 5-PRIME, mRNA sequence.
ACCESSION AL547774
VERSION AL547774.2 GI:31269603
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12882152.
Contact: Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI033CB06QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI033CB06QP1.

FEATURES
    source
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            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="CSODI033YD11"
            /issue_type="PLACENTA COT 25-NORMALIZED"
            /note="1st strand cDNA was primed with a NotI-oligo(dT)
            primer. Five prime end enriched, double-strand cDNA was
            digested with Not I and cloned into the Not I and EcoR V
            sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.: 1.05e-209 Length: 1201
Score: 237.00 Matches: 237
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 73.60% Indels: 0

US-10-079-111-1 (1-322) x AL547774 (1-1201)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu 20
Db ATGGCCAGGCTCTTGGCGTGCAGAAAGAGCTTCCATCCAGTGCATGCAGAAATATGGGG 382
QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db GTCCAGGCTCTTGGCGTGCAGAAAGAGCTTCCATCCAGTGCATGCAGAAATATGGGG 382
QY 41 IleThrLeuValSerIleLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db ATCACCTCTTGTAGCAAAAAGGCGAACACAGCAGCTGAATTCACAGAAAGTAAAGAGGCC 442
QY 61 CysArgLeuGlyLeuSerIleAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db TGTAGGCTCTGGGACTAAGTTTGGCCGCGAAGGACCAAGTTCGAAAGCTTTGAAAGCT 502
QY 81 SerPheGluThrCysSerTyrlGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db AGCTTTGAACCTTCAGACTATGCTGGTGGATGGATTCGTGTCATCTCTAGATT 562
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db AGCCCAAAACCCCAAGTGTGGMAAAATGGGTGGTGGTCTCTGATTGGTGGAGGTTCCAGTG 622

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QY 121 SerArgGlnPheAlaalaTyrlCysTyrlAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTTGGACTAACTCGTCATT 682
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db CCAGAAATATACACCACCAAGATCCATATTCAACACTCAAACTGCAACACCAACAACA 742
QY 161 GluPheIleValSerAspSerThrTyrlSerValAlaSerProTyrlSerThrIleProAla 180
Db GAATTTATTTGTCAGTCACAGTACTCTCGTGGCATCCCTTACTTACTACAACTCTGCC 802
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgLysLysLeuIle 200
Db CCTACTACTACTCTCTGCTCCAGCTTCCACTTCTATTCCACGAGAAAAAATTGATT 862
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db TGTGTACAGAAAGTTTTTATGGAACTAGCACCATGCTTACAGAAACTGAACCATTTGTT 922
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValPro 237
Db GAAATAAAGCAGCAATTCAGAAATGAAGCTGCTGGTGGAGGTGTCCTCCM 973

RESULT 11
BX402505 1201 bp mRNA linear EST 13-MAY-2003
LOCUS BX402505 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CSODI045YA10 5-PRIME, mRNA sequence.
ACCESSION BX402505
VERSION BX402505.1 GI:30630733
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS1A1012ZA06QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS1A1012ZA06QP1.

FEATURES
    Location/Qualifiers
        1..1201
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="CSODI045YA10"
            /tissue_type="PLACENTA COT 25-NORMALIZED"
            /note="1st strand cDNA was primed with a NotI-oligo(dT)
            primer. Five prime end enriched, double-strand cDNA was
            digested with Not I and cloned into the Not I and EcoR V
            sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.: 1.05e-209 Length: 1201
Score: 237.00 Matches: 237
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 73.60% Indels: 0

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DB: 13 Gaps: 0
US-10-079-111-1 (1-322) x BX402505 (1-1201)
QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 212 ATGCCAGGCTCTTACGCTGGTGGTTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTG 271
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 272 GTCCAAAGGCTCTTGGCTGCAGAGAGCTTTCATCCAGGTGTCATGCAGAAATATGGGG 331
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 332 ATCACCTTGTGAGCAAAAGGCAACACGACGCTGAATTTTCAGAAAGTAAAGAGGCC 391
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 392 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 451
QY 81 SerPheGluThrCysSerTyGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 452 AGCTTTTCAAACTTTCGACTATGGCTGGTGGAGATGGATTCGTGGTCACTCTAGGATT 511
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 512 AGCCCAAAACCCCAAGGTGGGAAATATGGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 571
QY 121 SerArgGlnPheAlaIleTyGlyCysTyAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 572 AGCCGACAGTTTCAGGCTATTGTATCAACTCATCTGATCTGATCTGATCTGATCTGAT 631
QY 141 ProGluIleIleThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 632 CCAGAAATATATACCAACCAAGATCCCATATTCACACTCAAACTCAAACTCAAACTCA 691
QY 161 GluPheIleValSerAspSerThrTySerValAlaSerProTySerThrIleProAla 180
Db 692 GAATTTATTTGTCAGTGACGACTACTCTGGTGGCATCCCTTACTCTACTCTACTCTG 751
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgLysLysLeuIle 200
Db 752 CCTACTACTACTCTCTCTCTCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATGATT 811
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 812 TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAAACCATTTGTT 871
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValPro 237
Db 872 GAAATAAAGCAGCATTCAGAAATGAAGCTGCTGGGTGGAGGTGTCCCA 922

RESULT 12
AL550615 970 bp mRNA linear EST 31-MAY-2003
LOCUS AL550615 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CSODI058XJ19 5-PRIME, mRNA sequence.
ACCESSION AL550615
VERSION AL550615.2 GI:31272432
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1. (bases 1 to 970)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12887757.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
```

Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5952.r For more information about this cluster, see <http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSODI058XJ19&cluster=5952.r>. Contact : Peng Liang Email : [liang@lifetech.com](mailto:liang@lifetech.com) URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Paraday Avenue Genoscope sequence ID : CSODI058XJ19QPl.

## FEATURES

source 1..970  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CSODI058XJ19"  
/tissue\_type="PLACENTA COT 25-NORMALIZED"  
/cisse\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
/notes="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

Alignment Scores:  
Pred. No.: 1,71e-200 Length: 970  
Score: 227.00 Matches: 227  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 70.50% Indels: 0  
DB: 9 Gaps: 0  
US-10-079-111-1 (1-322) x AL550615 (1-970)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20  
Db 249 ATGCCAGGCTCTTACGCTGGTGGTTCCTCCTCCTCCTCCTCCTCCTCCTG 308  
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
Db 309 GTCCAAAGGCTCTTGGCTGCAGAGAGCTTTCATCCAGGTGTCATGCAGAAATATGGGG 368  
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
Db 369 ATCACCTTGTGAGCAAAAGGCAACACGACGCTGAATTTTCAGAAAGTAAAGAGGCC 428  
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
Db 429 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 488  
QY 81 SerPheGluThrCysSerTyGlyTrpValGlyAspGlyPheValValIleSerArgIle 100  
Db 489 AGCTTTTGAACCTTTCAGCTATGGCTGGTGGAGATGGATTCGTGGTCACTCTAGGATT 548  
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
Db 549 AGCCCAAAACCCCAAGGTGGGAAATATGGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 608  
QY 121 SerArgGlnPheAlaIleTyGlyCysTyAsnSerSerAspThrTrpThrAsnSerCysIle 140  
Db 609 AGCCGACAGTTTCAGGCTATTGTATCAACTCATCTGATCTGATCTGATCTGATCTGAT 668  
QY 141 ProGluIleIleThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
Db 669 CCAGAAATATATACCAACCAAGATCCCATATTCACACTCAAACTCAAACTCAAACTCA 728  
QY 161 GluPheIleValSerAspSerThrTySerValAlaSerProTySerThrIleProAla 180  
Db 729 GAATTTATTTGTCAGTGACGACTACTCTGGTGGCATCCCTTACTCTACTCTACTCTG 788  
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgLysLysLeuIle 200  
Db 789 CCTACTACTACTCTCTCTCTCTCCAGCTTCCATTTCTATCCACGGAGAAAAAATGATT 848  
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220



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Db      849 TGTGTACAGAGTATTTTATGGAAGACTAGCACCATTCTACAGAAACTGACACCATTTGTT 908
QY      221 GluAsnLysAlaAlaPheLys 227
Db      909 GAAATAAAGCAGCATTCAAG 929

RESULT 13
BX366718
LOCUS      1201 bp mRNA linear EST 08-MAY-2003
DEFINITION BX366718 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI040YD03 5-PRIME, mRNA sequence.
ACCESSION BX366718
VERSION    BX366718.1 GI:30451557
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS    1 (bases 1 to 1201)
TITLE      Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
JOURNAL    Full-length cDNA libraries and normalization
COMMENT     Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0AI040CB02QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0AI040CB02QP1.

FEATURES
source
1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI040YD03"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.: 1,55e-198 Length: 1201
Score: 225.00 Matches: 225
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 69.88% Indels: 0
DB: 13 Gaps: 0

US-10-079-111-1 (1-322) x BX366718 (1-1201)

QY      1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleThrThrArgLeuLeu 20
Db      212 ATGGCCAGGTCTTCAGCTGTGTGTTCTTCATCTCCATCTGGACGAGGCTCCTG 271
QY      21 ValGlnGlySerLeuArgLaGluGluLeuSerIleGlnValSerCysArgileMetGly 40
Db      272 GTCCAAGGCTCTTTGCGTGCAGAAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGG 331
QY      41 IleThrIeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db      332 ATCACCCCTTGTAGCAAAAGGCGAACCCAGCAGCTGAATTTCACAGAGCTAAGAGGCC 391
QY      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80

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Db      392 TGTAGGCTGTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACACGCTTGAAAGCT 451
QY      81 SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgile 100
Db      452 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTGCTCTTAGGATT 511
QY      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTyrLysValProVal 120
Db      512 AGCCCAAAACCCCAAGTGTGGGAAAATGGGTGGGTGCTCTGATTGGAGAGTTCCAGTG 571
QY      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrThrThrAsnSerCysile 140
Db      572 AGCCGACAGTTTGGAGCCTATTGTTTACAACTCATCTGATCTTGGACTAACTCGTGCA 631
QY      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db      632 CCAGAAATATATCACCAACCAAGATCCCATATATCAACACTCAAACTGCACACACAAACA 691
QY      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db      692 GAATTTATGTGAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACATATACCTGCC 751
QY      181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeu 200
Db      752 CCTACTACTCTCTCTGCTCCAGTCCACTTCTATTCACGGAGAAAAAATGATT 811
QY      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db      812 TGTGTGCACAGAGATTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 871
QY      221 GluAsnLysAlaAla 225
Db      872 GAAATTAAGCAGCA 886

RESULT 14
BX366718
LOCUS      1201 bp mRNA linear EST 31-MAY-2003
DEFINITION AL546623 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI029YM23 5-PRIME, mRNA sequence.
ACCESSION AL546623
VERSION    AL546623.2 GI:31268456
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS    1 (bases 1 to 1201)
TITLE      Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
JOURNAL    Full-length cDNA libraries and normalization
COMMENT     Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI029AG12QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0DI029AG12QP1.

FEATURES
source
1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI029YM23"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

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QY 161 GluPheIleValSerAspSerThrTySerValAlaSerProTySerThrThrProAla 180
DB 724 GAATTTATTGTGAGTACAGTACTCGTGGCATCCCTTACTCTCAATACCTGCC 783
QY 181 ProThrThrProProAlaProAlaSerThrSerIleProArgArg-LysLysLeu11 200
DB 784 CCTACTACTACTCTCTGCTCAGCTTCCACTTCTATTCCAGGAGAAAAAATTGAT 843
QY 200 eCysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVa 220
DB 844 TTGTGTACAGAAAGTTTTATGAAACTAGCACMATGTCTACAGAACTGAACCACTTGT 903
QY 220 lGluAenLysAlaAlaPheIysAsnGluAlaGly 232
DB 904 TGAATAAAGCAGCATTCAAGAAATGAAGTGTGCTGGG 940

RESULT 16
AL552127
LOCUS
DEFINITION
AL552127 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
ACCESSION
VERSION
AL552127.2 GI:31273943
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1172)
AUTHORS
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished (2001)
COMMENT
On Feb 15, 2001 this sequence version replaced gi:12890728.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI059BA06QP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI059BA06QP1.
Location/Qualifiers
1. .1172
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI059YA12"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES
source
1. .1172
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI059YA12"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.: 4,238-191 Length: 1172
Score: 217.00 Matches: 246
Percent Similarity: 99.19% Conservative: 0
Best Local Similarity: 99.19% Mismatches: 2
Query Match: 67.39% Indels: 2
DB: 9 Gaps: 0

US-10-079-111-1 (1-322) x AL552127 (1-1172)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleThrThrArgLeuLeu 20
DB 242 ATGCCAGGTGCTTCAGCTGGTGTGCTTCTCACTTCCATTCGACCACGAGGCTCCG 301

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QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
DB 302 GTCCAGAGGCTCTTTGGCGTCAGAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 361
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
DB 362 ATCACCCTTGTGAGCAAAAAGGGAACACAGAGCTGAATTTACAGAACTAAGAGGCC 421
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
DB 422 TGTAGGCTCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCGCTTGAAGCT 481
QY 81 SerPheGluThrCysSerTyroValGlyValGlyValGlyValValIleSerArgIle 100
DB 482 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCTGTGTCATCTCTAGGATT 541
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
DB 542 AGCCCAAAACCCAGTGTGGGAAAATGGGTGGGTGCTGCTGATTTGGAGAGGTTCCAGTG 601
QY 121 SerArgGlnPheAlaAlaTyroCysTyroAsnSerSerAspThrTrpThrAsnSerCysIle 140
DB 602 AGCGACAGCTTTCAGCCTATTGTTCAAACTCATCTGATCTTGGACTTAACCTCGTCAIT 661
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
DB 662 CCAGAAATATCACCACCAAGATCCCATATTCAACACTCAAACTCAACACCAACAAACA 721
QY 161 GluPheIleValSerAspSerThrTyroValAlaSerProTyroSerThrIleProAla 180
DB 722 GAATTTATGTCAGTGACAGTACCTACTCGTGGGATCCCTTACTCTACATACCTGCC 781
QY 181 ProThrThrProProAlaProAlaSerThrSerIleProArgLysLysLeuLeu 200
DB 782 CCTACTACTACTCTCTCTCCAGCTTCCACTTCTATTCCAGGAGAAAAAATTGATT 841
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
DB 842 TGTGTACAGAGAGTTTTTATGAAACTAGCACCATCTGTACAGAACTGAACA-TTTGTT 900
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
DB 901 GA-ATAAAGCAGCATTCAAGATGAAGCTGTGGGTTTGGAGGTGTCCTCCACGGCTCTT 959
QY 241 LeuValLeuAlaLeuLeuPhePhe 248
DB 960 CTAGTGCTTGTCTCTCTCTTT 983

RESULT 17
AL549512
LOCUS
DEFINITION
AL549512 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI044YN16 5-PRIME, mRNA sequence.
ACCESSION
VERSION
AL549512.2 GI:31271330
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 972)
AUTHORS
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished (2001)
COMMENT
On Feb 15, 2001 this sequence version replaced gi:12885569.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see

```



```

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 303 TGTAGGCTGCTGGGACTAAGTTTGGCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 362

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 363 AGCTTTGAAACTTGCAGCTATGCTGGTGGAGATGGATTCGTGTCATCTTAGGATT 422

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 423 AGCCCAAAACCCCAAGTGTGGGAAAATGGGTGGGTGCTCTGATTGGGAAGGTTCCAGTG 482

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 483 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTTGGACTAACTCGTGCATT 542

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 543 CCAGAAATATCACCAAGATCCCATATTCACACTCAAACTGCAACACAAACACACA 602

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 603 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 662

QY 181 Pro 181
Db 663 CCT 665

RESULT 19
AL550621
LOCUS
DEFINITION
AL550621 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1058YNI4 5-PRIME, mRNA sequence.
ACCESSION
VERSION
AL550621
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
COMMENT
On Feb 15, 2001 this sequence version replaced gi:12887769.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by life technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D1058DG07QPL&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0D1058DG07QPL.
Location/Qualifiers
1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1058YNI4"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES
source
1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1058YNI4"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:

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Pred. No.: 1.75e-145 Length: 1201
Score: 168.00 Matches: 268
Percent Similarity: 99.26% Conservative: 0
Best Local Similarity: 99.26% Mismatches: 1
Query Match: 52.17% Indels: 2
DB: 9 Gaps: 0

US-10-079-111-1 (1-322) x AL550621 (1-1201)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 158 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACACAGGCTCCTG 217

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 218 GTCCAGGCTCTTTCGTGCAGAGAGCTTTCATCCAGGTGTCATGCAGAAATATGGGG 277

QY 41 IleThrLeuValSerIlyslsAlaAsnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 278 ATCACCCTTGTGAGCAAAAGGCGAACAGCAGCTGAATTTCCAGAGACTAAGGAGGCC 337

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 338 TGTAGGCTGCTGGACTAAGTTTGGCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 397

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 398 AGCTTTGAAACTTGCAGCTATGCTGGTGGAGATGGATTCGTGTCATCTTAGGATT 457

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 458 ACCCAAAACCCCAAGTGTGGGAAAATGGGTGGGTGCTCTGATTTGGGAAGGTTCCAGTG 517

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 518 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTTGGACTAACTCGTGCATT 577

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 578 CCAGAAATATCACCAAGATCCCATATTCACACTCAAACTGCAACACAAACACA 637

QY 161 Glu-PheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAl 180
Db 638 AA-ATTATTATGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGC 696

QY 180 aProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLeuIle 200
Db 697 CCTACTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 756

QY 200 eCysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVa 220
Db 757 TTGTGTGCAGAGAGTTTATGGAACCTAGCACCATGCTACAGAACTGAAACCACTTTGT 816

QY 220 lGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLe 240
Db 817 TGAAAATAAAGCAGCATTCAGAAATGAAGCTGCTGGTGGAGGTGTCCTCCACCGCTCT 876

QY 240 uLeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrVally 260
Db 877 GCTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 936

QY 260 sArgTyrValLysAlaPheProPheThr 269
Db 937 AAGGTATGTGAAGGCTTCCCTTTTACA 964

RESULT 20
CB959809
LOCUS
DEFINITION
CB959809
IMAGE:30345878 5', mRNA sequence.
ACCESSION
VERSION
CB959809.1 GI:30215925
KEYWORDS
EST.

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CB959809 760 bp mRNA linear EST 29-APR-2003  
 AGENCOURT 13889469 NIH\_MGC\_147 Homo sapiens cDNA clone  
 IMAGE:30345878 5', mRNA sequence.  
 CB959809  
 CB959809.1 GI:30215925  
 EST.

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 760)  
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaps-remail.nih.gov  
 Tissue Procurement: Dr. Stefan Hansson  
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help  
 and advice from Piero Carninci (RIKEN)  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: NDAM384 row: h column: 15  
 High quality sequence stop: 545.  
 Location/Qualifiers  
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 /clone="IMAGE:30345878"  
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 /lab\_host="DH10B Tona"  
 /clone\_lib="NIH\_MGC\_147"  
 /notes="Organ: Placenta; Vector: pBluescriptR; Site: 1:  
 all-XhoI; Site 2: BamH; Oligo-dT primed using primer  
 5'-TTTTTTTTTTTTTWN-3', size-selected for average  
 insert size 2.3 kb and normalized to R0T 5. This is a  
 primary library enriched for full-length clones and  
 constructed using the Cap-trapper method (Carninci, in  
 preparation). Library constructed by M. Brownstein  
 (NIH/NHGRI, National Institutes of Health). Note: This is  
 a NIH\_MGC library."  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 1.37e-133 Length: 760  
 Score: 155.00 Matches: 155  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 48.14% Indels: 0  
 DB: 14 Gaps: 0  
 US-10-079-111-1 (1-322) x CB959809 (1-760)  
 QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20  
 Db 99 ATGGCCAGGTGCTTCAGCTGGTGGTGTCTTCACATTCATCCAGCCAGGCTCCTG 158  
 QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
 Db 159 GTCCAAAGGCTCTTTCGTCGAGAGAGCTTCCATCCAGGTGTCTATGCAGATTAATGGG 218  
 QY 41 IleThrLeuValSerIleValAsnGlnGlnLeuAsnPhetheThrGluAla 60  
 Db 219 ATCACCTTGTGAGCAAAAGCGCAACACAGAGCTGAATTTTCAGAAAGCTAAGGAGGC 278  
 QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyValAspGlnValGluThrAlaLeuVal 80  
 Db 279 TGTAGGCTGCTGGACTAGTTTGGCGGCGNAGGACCAAGTTGAACACAGCTTGAAGCT 338  
 QY 81 SerPheGluThrCysSerTrpValGlyAspGlyPheValValIleSerArgIle 100  
 Db 339 AGCTTTGAAACCTTCAGCTATGCTGGCTGGAGATGATTCGTGTCATCTCTAGGATT 398  
 QY 101 SerProAsnProLysCysGlyValAsnGlyValGlyValIleTrpValProVal 120  
 Db 399 AGCCCAACCCCAAGTGTGGGAAATGGGGTGGGTGCTCTGATTGGGAAGGTTCAGGTG 458

QY 121 SerArgGlnPheAlaIleTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
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 QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThr 155  
 Db 519 CCGAAATATATACCAACCAAGATCCCATATTCAACACTCAAACT 563  
 RESULT 21  
 LOCUS AL545331 864 bp mRNA linear EST 31-MAY-2003  
 DEFINITION AL545331 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA  
 clone CS0DI027YD19 5-PRIME, mRNA sequence.  
 ACCESSION AL545331  
 VERSION AL545331.2 GI:31267167  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 864)  
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT On Feb 15, 2001 this sequence version replaced gi:12877812.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 5952.r For  
 more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgi-bin/cluster.cgi?seq=CS0DI027CB10QPl&cluster=5952.r. Contact :  
 Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CS0DI027CB10QPl.  
 FEATURES  
 Location/Qualifiers  
 1..864  
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 /db\_xref="taxon:9606"  
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 /tissue\_type="PLACENTA COT 25-NORMALIZED"  
 /clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
 /note="1st strand cDNA was primed with a NotI-oligo(dT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and cloned into the Not I and Ecor V  
 sites of the pCMVSPORT 6 vector. Library was normalized."  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 1.13e-131 Length: 864  
 Score: 153.00 Matches: 226  
 Percent Similarity: 99.56% Conservative: 0  
 Best Local Similarity: 99.56% Mismatches: 1  
 Query Match: 47.52% Indels: 1  
 DB: 9 Gaps: 0  
 US-10-079-111-1 (1-322) x AL545331 (1-864)  
 QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20  
 Db 183 ATGGCCAGGTGCTTCAGCTGGTGGTGTCTTCACATTCATCCAGCCAGGCTCCTG 242  
 QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
 Db 243 GTCCAAAGGCTCTTTCGTCGAGAGAGCTTCCATCCAGGTGTCTATGCAGATTAATGGG 302  
 QY 41 IleThrLeuValSerIleValAsnGlnGlnLeuAsnPhetheThrGluAla 60  
 Db 303 ATCACCTTGTGAGCAAAAGCGCAACACAGAGCTGAATTTTCAGAAAGCTAAGGAGGC 362

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QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 363 TGTAGGCTCTGGACTAGATTGGCCGCGAAGACCAAGTTGAACACGCCCTTGAAGCT 422
QY 81 SerPheGluThrCysSerTyrGlyTTPValGlyVAspGlyPheValValIleSerArgIle 100
Db 423 AGCTTTGAAACTTGCAGCTATGCTGGTGGAGATGGATTCTGTGTCATCTCTAGATT 482
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 483 AGCCCAAAACCCCAAGTGTGGAA-AAATGGGGTGGTGTCTGATTGGGAAGGTTCCAGTG 541
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 542 AGCCGACAGTTTGCAGCCCTATTGTTCAACTCATCTGATCTTGGACTTAACCTGTCATT 601
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 602 CCAGAAATTTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA 661
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 662 GAATTTATTGTCTAGTCACAGTACTACTCGTGGCATCCCTTTACTCTCAATACCTGCC 721
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 722 CTTACTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 781
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 782 TGTGTCTACAGAAAGTTTTTATGGAACCTAGCACCATGCTCTACAGAACTGAACCAATT 841
QY 221 GluAsnLysAlaAlaPheLys 227
Db 842 GAAATAAAGACGACATTCAAG 862
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LOCUS
DEFINITION
AGENCOURT_13620505 NIH_MGC_148 Homo sapiens cDNA clone
IMAGE:30335820 5', mRNA sequence.
CB994314
ACCESSION
CB994314.1 GI:30288834
VERSION
EST.
KEYWORDS
SOURCE
Homo sapiens
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 802)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM358 row: e column: 13
High quality sequence stop: 646.
Location/Qualifiers
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/organism="Homo sapiens"
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/tissue_type="pre-eclampsia placenta"
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FEATURES

source

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/notes="Organ: Placenta; Vector: pBluescriptR; Site_1:
all-XhoI; Site_2: BamH; Library is oligo-dr primed and
directionally cloned using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert
size 2.3 kb and normalized to ROT 5. This is a primary
library enriched for full-length clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NIH/NHGRI,
National Institutes of Health). Note: this is a NIH_MGC
Library."
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ORIGIN

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Alignment Scores:
Pred. No.: 6,97e-116 Length: 802
Score: 136.00 Matches: 167
Percent Similarity: 98.82% Conservative: 0
Best Local Similarity: 98.82% Mismatches: 1
Query Match: 42.24% Indels: 2
DB: 14 Gaps: 0
US-10-079-111-1 (1-322) x CB994314 (1-802)
QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 231 ATGGCCAGGTGCTTCAGCCTGGTGTGTCTTCTCCTCCATCTGGACACAGGCTCTTG 290
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 291 GTCCAAAGGCTCTTTCGTGCAGAAAGCTTCCATCCAGGTGTCTGCAAGAATTATGGGG 350
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 351 ATCACCCTTGTGAGCAAAAGGCAACAGCAGCTGAAATTCACAGAACTAAGGAGGCC 410
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 411 TGTAGGCTCTGGACTAGTTTGGCCGCGAAGGACCAAGTTGAAACACGCTTGAAGCT 470
QY 81 SerPheGluThrCysSerTyrGlyTTPValGlyVAspGlyPheValValIleSerArgIle 100
Db 471 AGCTTTGAAACTTGCAGCTATGCTGGTGGTGGAGATGGATTCTGTGTCATCTCTAGATT 530
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 531 AGCCCAAAACCCCAAGTGTGGGAAAATGGGTGGGTGTGCTGATTGGGAAGGTTCCAGTG 590
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsn-SerCysIle 140
Db 591 AGCCGACAGTTTGCAGCCTATTGTTCAACTCATCTGATCTTGGACTAG-CTCGTGCAT 649
QY 140 eProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrTh 160
Db 650 TCCAGAAATTTATCACCAACCAAGATCCCATATTCAACTCAAACTCAAACTGCAACAAACAAC 709
QY 160 rGluPheIleValSerAspSerThr 168
Db 710 AGAATTTATTGTGACGTGACAGTACC 734
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AL552661 1116 bp mRNA linear EST 31-MAY-2003  
AL552661 Homo sapiens PLACENTA COT 23-NORMALIZED Homo sapiens cDNA  
clone CS0DI067YG15 5-PRIME, mRNA sequence.

AL552661  
VERSION  
AL552661.2 GI:31274476

EST.

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1116)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT On Feb 15, 2001 this sequence version replaced gi:12891779.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
Bp 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 5952.r For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0DI067AD08QPL&cluster=5952.r. Contact :  
Peng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CS0DI067AD08QPL.

## FEATURES

source

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/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

Alignment Scores: 4.42e-111 Length: 1116  
Pred. No.: 131.00 Matches: 231  
Score: 99.14% Conservative: 0  
Percent Similarity: 99.14%  
Best Local Similarity: 99.14% Mismatches: 1  
Query Match: 40.68% Indels: 2  
DB: 9 Gaps: 0

US-10-079-111-1 (1-322) x AL552661 (1-1116)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrTrpThrArgLeuLeu 20  
Db 249 ATGGCCAGGTGCTTCAGCCCTGGTGTTCCTTCACATTCGACACGAGGCTCCCTG 308  
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
Db 309 GTCCAGAGGCTCTTGGCTGCAGAAAGAGCTTTCATCCAGTGTGTCGAGAAATTATGGGG 368  
QY 41 IleThrLeuValSerIleLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
Db 369 ATCACCCCTTGTGAGCAAAAAGGCGAACACGACGAGCTGAATTCACAGAAGCTAAGGAGGC 428  
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
Db 429 TGTAGCTCTGGGACTAGTATTGGCCGCGACAGGACCAAGTTGAAACAGCCCTTGAAGCT 488  
QY 81 SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle 100  
Db 489 AGCTTTGAACCTTGACGCTATGCTGGTTGGAGATGGATTCGTGGTCACTCTAGGATT 548  
QY 101 SerProAsnProLysCysGlyLysAsn-GlyValGlyValLeuIleTrpLysValProVa 120  
Db 549 AGCCCAAAACCCCAAGTGTGGGAAAMA-TGGGGTGGGTGCTCTGATTGGAGGTTCCAGT 607  
QY 120 lSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
Db 608 GAGCCGACAGTGTGACGCTATTGTTACAACTCATCTGATACCTTGACTAACTCGGGCAT 667  
QY 140 eProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrTh 160  
Db 668 TCCAGAAATTATCACCAACAAGATCCCATATTCAACTCAAACTGCAACACAAACAC 727  
QY 160 rGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAl 180

Db 728 AGAATTTATTGTTCAGTGACAGTACTACTCGGTGGCATCCCTTACTCTACAATACCTGC 787  
QY 180 aProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200  
Db 788 CCTACTACTACTCTCTCCCTCCAGTTCACCTTCTATTCCACGGAGAAAAAATTGAT 847  
QY 200 eCysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVa 220  
Db 848 TTGTGTGCACAGAAGTTTTTATGGAAACTAGCACCATTGTCTACAGAAACTGAACATTGT 907  
QY 220 lGluAsnLysAlaAlaPheLysAsnGluAlaAlaGly 232  
Db 908 TGAATAATAAGCAGCATTTCAGAAATCAGCTGCTGGG 944  
AA046671 596 bp mRNA linear EST 06-SEP-1996  
zf12d09.r1 Soares fetal heart NbHL19W Homo sapiens cDNA clone  
IMAGE:376721 5' similar to PIR:A38745 A38745 cell adhesion molecule  
CD44 precursor - rat [1] ; mRNA sequence.  
AA046671  
AA046671.1 GI:1524772  
Homo sapiens (human)  
EST.  
Homo sapiens  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS  
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,  
Trevasaki,E., Waterston,R., Williamson,A., Wohlmann,P. and  
Wilson,R.  
The WashU-Merck EST Project  
Unpublished (1995)  
CONTACT: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: estowatson.wustl.edu  
This clone is available royalty-free through LML ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: -28M13 rev2 from Amersham  
High quality sequence stop: 419.  
Location/Qualifiers  
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/db\_xref="GDB:1284977"  
/db\_xref="taxon:9606"  
/clone="IMAGE:376721"  
/sex="unknown"  
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/lab\_host="DH10B (ampicillin resistant)"  
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/note="Organ: heart; Vector: pT73D (Pharmacia) with a  
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5',  
TGTTACCAATCTGAAGTGGAGCGGCGCATCTTTTTTTTTTTTTTTT 3'],  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT73 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by  
M.Fatima Bonaldo. This library was constructed from the  
same fetus as the fetal lung library, Soares fetal lung  
NbHL19W."

ORIGIN

Alignment Scores: 8.86e-106 Length: 596  
Pred. No.: 125.00 Matches: 181



Percent Similarity: 98.91%  
 Best Local Similarity: 98.91%  
 Query Match: 38.82%  
 DB: 9

Conservative: 0  
 Mismatches: 2  
 Indels: 2  
 Gaps: 0

Plate: NDAM384 row: h column: 14  
 High quality sequence stop: 456.  
 Location/Qualifiers  
 1..974

US-10-079-111-1 (1-322) x AA046671 (1-596)

QY 41 IleThrLeuValSerLysLysAlaAsnGlnLeuAsnPheThrGluAlaLysGluAla 60  
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 Db 3 ATCACCTTGTGACAAAAGGCGAACACGACTGAATTTCACAAAGCTAAAGAGGCC 62  
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 QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
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 Db 63 TGTAGGTGCTGGGACTAGTTTGGCGGCAAGACCAAGTTGAACAGCCTTGAAGCT 121  
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 QY 81 SerPheGluThrCysSerTyrGlyTTPValGlyAspGlyPheValValleSerArglie 100  
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 QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValleuileTTPlysValProVal 120  
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 Db 182 AGCCNAACCCCAAGTGTGGAAAAATGGGTGGGTCTGATTTGGAGGTTCAGTG 241  
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 QY 121 SerArgGlnPheAlaIatYrCysTyrAsnSerSerAspThrTTPThrAsnSerCyslie 140  
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 Db 242 AGCGACAGCTTGCAGCCTATTGTTACAACTCATCTGATCTTGGACTTAACCTGTCATT 301  
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 QY 141 ProGluIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
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 Db 302 CCAGAAATTTATCACCAACCAAGATCCCATTTTCAACACTCAAACTCAACACACAACA 361  
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 QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
 |||||  
 Db 362 GAATTTATTTGTCAGTGACAGTACCTACTCGTGCGCATCCCTTACTCTCAATACCTGCC 421  
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 QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeulle 200  
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 Db 422 CCTACTACTACTCTCTCTCTCCAGI-TCCACTTCTATTCACGGAGAAAAAATGATT 480  
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 QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
 |||||  
 Db 481 TGTGTACAGAAAGTTTATTTGAAACTAGCACCATGCTACAGAAACTGAACCATTTGTT 540  
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 QY 221 GluAsnLys 223  
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 Db 541 GAAATTAAG 549

RESULT 25  
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 AGENCOURT\_13892970 NIH\_MGC\_147 Homo sapiens cDNA clone  
 IMAGE:30345877 5', mRNA sequence.  
 CB988195  
 VERSION  
 CB988195.1 GI:30282715  
 EST.  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 974)  
 NIH-MGC <http://mgi.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapsb@mail.nih.gov](mailto:cgapsb@mail.nih.gov)  
 Tissue Procurement: Dr. Stefan Hansson  
 cDNA library Preparation: Michael J. Brownstein (NHGRI) with help  
 and advice from Piero Carninci (RIKEN)  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

## ORIGIN

Alignment Scores:  
 Pred. No.: 5.66e-100 Length: 974  
 Score: 119.00 Matches: 119  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 36.96% Indels: 0  
 DB: 14 Gaps: 0

US-10-079-111-1 (1-322) x CB988195 (1-974)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleThrThrArgLeuLeu 20  
 Db 99 ATGGCCAGGTGCTCAGCCTGTGTGCTTCTCCTCCATCTGGACACAGAGCTCTG 158  
 |||||  
 QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
 |||||  
 Db 159 GTCCAGGCTCTTGGTGCAGAGAGCTTCCATCCAGTGTGTCATGCAAGATTATGGGG 218  
 |||||  
 QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
 |||||  
 Db 219 ATCACCTTGTGAGCAAAAAGGCGAACACAGCAGCTGAATTCACAGAACTAAGAGGCC 278  
 |||||  
 QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
 |||||  
 Db 279 TGTAGGCTCTGGGACTAAGTTTGGCGGCAAGGACCAAGTTGAAACGCTTGAAGCT 338  
 |||||  
 QY 81 SerPheGluThrCysSerTyrGlyTTPValGlyAspGlyPheValValleSerArglie 100  
 |||||  
 Db 339 AGCTTTGAAACTTGCAGCTATGCTGGGTGGAGATGGATTCTGCTCTCTAGGATT 398  
 |||||  
 QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValleuileTTPlysValPro 119  
 |||||  
 Db 399 AGCCCAACCCCAAGTGTGGAAAAATGGGTGGGTGCTCTGATTTGGAGAGTTTCCA 455  
 |||||

## RESULT 26

AL552777  
 LOCUS  
 DEFINITION  
 AL552777 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
 clone CS0D1068YF16 5-PRIME, mRNA sequence.  
 AL552777  
 ACCESSION  
 AL552777.2 GI:31274592  
 VERSION  
 EST.  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 1074)  
 Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
 Full-length cDNA libraries and normalization  
 Unpublished (2001)  
 JOURNAL  
 COMMENT  
 On Feb 15, 2001 this sequence version replaced gi:12892000.



DB: 14 Gaps: 0

US-10-079-111-1 (1-322) x H69328 (1-465)

QY 142 GluIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThrGlu 161

DB 1 GAAATATACACCAAGATCCATATTCACACTCAAACTGCAACACAAACAGAA 60

QY 162 PheIleValSerAspSerThrThrValAlaSerProTyrSerThrThrleProAlaPro 181

DB 61 TTTATTTGTGAGTGACAGTACTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCCT 120

QY 182 ThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIleCys 201

DB 121 ACTACTACTCTCTCTGCTCAGCTTCCACTTCTATTCCACGGAGAAAAATGATTGT 180

QY 202 ValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheValGlu 221

DB 181 GTCACAGAAGTTTTTATGGAACCTAGCACCATGCTCTACAGAACTGAACCAATTTGTTGAA 240

QY 222 AsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeuLeu 241

DB 241 AATAAAGCAGCATTTCAAGATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTGCTA 300

QY 242 ValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGly 255

DB 301 GTGCTGTCTCTCTCTCTCTTGTGGTGTCGACGTGCTGCTGGG 342

RESULT 28

BG012717

LOCUS 368 bp mRNA linear EST 24-JAN-2001

DEFINITION IL5-GN0239-141200-341-c05 GN0239 Homo sapiens cDNA, mRNA sequence.

ACCESSION BG012717

VERSION BG012717.1 GI:12462184

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 368)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL5&t2=IL5-GN0239-141200-341-c05&t3=2000-12-14&t4=1) Seq primer: puc 18 forward High quality sequence stop: 339. Location/Qualifiers 1. .368 /organism="Homo sapiens" /mol\_type="mRNA" /db\_xref="taxon:9606" /dev\_stage="Adult" /clone\_lib="GN0239" /note="Organ: placenta\_normal; Vector: puc18; Site\_1:

FEATURES source

SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Alignment Scores:

Pred. No.: 7,92e-95 Length: 368

Score: 113.00 Matches: 113

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 35.09% Indels: 0

DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x BG012717 (1-368)

QY 22 GlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGlyIle 41

DB 2 CAAGGCTCTTTGCGTGCAGAAAGAGCTTCCATCCAGGTGTCATGCAGAAATTTATGGGATC 61

QY 42 ThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAlaCys 61

DB 62 ACCCTGTGAGCAAAAGCGCAACAGCAGCTGAATTCACAGAGCTAAGGAGGCTGT 121

QY 62 ArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAlaSer 81

DB 122 AGGCTGCTGGGACTAAGTTTGGCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCTAGC 181

QY 82 PheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIleSer 101

DB 182 TTGAAACCTTGAGCTATGCTGGGTGGAGATGGATTCGTGCTCATCTCTAGGATTAGC 241

QY 102 ProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProValSer 121

DB 242 CCAACCCCAAGTGTGGGAAATGGGTGGGTGCTCTGATTTGGNAGGTTCCAGTAGC 301

QY 122 ArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThr 134

DB 302 CGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACT 340

## RESULT 29

BG541447 872 bp mRNA linear EST 03-APR-2001

LOCUS 602570880F1 NTH\_MGC\_77 Homo sapiens cDNA clone IMAGE:4695427 5',

DEFINITION mRNA sequence.

ACCESSION BG541447

VERSION BG541447.1 GI:13533680

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 872)

TITLE NIH-MGC http://mgc.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D. Email: cgabbs-r@mail.nih.gov Tissue Procurement: CLONTECH Laboratories, Inc. cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Sequencing by: Incyte Genomics, Inc. DNA distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: LLCMI520 row: p column: 20 High quality sequence stop: 669. Location/Qualifiers 1. .872 /organism="Homo sapiens" /mol\_type="mRNA"

FEATURES source



JOURNAL  
COMMENT

Unpublished (2002)  
Contact: Gong Da-Wei  
Division of Endocrinology, Diabetes and Nutrition  
University of Maryland  
660 Redwood St, HH497, Baltimore, MD 21201, USA  
Tel: 410 706 1672  
Fax: 410 706 1622  
Email: dgong@medicine.umaryland.edu  
PCR Primers  
FORWARD: CTCGGAAGCGCCGATGTGGT  
BACKWARD: AATACGACTCATAGCGGAATTGG  
Seq primer: GTTGGTACCGGAATTC  
Location/Qualifiers

FEATURES  
source

1. .487  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/sex="Male and Female"  
/tissue\_type="Adipose"  
/clone\_lib="Human Fat Cell 5'-Stretch Plus cDNA Library"  
/note="Vector: lambdaTriplex"

## ORIGIN

Alignment Scores:  
Pred. No.: 2.96e-87 Length: 487  
Score: 105.00 Matches: 105  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 32.61% Indels: 0  
DB: 14 Gaps: 0

US-10-079-111-1 (1-322) x CA407758 (1-487)

QY 86 SerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIleSerProAsnProLys 105  
DB 21 AGCTATGGCTGGGTGGAGATGATTGGTGTCTCTAGGATTAGCCAAACCCCAAG 80  
QY 106 CysGlyLysAsnGlyValGlyValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 125  
DB 81 TGTGGGAAAATGGGTGGGTGCTCTGATTGGAAAGTTCCAGTGAGCCGACAGTTGCA 140  
QY 126 AlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIleProGluLeuIleThr 145  
DB 141 GCCTATTGTTACAACTCATCTGATCTTGGACTAATCGTGCATTCCAGAAATTATCACC 200  
QY 146 ThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThrGluPheIleValSer 165  
DB 201 ACCAAAGATCCCATATTCACACTCAAACTGCAACACAAACACAGAAATTATTGTGAGT 260  
QY 166 AspSerThrTyrSerValAlaSerProTyrSerThrIleProAlaProThrThrPro 185  
DB 261 GACAGTACCTACTCGTGGCATCCCTTACTCTACATACCTGCCCTACTACTCCT 320  
QY 186 ProAlaProAlaSer 190  
DB 321 CCTGCTCCAGCTTCA 335

RESULT 32  
AL598709  
LOCUS

DEFINITION 743 bp mRNA linear EST 04-SEP-2003  
DKF2p313B2422 r1 313 (synonym: hlcc2) Homo sapiens cDNA clone  
DKF2p313B2422 5', mRNA sequence.

## ACCESSION

AL598709

## VERSION

AL598709.1 GI:15161400

## KEYWORDS

EST.

Homo sapiens (human)

Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 743)

Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and

Wiemann, S.

EST (Duesterhoeft, et al.)

JOURNAL  
COMMENT

Unpublished (1999)  
Contact: MIPS  
MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing  
consortium of the German Genome Project.  
No s1 sequence available.

This clone (DKFZp313B2422) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES  
source

1. .743  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZp313B2422"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="313 (synonym: hlcc2)"  
/note="Vector: pTriplex2; Site\_1: SfiIA; Site\_2: SfiIB;  
cDNA-collection"

## ORIGIN

Alignment Scores:  
Pred. No.: 4.58e-87 Length: 743  
Score: 105.00 Matches: 188  
Percent Similarity: 96.91% Conservative: 0  
Best Local Similarity: 96.91% Mismatches: 3  
Query Match: 32.61% Indels: 6  
DB: 9 Gaps: 0

US-10-079-111-1 (1-322) x AL598709 (1-743)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 20  
DB 158 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCCTCCTCCAGCCAGAGGCTCTG 217  
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuLeuSerIleGlnValSerCysArgIleMetGly 40  
DB 218 GTCCAGGCTCTTGGCTGCAGAGAGCTTTCATCCAGGTGTCATGAGAAATTATGGGG 277  
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
DB 278 ATCACCTTGTGAGCAAAAAGCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 337  
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
DB 338 TGTAGCTCTGGGACTAAGTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAGACT 397  
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100  
DB 398 AGCTTTGAAACTTGCAGCTATGCTGGTGGATGGATGGATTCGTGTCATCTAGGATT 457  
QY 101 SerProAsnProLysCys-GlyLysAsnGlyValGlyValLeu-IleThrLysValPro 120  
DB 458 AGCCCAAAACCCCAAGCG-TGGGAAAAATGGGGTGGGTGCCA-GATTTGGAAGTTCCAG 515  
QY 120 aLserArgGlnPheAlaIleTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysI 140  
DB 516 TGAGCCGACAGTTTGCAGCTTATTGTTCACTCATCTGATGACTTGGACTTAATCGTGCA 575  
QY 140 leProGluIleIleThrThrLysAspProIlePhe-AsnThrGlnThrAlaThrGlnThr 159  
DB 576 TTCCAGAAATTATCACCACCAAGATCCCATACT-CAACACTCAAACTGCACACAAACA 634  
QY 160 ThrGluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIlePro 179  
DB 635 ACAGAAATTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTTCTACAATACCT 694  
QY 180 AlaProThrThrProProAlaProAlaSerThr 191



```

QY      153 hr 153
Db      592 CT 593

RESULT 35
CB269023
LOCUS   1007930 Human Fat Cell 5'-Stretch Plus cDNA Library Homo sapiens
DEFINITION
cDNA 5', mRNA sequence.
ACCESSION
CB269023
VERSION  CB269023.1 GI:28443608
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
1 (bases 1 to 473)
AUTHORS Yang,R.-Z., Shuldiner,A. and Gong,D.-W.
TITLE   EST analysis of human adipose gene expression
JOURNAL Unpublished (2002)
COMMENT Contact: Gong Da-Wei
Division of Endocrinology, Diabetes and Nutrition
University of Maryland
660 Redwood St, HH497, Baltimore, MD 21201, USA
Tel: 410 706 1672
Fax: 410 706 1622
Email: dgong@medicine.umaryland.edu
PCR Primers
FORWARD: CTCGGGAAGCGCCCATTTGTGTGGT
BACKWARD: AATACGACTACTATAGGCGGAATTGG
Seq primer: GTTGGTACCGGGAATTC.

FEATURES             source
    Location/Qualifiers
        1..473
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /sex="Male and Female"
            /tissue type="Adipose"
            /clone_lib="Human Fat Cell 5'-Stretch Plus cDNA Library"
            /note="Vector: lambdaTriplex"

ORIGIN
Alignment Scores:
Pred. No.:      5,82e-78      Length:      473
Score:          95.00      Matches:      95
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches:  0
Query Match:     29.50%      Indels:      0
DB:              14      Gaps:          0

US-10-079-111-1 (1-322) x CB269023 (1-473)

QY      1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu 20
Db      127 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCATTCCATCTGGACCGAGGCTCCTG 186

QY      21 ValGlnGlySerLeuArgLaGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db      187 GTCCAAAGGCTCTTTGGCGTGAGAAAGAGCTTTCCATCCAGGTGTCAGCAATATTGGGG 246

QY      41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db      247 ATCACCCCTTGTGAGCAAAAAGGCGAACCCAGCAGCTGATTTTCACAGAAGCTTAAGGAGGCC 306

QY      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db      307 TGTAGGCTGTGGGACTAAGTTTGGCGGCAAGGACCAAGTTTGAACACAGCTTGAAGCT 366

QY      81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheVal 95
Db      367 AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTCGTG 411

RESULT 36

```

```

BX366589      1201 bp      mRNA      linear      EST 08-MAY-2003
LOCUS         BX366589 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION    clone CSODI024YPI17 5-PRIME, mRNA sequence.
ACCESSION     BX366589
VERSION       BX366589.1 GI:30437038
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens

REFERENCE
1 (bases 1 to 1201)
AUTHORS       Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL       Full-length cDNA libraries and normalization
COMMENT       Unpublished (2001)
              Contact: Genoscope
              Genoscope - Centre National de Sequencage
              BP 191 91006 EVRY cedex - France
              Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
              Library was constructed by Life Technologies, a division of
              Invitrogen. This sequence belongs to sequence cluster 5952.r For
              more information about this cluster, see
              http://www.genoscope.cns.fr/
              cgi-bin/cluster.cgi?seq=CSOA1024CH09QPI&cluster=5952.r. Contact :
              Peng Liang Email : fliang@lifetech.com URL :
              http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
              Paraday Avenue Genoscope sequence ID : CSOA1024CH09QPI.

FEATURES             source
    Location/Qualifiers
        1..1201
            /organism="Homo sapiens"
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            /db_xref="taxon:9606"
            /clone="CSODI024YPI17"
            /tissue type="PLACENTA COT 25-NORMALIZED"
            /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
            /note="1st strand cDNA was primed with a NotI-oligo(dT)
            primer. Five prime end enriched, double-strand cDNA was
            digested with Not I and cloned into the Not I and EcoR V
            sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.:      1,53e-77      Length:      1201
Score:          95.00      Matches:      222
Percent Similarity: 97.80%      Conservative: 0
Best Local Similarity: 97.80%      Mismatches:  2
Query Match:     29.50%      Indels:      5
DB:              13      Gaps:          0

US-10-079-111-1 (1-322) x BX366589 (1-1201)

QY      14 IleTrpThrArgLeuLeuValGlnGlySerLeuArgAlaGluLeuSerIleGln 33
Db      203 ATCTGACACACGAGGCTCTCTGTCACAGGCTCTTTGCGTGCAGAGAGCTTTCATCCAG 262

QY      34 ValSerCysArgIleMetGlyIleThrLeuValSerLysLysAlaAsnGlnLeuAsn 53
Db      263 GTGTCAATGAGAAATATGGGATCACCCCTGTGTGAGCAAAAGCGCAACAGCAGCTGAAT 322

QY      54 PheThrGluAlaLysGluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGln 73
Db      323 TTCACAGAAGCTTAAGGAGGCTGTAGGCTGCTGGGACTAAGTTTGGCCGCGAAGGACCAA 382

QY      74 ValGluThrAlaLeuLysAlaSerPheGluThrCysSerTyrGlyTrpValGlyAspGly 93
Db      383 GTTGAACAGCCTTGAAGCTAGCTTTGAACTTTCAGCAGTATGGCTGGGTTGGAGATGA 442

QY      94 PheValValIleSerArgIleSerProAsnProLysCysGlyLysAsn-GlyValGlyVa 113
Db      443 TTCTGGTGTCTCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAWA-TGGGGTGGGTGT 501

QY      113 IleuIleTrpLysValProValSerArgGlnPheAlaIleTyrCysTyrAsnSerSerAs 133

```

```

Db      502 CCTGATTTGGAGGTTCCAGTGAGCGCAGAGTTTGTCAGCCTATTGTACAACTCATCTGA 561
QY      133 pThrTrpThrAsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnTh 153
Db      562 TACTTGAGCTAACTCGTGATTCAGAAATATATCACCACCAAGATCCCATATTTCAACAC 621
QY      153 rGlnThrAlaThrGlnThrThrGluPheIleValSerAspSerThr-TyrSerValAla 173
Db      622 TCAAACTGCAACACAAACACAGAAATTTATGTGAGTGACAGTTC-CTACTCGGTGGCAT 680
QY      173 exProTyrSerThrIleProAlaProThrThrThrProAlaProAlaSerThrSerI 193
Db      681 CCCTTACTCTCAATACCTGCCCTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 740
QY      193 leProArgArgLysLysLeuIleCysValThrGluValPheMetGluThrSerThrWets 213
Db      741 TTCACGGAGAAAAAATGATTTGTGTACAGAAAGTTTTTATCGAAACTAGCACCATGT 800
QY      213 erThrGluThrGluPro-PheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGly 232
Db      801 CTACAGAACTGAACCATTTTGTGAAATTAAGACAGCATTCAGAAATGAAGCTGCTGG 860
QY      233 PheGlyGlyValPro 237
Db      861 TTTGGAGGTGTCCTCCM 875

RESULT 37
H02823
LOCUS   Y141b11.r1 Soares placenta Nb2HP Homo sapiens cDNA clone
DEFINITION IMAGE:151365 5', mRNA sequence.
ACCESSION H02823.1 GI:865756
VERSION   H02823.1
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          1 (bases 1 to 411)
          Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
          Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
          Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
          Trevaskis,E., Waterston,R., Williamson,A., Woldmann,P. and
          Wilson,R.
          The WashU-Merck EST Project
          Unpublished (1995)
          Contact: Wilson RK
          Washington University School of Medicine
          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
          Tel: 314 286 1800
          Fax: 314 286 1810
          Email: est@wustl.wustl.edu
          High quality sequence stops: 326
          Insert Size: 2127
          Source: IMAGE Consortium, LLNL
          This clone is available royalty-free through LLNL; contact the
          IMAGE Consortium (info@image.llnl.gov) for further information.
          Insert length: 2127 Std Error: 0.00
          Seq primer: M13RP1
          High quality sequence stop: 326.
          Location/Qualifiers
            1..411
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              /mol_type="mRNA"
              /db_xref="GDB:563454"
              /db_xref="taxon:9606"
              /clone="IMAGE:151365"
              /sex="Female"
              /dev_stage="placenta obtained at birth (full term)"
              /lab_host="DH10B (ampicillin resistant)"
              /clone_lib="Soares placenta Nb2HP"
              /note="Organ: placenta; Vector: p773D (Pharmacia) with a
              modified polylinker; Site_1: Not 1; Site_2: Eco RI; 1st

```

```

strand cDNA was primed with a Not I - oligo(dT) primer [5',
AACTGGAAGAATTCGGCGCGCAGGAATTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p773 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo. "

ORIGIN
Alignment Scores:
Pred. No.: 4,29e-77 Length: 411
Score: 94.00 Matches: 94
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 29.19% Indels: 0
DB: 14 Gaps: 0

US-10-079-111-1 (1-322) x H02823 (1-411)
QY      114 LeuIleTrrPlySValProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAsp 133
Db      1 CTGATTGGAAGTTCCAGTGACCCACAGTTTGGAGCCTATTGTTCACAACTCATCTGAT 60
QY      134 ThrTrpThrAsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThr 153
Db      61 ACTTGGACTAACTCGTGCAATTCAGAAATTTATCACCACCAAGATCCCATATTTCAACACT 120
QY      154 GlnThrAlaThrGlnThrThrGluPheIleValSerAspSerThrThrValAlaSer 173
Db      121 CAAACTGCACACAAACACAGAAATTTATGTGAGTGACAGTACCTACTCGGTGGCATCC 180
QY      174 ProTyrSerThrIleProAlaProThrThrThrProAlaProAlaSerThrSerIle 193
Db      181 CCTTACTCTCAATACTGCTCCCTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTATT 240
QY      194 ProArgArgLysLysLeuIleCysValThrGluValPheMet 207
Db      241 CCACGGAGAAAAAATGATTTGTGTACAGAAAGTTTATG 282

RESULT 38
BI763579 877 bp mRNA linear EST 25-SEP-2001
LOCUS 603050140F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5190393 5',
DEFINITION mRNA sequence.
ACCESSION BI763579
VERSION   BI763579.1 GI:15755157
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          1 (bases 1 to 877)
          NIH-MGC http://mgc.nci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished (1999)
          Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Life Technologies, Inc.
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM11475 row: p column: 10
          High quality sequence stop: 715.
          Location/Qualifiers
            1..877
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="IMAGE:5190393"
              /lab_host="DH10B"

```







Peng Liang Email : fliang@lifetech.com URL :  
<http://fulllength.invitrogen.com/InvitrogenCorporation1600>  
 Faraday Avenue Genoscope sequence ID : CS0D1030AB05QP1.

## FEATURES

source  
 1. .1201  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CS0D1030YC09"  
 /issue\_type="PLACENTA COT 25-NORMALIZED"  
 /clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
 /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

Alignment Scores:  
 Pred. No.: 2,64e-67 Length: 1201  
 Score: 84.00 Matches: 84  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 26.09% Indels: 0  
 DB: 9 Gaps: 0

US-10-079-111-1 (1-322) x AL546565 (1-1201)

QY 77 AlaLeuLysAlaSerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValVal 96  
 DB 434 GCCTTGAAGTAGCTTTGAACTTCAGCTATGGCTGGTGGAGATGGATTCGGTGC 493  
 QY 97 IleSerArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTyr 116  
 DB 494 ATCTCAGATTAGCCCAACCCAGTGTGGAAATGGGGTGGTGTCTGATTTGG 553  
 QY 117 LysValProValSerArgGlnPheAlaIleTyrCysTyrAsnSerSerAspThrTyrThr 136  
 DB 554 AAGGTTCCAGTCAGCGACAGTTTGAGCTATTGTACACTCATCTGACTTGGACT 613  
 QY 137 AnSerCysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAla 156  
 DB 614 AACTCGTGCAATCCGAAATTATCACCAAGATCCCATATTCACACTCAAACTGCA 673  
 QY 157 ThrGlnThrThr 160  
 DB 674 ACACAAACAACA 685

## RESULT 43

T96904  
 LOCUS Ye52g09\_r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone  
 DEFINITION IMAGE:121408 5', mRNA sequence.

T96904

VERSION T96904.1 GI:735528

KEYWORDS EST.

SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 444)  
 Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,  
 Trevaskis,B., Waterson,R., Williamson,A., Wohldmann,P. and  
 Wilson,R.

## TITLE

The WashU-Merck EST Project

## JOURNAL

Unpublished (1995)

## COMMENT

Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu

Insert Size: 1301

High quality sequence stops: 254 Source: IMAGE Consortium, LLNL  
 This clone is available royalty-free through LLNL ; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1301 Std Error: 0.00

Seq primer: M13RPI

High quality sequence stop: 254.

## FEATURES

source

1. .444

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:473953"

/db\_xref="taxon:9606"

/clone="IMAGE:121408"

/sex="male"

/dev\_stage="20 week-post conception fetus"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares fetal liver spleen INFLS"

/note="Organ: Liver and Spleen; Vector: p77T3D (Pharmacia)  
 with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;  
 1st strand cDNA was primed with a Pac I - oligo(dT) primer  
 [5' AACTGGAAGAAATAATTAAAGATCTTTTTTTTTTTTTTTT 3'],  
 double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Pac I and cloned into the Pac I  
 and Eco RI sites of the modified p77T3 vector. Library  
 went through one round of normalization. Library  
 constructed by Bento Soares and M.Fatima Bonaldo."

## ORIGIN

Alignment Scores:  
 Pred. No.: 8,03e-67 Length: 444  
 Score: 83.00 Matches: 83  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 25.78% Indels: 0  
 DB: 14 Gaps: 0

US-10-079-111-1 (1-322) x T96904 (1-444)

QY 213 SerThrGluThrGluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGly 232  
 DB 13 TCTACAGAACTGAACCATTTCTGAAATAAAGCAGCATTCAGATGAAGCTGCTGG 72

QY 233 PheGlyGlyValProThrAlaLeuLeuValLeuAlaLeuLeuPhePheGlyAlaAla 252  
 DB 73 TTGGAGGTGTCCCGCGCTCTGCTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 132

QY 253 GlyLeuGlyPheCysTyrValLysArgTyrValLysAlaPheProPheThrAsnLysAsn 272  
 DB 133 GGCTCTGGATTTCATGTCATAAGGTATGTGAAGGCCCTCCCTTTTCAACCAAGAAT 192

QY 273 GlnGlnLysGluMetIleGluThrLysValValLysGluLysAlaAsnAspSerAsn 292  
 DB 193 CAGCAGAGGAATGATCGAAACCAAGTAGTAAAGGAGGAGAGCCCAATCATAGCAC 252

QY 293 ProAsnGlu 295

DB 253 CCTAATGAG 261

## RESULT 44

BG566260

LOCUS BG566260

DEFINITION BG566260.1 GI:13573913

ACCESSION BG566260

VERSION EST.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 794)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

794 bp mRNA linear EST 10-APR-2001

602585128F1 NIH\_MGC\_76 Homo sapiens cDNA clone IMAGE:4712863 5',

mRNA sequence.

EST.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 794)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

```

TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgabp@remail.nih.gov
           Tissue Procurement: CLONETECH Laboratories, Inc.
           cDNA Library Preparation: CLONETECH Laboratories, Inc.
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLC1555 row: 9 column: 08
           High quality sequence stop: 615.

FEATURES   Location/Qualifiers
            source
            1..794
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:4712863"
            /lab_host="DH10B (T1 phage-resistant)"
            /clone_lib="NIH_MGC_76"
            /notes="Organ: liver; Vector: pDNR-LIB (Clontech); Site_1:
            SfII (ggcgctcgcc); Site_2: SfII (ggccattggcc); 5' and
            3' adaptors were used in cloning as follows: 5' adaptor
            sequence: 5'-CACGGCATTATGGCC-3' and 3' adaptor sequence:
            5'-ATTCTAGAGCGGAGCGCGGCACATG-dT(30)BN-3' (where B = A,
            C, or G and N = A, C, G, or T). Average insert size 1.85
            kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
            by PCR. This library was enriched for full-length clones
            and was constructed by Clontech Laboratories (Palo Alto,
            CA). Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.:      1.47e-66      Length:      794
Score:          83.00         Matches:     96
Percent Similarity: 98.97%    Conservative: 0
Best Local Similarity: 98.97% Mismatches:    0
Query Match:    25.78%       Indels:       1
DB:             12           Gaps:       0

US-10-079-111-1 (1-322) x BG556260 (1-794)

QY      7  LeuValLeuLeuThrSerIleTrrThrArgLeuLeuValGlnGlySerLeuArg 26
Db      68 CTGGTGTTGCTTCTCACTTCCATCTGACACAGAGCTCTGTGTCAGAGCTCTTTGCGT 127

QY      27 AlaGluGluSerIleGlnValSerCysArgIleMetGlyIleThrLeuValSerLys 46
Db      128 GCAGAGAGAGCTTTCCATCCAGGTGTCTATGCAGAAATTATGGGATCACCTTTGTGCAAAA 187

QY      47 LysAlaAsnGlnLeuAsnPhetrrGluAlaLysGluAlaCysArgLeuLeuGlyLeu 66
Db      188 AAGCGCAACAGCAGCTGAATTTACAGAGCTTAAGGAGCCCTGTAGGCTGTGGGACTA 247

QY      67 SerLeuAlaGlyLysAspGlnValGlu-ThrAlaLeuLysAlaSerPheGluThrCysSe 86
Db      248 AGTTGGCCGCGCAGACCAAGTTGAACAGAGCTTTGAAGCTAGCTTTGAACCTTGCAG 307

QY      86 rTrpGlyTrpValGlyAspGlyPheValValIleSerArgIleSerPro 102
Db      308 CTATGCGTGGTGGAGATGATTCGTGGTGCATCTCTAGGATTAGCCCA 356

RESULT 45
AA297240
LOCUS   EST112782 Embryo, 12 week II Homo sapiens cDNA 5' end, mRNA
DEFINITION
ACCESSION   AA297240
VERSION     AA297240.1
KEYWORDS    GI:1949574
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 328)
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitchugh,W.M., Hedblom,E., Hitchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hitchman,J.L., Geoghagen,N.S.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palances,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
96026280
Other ESTs: THCL179312
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tcdb/hgi/hgi.html)
Seq primer: M13 Reverse.

FEATURES   Location/Qualifiers
            source
            1..328
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="ATCC (inhost):131278"
            /db_xref="taxon:9606"
            /dev_stage="embryo, 12 wks"
            /clone_lib="Embryo, 12 week II"
            /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
            XhoI"

ORIGIN
Alignment Scores:
Pred. No.:      1.4e-58      Length:      328
Score:          74.00         Matches:     74
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    22.98%       Indels:       0
DB:             9           Gaps:       0

US-10-079-111-1 (1-322) x AA297240 (1-328)

QY      1  MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrrThrArgLeuLeu 20
Db      70 ATGGCCAGGTGTTTACGCTGGTGTCTTCTTCTTCCATCTGGACACAGAGCTCTCTG 129

QY      21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db      130 GTCCAAAGGCTCTTGTGCTGCAAGAGCTTCCATCCAGGTGTCTGCAAGATTATGGGG 189

QY      41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPhetrrGluAlaLysGluAla 60
Db      190 ATCACCCCTTGTGAGCAAAAAGGCGACACAGAGCTGAATTTCCACAGAAGCTAGAGGCC 249

QY      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnVal 74

```

```

Db      250 TGTAGGCTGCTGGCACTAAGTTTGGCGGCAAGGACCAAGTT 291
RESULT 46
AY411057
LOCUS   Homo sapiens XLK1D1 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION
ACCESSION AY411057 793 bp DNA linear GSS 16-DEC-2003
VERSION   AY411057 genomic survey sequence.
KEYWORDS  GSS.
SOURCE    AY411057.1 GI:39767025
ORGANISM  Homo sapiens (human)
REFERENCE 1 Homo sapiens
AUTHORS   Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
          1 (bases 1 to 793)
          Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
          Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
          Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
          Adams,M.D. and Cargill,M.
          Inferring nonneutral evolution from human-chimp-mouse orthologous
          gene trios
          Science 302 (5652), 1960-1963 (2003)
          14671302
          2 (bases 1 to 793)
          Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
          Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
          Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
          Adams,M.D. and Cargill,M.
          Direct Submission
          Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
          Rockville, MD 20850, USA
          This sequence was made by sequencing genomic exons and ordering
          them based on alignment.
          Location/Qualifiers
          1..793
             /organism="Homo sapiens"
             /mol_type="genomic DNA"
             /db_xref="taxon:9606"
             <!-->793
             /genes="XLK1D1"
             /locus_tag="HCM4097"
gene
ORIGIN
Alignment Scores:
Pred. No.:      2,97e-57      Length:      793
Score:          73.00        Matches:     73
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    22.67%       Indels:      0
DB:             29          Gaps:       0

US-10-079-111-1 (1-322) x AY411057 (1-793)
QY      60 AlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLys 79
Db      2 GCCTGTAGGCTGCTGGCACTAAGTTTGGCGGCAAGGACCAAGTTGAAAGCCTTGAAA 61
QY      80 AlaSerPheGluThrCysSerTyTGlyTrpValGlyAspGlyPheValValIleSerArg 99
Db      62 GCTAGCTTTGAAACTTGCAGCTATGCTGGCTGGGTTGGAGATGGATTCTGTCATCTC 121
QY      100 IleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValPro 119
Db      122 ATTAGCCCAACCCCAAGTGTGGAAAAATGGGGTGGGTCTCTGATTGGAGAGTTCCA 181
QY      120 ValSerArgGlnPheAlaAlaTyCysTyAsnSerSer 132
Db      182 GTGAGCGGACAGTTTGCAGCCATTGTTACAATCACTCT 220

RESULT 47
BX418211
LOCUS   Homo sapiens FETAL BRAIN Homo sapiens cdna clone
DEFINITION
BX418211 Homo sapiens FETAL BRAIN Homo sapiens cdna clone
EST.
BX418211.1 GI:30765763
SOURCE   CSODF001YF23 5-PRIME, mRNA sequence.
ORGANISM Homo sapiens (human)
REFERENCE 1 Homo sapiens
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          1 (bases 1 to 990)
          Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
          Full-length cDNA libraries and normalization
          Unpublished (2001)
          Contact: Genoscope
          Genoscope - Centre National de Sequencage
          BP 191 91006 Evry cedex - France
          Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
          Library was constructed by Life Technologies, a division of
          Invitrogen. This sequence belongs to sequence cluster 5952.r For
          more information about this cluster, see
          http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSODF001CC12QP1&cluster=5952.r. Contact :
          Feng Liang Email : fliang@lifetech.com URL :
          http://fulllength.invitrogen.com/Invitrogen Corporation 1600
          Paraday Avenue Genoscope sequence ID : CSODF001CC12QP1.
          Location/Qualifiers
          1..990
             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /clone="CSODF001YF23"
             /tissue_type="FETAL BRAIN"
             /dev_stage="fetal"
             /clone_lib="Homo sapiens FETAL BRAIN"
             /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
                   was primed with a NotI-oligo(dT) primer. Five prime end
                   enriched, double-strand cDNA was digested with Not I and
                   cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                   vector. Library was not normalized."
ORIGIN
Alignment Scores:
Pred. No.:      2,32e-54      Length:      990
Score:          70.00        Matches:     117
Percent Similarity: 98.32%    Conservative: 0
Best Local Similarity: 98.32% Mismatches:    1
Query Match:    21.74%       Indels:      2
DB:             13          Gaps:       0

US-10-079-111-1 (1-322) x BX418211 (1-990)
QY      6 SerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeuValGlnGlySerLeu 25
Db      199 AGCTGTGTTGTCTTCTCACTTCCATCTGCACGAGGCTCTGTCGCAAGGCTCTTTG 258
QY      26 ArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGlyIleThrLeuValSer 45
Db      259 CGTGCAAGAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGGATCACCTTTG 318
QY      46 LysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAlaCysArgLeuLeuGly 65
Db      319 AAAAGGCGCAACACGACGCTGAATTTACAGAAGCTAGAGAGCCTGTAGGCTGTGGGA 378
QY      66 LeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAlaSerPheGluThrCy 85
Db      379 CTAAGTTTGGCGGCAAGGACCAAGTTGAAAM-AGCCTTGAAGAGTAGCTTTGAAACTTG 437
QY      85 sSerTyTGlyTrpValGlyAspGlyPheValValIleSerArgIleSerProAsnProLy 105
Db      438 CAGCTATGCTGGGTGGAGATGGATTCTGTGTCATCTCTAGGATTAGCCCAACCCCAA 497
QY      105 sCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProValSerArgGln 123
Db      498 GTGTGGAAAAATGGGGTGGGTGTTACTGATTGGAAGAGTTCCAGTGAGCAGACAG 552

```

```

RESULT 48
AY411058
LOCUS
DEFINITION
Pan troglodytes XLK01 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
AY411058
VERSION
AY411058.1 GI:39767026
KEYWORDS
GSS.
SOURCE
Pan troglodytes (chimpanzee)
ORGANISM
Pan troglodytes
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE
1 (bases 1 to 790)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
2 (bases 1 to 790)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Direct Submission
JOURNAL
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
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/gene="XLK01"
/locus_tag="HCM4097"
gene
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
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/gene="XLK01"
/locus_tag="HCM4097"
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Score: 58.00 Matches: 58
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 18.01% Indels: 0
DB: 29 Gaps: 0
US-10-079-111-1 (1-322) x AY411058 (1-790)
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QY 83 GluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIleSerPro 102
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Db 68 GAGACTTGACGCTATCGCTGGTGGTGGAGATGGATTCTGTGCTATCTCTAGGATTAGCCCA 127
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QY 103 AsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
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RESULT 49
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LOCUS
DEFINITION
fg03c09.y1 Human Iris cDNA (Normalized): fg Homo sapiens cDNA clone
fg03c09 5', mRNA sequence.
ACCESSION
CD671330
VERSION
CD671330.1 GI:32173061
KEYWORDS
EST.
SOURCE
Homo sapiens (human)

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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 529)
Wistow,G., Bernstein,S.L., Ray,S., Wyatt,M.K., Behal,A.,
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
TITLE
Expressed sequence tag analysis of adult human iris for the NRIBank
Project: steroid-response factors and similarities with retinal
pigment epithelium
JOURNAL
Mol. Vis. 8 (4), 185-195 (2002)
MEDLINE
22103462
PUBMED
12107412
COMMENT
Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 03 row: c column: 09
Seq primer: M13RPI reverse primer (ABI).
FEATURES
Location/Qualifiers
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1..529
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/db_xref="taxon:9606"
/clone="fg03c09"
/tissue_type="Iris"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Human Iris cDNA (Normalized): fg"
/notes="Organ: Eye; Vector: pCMVSPORT6; A human iris
library (bx) was normalized by self-subtraction. One
portion of double stranded plasmid DNA representing the
library was linearized by NotI. This NotI digested library
was used as a template for biotinylated RNA synthesis
using SP6 RNA polymerase. Another portion of the double
stranded plasmid library was converted to single-stranded
circles in vitro using Gene II and Exonuclease III (Life
Technologies). Single-stranded DNA (1 mg) was hybridized
(Cot 500) with 41 mg of Bio-RNA and vector blocking
oligonucleotides. The hybridized Bio-RNA/ss-circles were
removed by streptavidin:phenol extraction. EST analysis
was performed on the library at the NIH Intramural
Sequencing Center(NISC)."
ORIGIN
Alignment Scores:
Pred. No.: 1,3e-41 Length: 529
Score: 56.00 Matches: 56
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 17.39% Indels: 0
DB: 14 Gaps: 0
US-10-079-111-1 (1-322) x CD671330 (1-529)
QY 267 ProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThrLysValLysGluGlu 286
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QY 287 LysAlaAsnAspSerAsnProAsnGluGluSerLysLysThrAspLysAsnProGluGlu 306
|||||
Db 62 AAGCCCAATGATAGTACACCTTAATGAGGAATCAAGAGAAACTGATATAAAACCAGAGAG 121
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QY 307 SerLysSerProSerLysThrThrValArgCysLeuGluAlaGluVal 322
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Db 122 TCCAGAGTCCCAAGCAAAACTACCGTGGATGCTGGAAGCTGAAGTT 169
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RESULT 50
AA463325
LOCUS
DEFINITION
zx71f04.r1 Soares_total_fetus_ND2HF8_9w Homo sapiens cDNA clone

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IMAGE:796927 5', mRNA sequence.

ACCESSION AA463325  
 VERSION AA463325.1 GI:2188209  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 415)

AUTHORS Hillier, L., Allen, M., Bowles, J., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.  
 WashU-Merck EST Project 1997  
 Unpublished (1997)

TITLE  
 JOURNAL  
 COMMENT  
 Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -28ml3 rev2 ET from Amer sham

High quality sequence stop: 272.

#### FEATURES

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 /lab\_host="DH108"  
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 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from pooled 8-9 week (total) fetus material with a Not I - oligo(dT) primer [5' TGTTACATCTGAAGTGGAGGCGGCTTAATTTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

#### ORIGIN

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 Score: 55.00 Matches: 83  
 Percent Similarity: 98.81% Conservative: 0  
 Best Local Similarity: 98.81% Mismatches: 1  
 Query Match: 17.08% Indels: 1  
 DB: 9 Gaps: 0

US-10-079-111-1 (1-322) x AA463325 (1-415)

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 QY 27 AlaGluGluLeuSerIleGlnValSerCysArgIleMetGlyIleThrLeuValSerLys 46  
 Db |||||  
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 QY 47 LysAlaAsnGlnLeuAsnPheThrGluAlaLysGluAlaCysArgLeuLeuGlyLeu 66  
 Db |||||  
 256 AAGGCCAACGACGAGCTGAATTCACAGAAGCTAAGAGGCTGTAG-CTGCTGGGACTA 314  
 QY 67 SerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAlaSerPheGluThrCysSer 86  
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Search completed: September 16, 2004, 04:48:42  
 Job time : 3107 secs

Blank





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QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 783 TGTGTACAGAAGTGTATATGGAACCTAGCACCAGTGTCTACAGAACTGAACCATTTGTT 842
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db 843 GAAATATAACGACAGATTCAAGATGAAGCTGTGGTTCGAGGTGTCCCAACGGCTCTG 902
QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
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QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
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QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
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QY 321 GluVal 322
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## RESULT 2

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US-09-907-794A-200
; Sequence 200, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
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; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-794A-200

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Score: 322.00 Matches: 322
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-079-111-1 (1-322) x US-09-907-794A-200 (1-2372)

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QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
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QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
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QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValIleLeuTrpLysValProVal 120
Db 460 AGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCTGATTTGGAAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
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Db 460 AGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGTCTCTGATTTGGAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGGAGCTATTGTTACAACTCATCTGATCTTGGACTAACTCGTGCAAT 579
QY 141 ProGluLeuLeuThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTATCACCAACCAAGATCCCATATTTCAACACTCAACTGCAACACAAACA 639
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QY 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgLysLysLeuIle 200
Db 700 CCTACTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
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QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATTAAGACAGCATTCAGAAATGAAGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGCCCTTCCCTTTTACAAACAGAAATCAGCAGAGGAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysThr 300
Db 1000 AAGTAGTAGTAAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1059
QY 301 AspLysAsnProGluLysSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
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QY 321 GluVal 322
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## RESULT 4

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US-09-902-775A-200
; Sequence 200, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
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; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,775A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-902-775A-200
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## Alignment Scores:

Pred. No.:	8,62e-316	Length:	2372
Score:	322.00	Matches:	322
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-079-111-1 (1-322) x US-09-902-775A-200 (1-2372)

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QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGGCCAGGTGCTTCAGCGTGGTGTCTTCTCACTTCCATCTGCACCGAGGCTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTCGTCGAGAGAGCTTTCCATCCAGGTCATGCAGAAATTATGGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
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Db	280	ATCACCTTGTGAGCAAAAAGGGGAACCCAGCAGCTGAATTTCACAGAAGCTAGGAGGCC	339
Qy	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	340	TGTAGGCTGTGGGACTAAGTTTGGCCGGCAGACCAAGTTGGAACAGCCTTGAAGACT	399
Qy	81	SerPheGluThrCysSerTyrGlyTyrPValGlyAspGlyPheValValIleSerArgile	100
Db	400	AGCTTTGAAACTTCAGCTATGGCTGGTGGAGATGATTTCGTGGTCACTCTAGGATT	459
Qy	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleThrLysValProVal	120
Db	460	AGCCCAAAACCCAAAGTGTGGGAAAAATGGGGTGGGTCTCTGATTTGGAAAGGTTCAGTG	519
Qy	121	SerArgGlnPheAlaIaTyrCysTyrAsnSerSerAspThrThrThrAsnSerCysIle	140
Db	520	AGCCGACAGTTTGCAGCCTATTGTTTCAACTCATCTGATACTTGGACTAACTCGTGCATT	579
Qy	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	580	CCAGAAATATACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA	639
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Db	640	GAATTTATTTGCAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTCAAACTACCTGCC	699
Qy	181	ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Db	700	CCTACTACTCTCTCTCTCTCGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTCATT	759
Qy	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	760	TGTGTCAACAAGTTTTTATGGAACTAGCACCATGTCTACAGAAAACTGAACCATTTGTT	819
Qy	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	820	GAATAATAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGAGGTGCCCAAGCGCTCTG	879
Qy	241	LeuValLeuAlaLeuLeuPhePheGlyValAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	880	CTAGTCTTGTCTCTCTCTTCTTGGTGTCTGACGCTGGTCTTGATTTTGCATGTCAAA	939
Qy	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr	280
Db	940	AGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAAATCAGCAGAAGAGAAATGATCGAAACC	999
Qy	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
Db	1000	AAAGTAGTAAAGGAGGAGGAGGCCAATGATAGCAACCTTAATGAGGAATCAAGAAACT	1059
Qy	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1060	GATAAAACCCAGAGAGTCCAGAGAGTCCAGCAAAACACTACCGTGCATGCTCGAAGCT	1119
Qy	321	GluVal 322	
Db	1120	GAAGTT 1125	

## RESULT 5

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RESOL1_5					
US-09-833-381-849					
; Sequence 849, Application US/09833381					
; Patent No. 6672186					
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; GENERAL INFORMATION:					
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; APPLICANT: Robison, Keith E.					
:					
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs					
:					
; FILE REFERENCE: 5800-119					
:					
; CURRENT APPLICATION NUMBER: US/09/833,381					
:					
; CURRENT FILING DATE: 2001-04-11					
:					
; PRIOR APPLICATION NUMBER: 09/516,448					
:					
; PRIOR FILING DATE: 2000-02-29					
:					
; NUMBER OF SEQ ID NOS: 2050					
:					
; SOFTWARE: Fast-SEO for Windows Version 3.0					
:					
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RESULT 11
US-09-724-864-28
; Sequence 28, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Muirson, James G.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; FILE REFERENCE: 11000.1050U1
; CURRENT APPLICATION NUMBER: US/09/724,864
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 1896
; TYPE: DNA
; ORGANISM: Mouse
US-09-724-864-28

Alignment Scores:
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Score: 29.00 Matches: 29
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.01% Indels: 0
DB: 4 Gaps: 0

US-10-079-111-1 (1-322) x US-09-724-864-28 (1-1896)
QY 224 AlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThraLeuLeuValLeu 243
Db 719 GCAGCATTCAGAACGACGCTGGTTTGGAGGTGTCGCCACCGCCCTGCTGGTGTG 778
QY 244 AlaLeuLeuPhePheGlyAlaAlaAla 252
Db 779 GCTCTCTCTTCTTTGGTGTGCTGCCGCT 805

RESULT 12
US-09-907-794A-205
; Sequence 205, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14

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; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 205
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-907-794A-205

Alignment Scores:
Pred. No.: 4.39e-08 Length: 50
Score: 16.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.97% Indels: 0
DB: 4 Gaps: 0

US-10-079-111-1 (1-322) x US-09-907-794A-205 (1-50)
QY 59 GluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspClnVal 74
Db 3 GAGGCTGTAGGCTGCTGGACTAGTTTGGCGCGCAGGACCAAGTT 50

RESULT 13
US-09-905-125A-205
; Sequence 205, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman

```

APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/905,125A  
CURRENT FILING DATE: 2001-07-12  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR FILING DATE: 1999-07-07  
PRIOR FILING DATE: 1999-07-26  
PRIOR FILING DATE: 1999-07-28  
PRIOR FILING DATE: 1999-09-15  
PRIOR FILING DATE: 1999-09-15  
PRIOR FILING DATE: 1999-09-15  
PRIOR FILING DATE: 1999-10-05  
PRIOR FILING DATE: 1999-11-29  
PRIOR FILING DATE: 1999-11-30  
PRIOR FILING DATE: 1999-11-30  
PRIOR FILING DATE: 1999-12-02  
PRIOR FILING DATE: 1999-12-02  
PRIOR FILING DATE: 1999-12-16  
PRIOR FILING DATE: 1999-12-20  
PRIOR FILING DATE: 1999-12-20  
PRIOR FILING DATE: 1999-12-20  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 205  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-905-125A-205

Alignment Scores:  
Pred. No.: 4,39e-08  
Score: 16.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 4.97%  
DB: 0  
Length: 50  
Matches: 16  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Gaps: 0

US-10-079-111-1 (1-322) x US-09-905-125A-205 (1-50)  
Qy 59 GluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnVal 74  
Db 3 GAGGCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGCAAGTT 50  
RESULT 14  
US-09-902-775A-205  
Sequence 205, Application US/09902775A  
Patent No. 6686451  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/902,775A  
CURRENT FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR FILING DATE: 1999-07-07  
PRIOR FILING DATE: 1999-07-26  
PRIOR FILING DATE: 1999-07-28  
PRIOR FILING DATE: 1999-09-08  
PRIOR FILING DATE: 1999-09-13  
PRIOR FILING DATE: 1999-09-15  
PRIOR FILING DATE: 1999-09-15  
PRIOR FILING DATE: 1999-09-15  
PRIOR FILING DATE: 1999-10-05  
PRIOR FILING DATE: 1999-10-05  
PRIOR FILING DATE: 1999-11-29  
PRIOR FILING DATE: 1999-11-30  
PRIOR FILING DATE: 1999-12-02  
PRIOR FILING DATE: 1999-12-02  
PRIOR FILING DATE: 1999-12-16  
PRIOR FILING DATE: 1999-12-20  
PRIOR FILING DATE: 1999-12-20  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 205  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-905-125A-205

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; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 205
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-902-775A-205

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Alignment Scores:
Pred. No.:      4.39e-08      Length:      50
Score:          16.00         Matches:    16
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:      4.97%       Indels:      0
DB:               4          Gaps:         0

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US-10-079-111-1 (1-322) x US-09-902-775A-205 (1-50)

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QY  59  GluAlaCysArgLeuGlyLeuSerLeuAlaGlyLysAspGlnVal 74
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Search completed: September 16, 2004, 04:50:06  
Job time : 109 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 15, 2004, 16:31:46 ; Search time 4676 Seconds  
(without alignments)  
2984.700 Million cell updates/sec

Title: US-10-079-111-1  
Perfect score: 322  
Sequence: 1 MARCFSLVLLTTSIWTTRLL.....NPESKSPSKTVRCLEAEV 322

Scoring table: OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Word size: 12

Total number of hits satisfying chosen parameters: 43

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Command line parameters:  
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-Q=/cgn2\_1/USPTO\_spool/US10079111/runat\_13092004\_102224\_13988/app\_query.fasta\_1.519  
-DB=GenEmbl -QWMT=fastap -SUFFIX=olig.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
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-DOCALIGN=200 -THR SCORE=quality -THR MIN=12 -ALIGN=50 -MODE=LOCAL -OUTFMT=ptc  
-NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

GenEmbl: \*  
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2: gb\_hg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vl: \*  
15: em\_ba: \*  
16: em\_fun: \*  
17: em\_hum: \*  
18: em\_in: \*  
19: em\_mu: \*  
20: em\_om: \*  
21: em\_or: \*  
22: em\_ov: \*  
23: em\_pat: \*  
24: em\_ph: \*  
25: em\_pl: \*  
26: em\_ro: \*  
27: em\_sts: \*  
28: em\_un: \*

em\_vi: \*  
30: em\_htg\_hum: \*  
31: em\_htg\_inv: \*  
32: em\_htg\_other: \*  
33: em\_htg\_mus: \*  
34: em\_htg\_pln: \*  
35: em\_htg\_rdt: \*  
36: em\_htg\_mam: \*  
37: em\_htg\_vrt: \*  
38: em\_sy: \*  
39: em\_htgo\_hum: \*  
40: em\_htgo\_mus: \*  
41: em\_htgo\_other: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	322	100.0	1285	9	AF127670	Homo sapi
2	322	100.0	1755	6	AX136227	Sequence
3	322	100.0	1755	6	BD123566	Secretory
4	322	100.0	1755	9	AK075443	Homo sapi
5	322	100.0	2029	6	AR204700	Sequence
6	322	100.0	2029	6	BD222718	Human sig
7	322	100.0	2372	6	AR410761	Sequence
8	322	100.0	2372	6	AX092274	Sequence
9	322	100.0	2372	6	AX454446	Sequence
10	322	100.0	2372	6	AX490924	Sequence
11	322	100.0	2372	6	AX697609	Sequence
12	322	100.0	2372	6	BD075532	Secretory
13	322	100.0	2372	6	BD172392	Secreted
14	322	100.0	2372	6	BD172711	Secreted
15	322	100.0	2372	6	BD173030	Secreted
16	322	100.0	2372	6	BD173349	Secreted
17	322	100.0	2372	6	BD175383	Secretory
18	322	100.0	2372	9	AY358925	Homo sapi
19	221	68.6	2282	9	BC026231	Homo sapi
20	183	56.8	2313	9	AF118108	Homo sapi
21	125	38.8	716	6	AX136529	Sequence
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23	116	36.0	451	6	BD076146	5' EST of
24	103	32.0	165698	9	AC009532	Homo sapi
25	39	12.1	363	6	BD077623	5' EST of
26	37	11.5	373	6	BD073800	5' EST of
27	32	9.9	1613	4	AY372937	Bos tauru
28	29	9.0	1516	10	MMU311501	Mus muscu
29	29	9.0	2027	10	BC038653	Mus muscu
30	29	9.0	2027	10	BC038892	Mus muscu
31	28	8.7	59529	2	AC110451_3	Continuation (4 of
32	28	8.7	235382	2	AC130104	Rattus no
33	28	8.7	239307	2	AC129402	Rattus no
34	22	6.8	603	4	AY304537	Sus scrofa
35	16	5.0	50	6	AR410765	Sequence
36	16	5.0	50	6	AX697614	Sequence
37	16	5.0	50	6	BD075536	Secretory
38	16	5.0	50	6	BD172396	Secreted
39	16	5.0	50	6	BD172715	Secreted
40	16	5.0	50	6	BD173034	Secreted
41	16	5.0	50	6	BD173353	Secreted
42	16	5.0	50	6	BD175387	Secretory
43	12	3.7	5883	8	SCEARP1	X77949 S. commune b

## ALIGNMENTS

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LOCUS

AF127670 1285 bp mRNA linear PRI 13-OCT-2000



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/db_xref="taxon:9606"
201..1169
/notes="unnamed protein product"
/codon_start=1
/protein_id="CAC39756.1"
/db_xref="GI:14272636"
/db_xref="REMBEL:CAC39756"
/translation="MARCFSLVLLTSIWTRLLVQGSURAELSIQVSCRMGITLV
SKKAAQQLNFTAKACRLGLSLAGKQDVETALKASFETCSYGMWDFVVISRISP
NPKCGKNGVGLVWKVPVSRQFAAYCYNSSDTWNSCIPEIITTKDPIENTATQTTP
EFIVSDSTYSVASPTSTIPATTPAPASTSIPIRKKLICVTEVFMESTWSTETP
FVENKAAPKNEAAGFGVPTALLVLALLFPGAAGLGFYKRYVKAFFPTKNQOKE
METKVKVEKANDSNPNEESKTKDNPEKSPSKTTVRCLEAEV"

ORIGIN
Alignment Scores:
Pred. No.: 0 Length: 1755
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-079-111-1 (1-322) x AX136227 (1-1755)
QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTyrThrThrArgLeuLeu 20
Db 201 ATGGCCAGGTGCTTCAGCGTGGTGTGCTTCTCACTTCCATCTGGACACGAGGCTCCTG 260
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 261 GTCCAAAGGCTCTTCGCTGCAGAAAGCTTCCATCCAGGTGTCAGCAAGATTATGGGG 320
QY 41 IleThrLeuValSerIlylsAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 321 ATCACCCITGTGAGCAAAAGGCAACAGCAGCTGAATTTACAGAGCTTAAGAGGCC 380
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 381 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 440
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100
Db 441 AGCTTTGAACCTTGACGCTATGGCTGGGTGGAGATGGAATTCGTGTCATCTCTAGGAT 500
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 501 AGCCCAAAACCCCAAGTGTGGGAAAATGGGGTGGGTGCTGATTTGGNAGGTTCCAGTG 560
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTyrThrAsnSerCysIle 140
Db 561 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTTGGACTAACTCGTGCA 620
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 621 CCAGAAATTAATACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA 680
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 681 GAATTTATTGTGAGTGACAGTACTTACTCGTGGCATCCCTTACTCTACATACTCTGCC 740
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuLe 200
Db 741 CCTACTACTACTCCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGAT 800
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 801 TGTGTACAGAAAGTTTTATGGAAACTAGCACCATGCTCTACAGAAACTGAACCATTTGT 860
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db 201 ATGGCCAGGCTGCTTCCAGCTGGTGTGCTTCTCACTTCCATCTGGACACGAGGCTCCTG 260

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Db 861 GAAATAAAGCAGCATTCAAGATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 920
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 921 CTAGTGCTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 980
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 981 AGGTATGTGAAGGCTCTCCCTTTTACAAACAAGAATCAGCAGAAGAAATGATCGAAACC 1040
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1041 AAAGTAGTAAAGAGAGAGAGAGCCCATGATACCAACCTTAATGAGAAATCAAGAAACT 1100
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1101 GATAAAACCCAGAGAGTCCAAAGAGTCCCAAGAACTACCGTGCATGCTCGGAAGCT 1160
QY 321 GluVal 322
Db 1161 GAAGTT 1166

RESULT 3
BD123566
LOCUS BD123566
DEFINITION Secretory protein or membrane protein.
ACCESSION BD123566
VERSION BD123566.1 GI:23218511
KEYWORDS JP 2002017376-A/75.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1755)
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
Hayashi,K.
TITLE Secretory protein or membrane protein
JOURNAL Patent: JP 2002017376-A 75 22-JAN-2002;
HELIX RESEARCH INSTITUTE
COMMENT OS Homo sapiens (human)
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PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253173
PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,YURI KAWAI,TOMOYASU
SUGIYAMA,
PI KOJI HAYASHI
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	LTVS-1 mRNA.		
ACCESSION	AK075443		
VERSION	AK075443.1 GI:22761535		
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Db	741	CCTACTACTACTCTCTCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	800
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Db	921	CTAGTCTTGTCTCTCTCTCTTCTTGTGCTGCAGCTGGTCTTGGATTTTGTATGTCAA	980
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	981	AGGTATGTGAAGCCCTTCCCTTTTACAAACAGAAATCAGCAGAAGAAATGATCGAAACC	1040
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LOCUS			
DEFINITION	AK075443 1755 bp mRNA linear PRI 03-SEP-2002		
	Homo sapiens cDNA PSEC0135 fis, clone PLACE1004850, highly similar		
	to Homo sapiens lymphatic endothelium-specific hyaluronan receptor		
	LTVS-1 mRNA.		
ACCESSION	AK075443		
VERSION	AK075443.1 GI:22761535		





Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 2029)  
**REFERENCE**  
**AUTHORS**  
 Lal, P., Tang, Y.T., Gorgone, G.A., Corley, N.C., Guegler, K.J.,  
 Baughn, M.R., Akerblom, I.E., Young, J.A., Yue, H., Patterson, C.,  
 Reddy, R., Hillman, J.L. and Bandman, O.  
**TITLE**  
**JOURNAL**  
 Human signal peptide-containing protein  
 Patent: JP 2002519030-A 64 02-JUL-2002;  
**COMMENT**  
 INCYTE PHARMACEUTICALS INC  
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 PN JP 2002519030-A/64  
 PD 02-JUL-2002  
 PF 25-JUN-1999 JP 2000557363  
 PR 26-JUN-1998 US 60/090762, 31-JUL-1998 US 60/094983 PR  
 01-OCT-1998 US 60/102686, 11-DEC-1998 US 60/112129 PI PREETI  
 LAL, Y TOM TANG, GINA A GORGONE, NEIL C CORLEY, KARL J PI GUEGLER,  
 PI MARIAH R BAUGHN, INGRID E AKERBLOM, JANICE AU YOUNG, HENRY YUE,  
 CHANDRA PATTERSON, ROOPA REDDY, JENNIFER L HILLMAN, OLGA BANDMAN  
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**ORGANISM** Unknown.  
**REFERENCE** Unclassified.  
**AUTHORS** 1 (bases 1 to 2372)  
 Ashkenazi, A., Botstein, D., Desnoyers, L., Eaton, D. L., Ferrara, N.,  
 Filvaroff, E., Fong, S., Gao, W.-Q., Gerber, H., Gerritsen, M. E.,  
 Goddard, A., Godowski, P. J., Grimaldi, J. C., Gurney, A. L., Hillan, K. J.,  
 Kldavin, I. J., Mather, J. P., Pan, J., Paoni, N. P., Roy, M. A.,  
 Stewart, T. A., Tumas, D., Williams, P. M. and Wood, W. I.  
**TITLE** Secreted and transmembrane polypeptides and nucleic acids encoding  
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**JOURNAL** Patent: US 6635468-A 200 21-OCT-2003;  
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Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,  
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,  
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.  
and Ye, W.  
Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis  
Patent: WO 0208284-A 31 31-JAN-2002;  
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone  
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,  
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;  
Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)  
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;  
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William  
I. (US)  
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ACCESSION AX490924  
VERSION AX490924.1 GI:22323799

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KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Homo sapiens
REFERENCE     1
AUTHORS      Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
              Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
              Paoni, N.F., Stephan, J.F., Watanabe, C.K., Williams, P.M., Wood, W.I.
              and Ye, W.
TITLE        Compositions and methods for the diagnosis and treatment of
              disorders involving angiogenesis
JOURNAL      Patent: WO 0200690-A 31 03-JAN-2002;
              Genentech, Inc. (US)
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ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Ashkenazi, A.J., Botstein, D., Desnoyers, L., Eaton, D.L., Ferrara, N.,
              Filvaroff, E., Fong, S., Gao, W.Q., Gerber, H., Gerritsen, M.E.,
              Goddard, A., Godowski, P.J., Grimaldi, C.J., Gurney, A.L., Hillan, K.J.,
              Kljavin, I.J., Mather, J.P., Pan, J., Paoni, N.F., Roy, M.A.,
              Stewart, T.A., Tumas, D., Williams, P.M. and Wood, W.I.
              Secreted and transmembrane polypeptides and nucleic acids encoding
              the same
              Patent: WO 0104311-A 200 18-JAN-2001;
              Genentech Inc. (US)
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Score:          322.00  Matches:      322
Percent Similarity: 100.00%  Conservative: 0
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LOCUS

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VERSION

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KEYWORDS

JP 2001516580-A/165

SOURCE

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ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 2372)

AUTHORS

Wood,W.I., Gurney,A.L., Goddard,A., Penica,D., Chen,J. and Yuan,J.

TITLE

JOURNAL

COMMENT

Patent: JP 2001516580-A 165 02-OCT-2001;

GENENTECH INC

OS Homo sapiens (human)

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PD 02-OCT-2001

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PI WILLIAM I WOOD,AUSTIN L GURNEY,AUDLEY GODDARD,DIANE PENICA, PI

JEAN CHEN,

PI JEAN YUAN

PC C12N15/09,C07K14/47,C07K14/705,C07K16/18,C07K16/28,C07K19/00,

PC C12N1/19,

PC C12N1/21,C12N5/10,C12P21/02,C12P21/08,C12Q1/02,C12P21/08, PC

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CC Secretory and transmembrane polypeptide and nucleic acid encoding the same

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AUTHORS	Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.		

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Db	820	GAATAATAAGCAGCATTTCAAGATGAAGCTGCTGGGTTTGGAGGTGTCCCAACGGCTCTG	879
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Db	880	CTAGTGCTGCTCTCTCTCTCTTTTGGTGTGTCAGCTGGTCTTGATTTGCTATGCAAA	939
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr	280
Db	940	AGGTATGTAGGCTTCCCTTTTACAAACAAGATCAGCAGAGGAATGATCGAAACC	999
QY	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysThr	300
Db	1000	AAAGTAGTAAGGAGGAGAGGCAATGATAGCAACCTTAATGAGGAATCAAGAAAACT	1059
QY	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1060	GATAAAACCCAGAGAGTCCAAAGTCCAAAGTCCAAAGTCCCGTGGATGCTTGGAGCT	1119
QY	321	GluVal 322	
Db	1120	GAAATT 1125	
RESULT 14			
LOCUS	BD172711		
DEFINITION	Secreted and transmembrane polypeptides and nucleic acids encoding the same.		
ACCESSION	BD172711		
VERSION	BD172711.1	GI:28414015	
KEYWORDS	JP 2002238586-A/165.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 2372)		
AUTHORS	Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.		

TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same									
JOURNAL	Patent: JP 2002238586-A 165 27-AUG-2002; GENENTECH INC									
COMMENT	OS Homo sapiens (human) PN JP 2002238586-A/165 PD 27-AUG-2002 JP 2001385205 PF 18-DEC-2001 JP 60/059115,17-SEP-1997 US 60/059184 PR PR 17-SEP-1997 US 60/059122,17-SEP-1997 US 60/059117 PR 17-SEP-1997 US 60/059113,17-SEP-1997 US 60/059121 PR 17-SEP-1997 US 60/059119,18-SEP-1997 US 60/059263 PR 18-SEP-1997 US 60/059266,15-OCT-1997 US 60/062125 PR 17-OCT-1997 US 60/062287,17-OCT-1997 US 60/062285 PR 21-OCT-1997 US 60/063486,24-OCT-1997 US 60/062816 PR 24-OCT-1997 US 60/062814,24-OCT-1997 US 60/063127 PR 24-OCT-1997 US 60/063045,24-OCT-1997 US 60/063128 PR 27-OCT-1997 US 60/063329,27-OCT-1997 US 60/063327 PR 28-OCT-1997 US 60/063549,28-OCT-1997 US 60/063541 PR 28-OCT-1997 US 60/063550,28-OCT-1997 US 60/063542 PR 28-OCT-1997 US 60/063544,28-OCT-1997 US 60/063564 PR 29-OCT-1997 US 60/063734,29-OCT-1997 US 60/063738 PR 29-OCT-1997 US 60/063704,29-OCT-1997 US 60/063435 PR 29-OCT-1997 US 60/064215,29-OCT-1997 US 60/063735 PR 29-OCT-1997 US 60/063732,31-OCT-1997 US 60/064103 PR 31-OCT-1997 US 60/063870,31-OCT-1997 US 60/064248 PR 07-NOV-1997 US 60/064809,12-NOV-1997 US 60/065186 PR 17-NOV-1997 US 60/065846,18-NOV-1997 US 60/065693 PR 21-NOV-1997 US 60/066120,21-NOV-1997 US 60/066364 PR 24-NOV-1997 US 60/066772,24-NOV-1997 US 60/066466 PR 24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR 24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI JIAN ZHENG, PI JEAN YUAN PC C12N15/09,C07K14/47,C07K16/18,C07K19/00,C12N1/19,C12N1/21, PC C12N5/10, PC C12P21/02//C12P21/08,(C12N1/19,C12R1:645),(C12N1/21,C12R1:19), PC (C12N5/10,C12R1:91),(C12P21/02,C12R1:91),(C12P21/02,C12R1:645), PC (C12P21/02,C12R1:19),(C12P21/08,C12R1:91),C12N5/00,C12N5/00, PC (C12N5/00,C12R1:91) CC Secreted and transmembrane polypeptides and nucleic acids encoding the same FH Key Location/Qualifiers FT source 1..2372 /organism='Homo sapiens (human)'. FEATURES source 1..2372 /organism='Homo sapiens' /mol_type='genomic DNA' /db_xref='taxon:9606' ORIGIN Alignment Scores: Pred. No.: 0 Length: 2372 Score: 322.00 Matches: 322 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0 DB: 6 Gaps: 0 US-10-079-111-1 (1-322) x BD172711 (1-2372) QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20 Db 160 ATGGCCAGGTGCTTCAGCGCTGGTGTGCTTCTCACTTCCATCTGGACACAGAGCTCTG 219 QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40 Db 220 GTCCAAAGGCTCTTTGGTGCAGAGAGCTTTCCATCCAGGTGTGCATGCAAGATTATG 279									



QY	41	IleThrLeuValSerIysAlaAsnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	280	ATCACCTTGTGAGCAAAAGCGAACCGAGCTGAATTCACAGAACTAAGGAGGCC	339
QY	61	CysArgLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	340	TGTAGCGTCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACGCTTGAAGCT	399
QY	81	SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle	100
Db	400	AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGAATTCGTCATCTCTAGGATT	459
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
Db	460	AGCCCAACCCCAAGTGTGGGAAATGGGTGGGTGCTCTGATTGGGAAGTTCGAGTG	519
QY	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	520	AGCCGACAGCTTTCAGCCCTATTGTTACAACTCATCTGATACTTGGACTAACTCGTGCATT	579
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	580	CCAGAAATATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA	639
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	640	GAATTTATGTGAGTGACAGTACTACTCGTGGCATCCCTTACTTCAATATCTGCC	699
QY	181	ProThrThrThrProProAlaProLaserThrSerIleProArgArgLysLysLeuIle	200
Db	700	CCTACTACTACTCTCTCTCCAGCTCCACTTCTATTTCCACGGAGAAAAAATTGATT	759
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	760	TGTGTACAGAAAGTTTTTATGGAATAGCACCATTCTACAGAACTGAACATTGTT	819
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	820	GAATATTAAGCAGCATTCAGAAATGAAGCTGTGGTTGGAGGTGTCCCCACGGCTCTG	879
QY	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	880	CTAGTGTCT	939
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr	280
Db	940	AGGTATGTGAAGCCCTTCCCTTTTACAAACAAGAAATCAGCAGAAGAAATGATCGAAAC	999
QY	281	LysValValLysGluLysAlaAsnAspSerAsnProAsnGluLysLysThr	300
Db	1000	AAAGTAGTAAGGAGGAGAGAGGCCAATGATACAAACCTTATGAGGAATCAAGAAACT	1059
QY	301	AspLysAsnProGluLysSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1060	GATAAAACCCAGAGAGTCCCAAGAGTCCCAAGAACTTACCCGAGTCCGCTGGAAGCT	1119
QY	321	GluVal	322
Db	1120	GAAGTT	1125
RESULT 15			
LOCUS	BD173030		
DEFINITION	Secreted and transmembrane polypeptides and nucleic acids encoding the same.		
ACCESSION	BD173030		
VERSION	BD173030.1	GI:28414336	
KEYWORDS	JP 2002238587-A/165.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1	(bases 1 to 2372)	

AUTHORS	Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same		
JOURNAL	Patent: JP 2002238587-A 165 27-AUG-2002;		
COMMENT	GENENTECH INC		
OS	Homo sapiens (human)		
PN	JP 2002238587-A/165		
PD	27-AUG-2002		
PF	18-DEC-2001	JP 2001385248	
PR	17-SEP-1997 US	60/059115,17-SEP-1997 US	60/059184 PR
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WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI			
JIAN ZHENG			
PI JEAN YUAN			
PC C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC C12N15/02,			
PC C12P21/02,C12P21/08/(C12P21/02,C12R1:91), (C12P21/02,C12R1:19), PC (C12P21/02,C12R1:645),C12N15/00,C12N5/00,C12N15/00 CC			Secreted and transmembrane polypeptides and nucleic CC acids encoding the same
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QY	21	ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly	40
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QY      61  CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
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QY      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
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QY      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db      580 CCAGAAATATTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA 639
QY      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
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QY      181 ProThrThrThrProProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db      700 CCTACTACTACTCCTCCTCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
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QY      241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db      880 CTAGTGTCTGCTCTCTCTCTTCTTGTGTGTGTCAGCTGGTCTTGGAATTTGCTATGTC 939
QY      261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db      940 AGGTATGTGAAGCCCTTCCCTTTTACAAACAAGAAATCAGCAGGAAGAAATGATCGAA 999
QY      281 LysValValLysGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db      1000 AAAGTAGTAAGAGGAGAGGAGCCCAATGATAGCAACCTTAATGAGGAATCAAGAANA 1059
QY      301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
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RESULT 16
LOCUS   BD173349
DEFINITION 2372 bp DNA linear PAT 18-FEB-2003
Secretd and transmembrane polypeptides and nucleic acids encoding
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ACCESSION BD173349
VERSION   BD173349.1 GI:28414660
KEYWORDS  JP 2002238588-A/165.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2372)
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AUTHORS  Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
Yuan,J.
TITLE     Secretd and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL   GENENTECH INC
COMMENT   OS Homo sapiens (human)
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24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR
24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI
WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI
JIAN ZHENG.
PI        JEAN YUAN
PC        C12N15/09, C07K14/435, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC
C12N5/10,
PC        C12P21/02/C12P21/08, (C12N1/19, C12R1:645), (C12N1/21, C12R1:19),
PC        (C12N5/10, C12R1:91), C12N15/00, C12N5/00, C12N5/00, C12N1:91) CC
Secretd and transmembrane polypeptides and nucleic CC
encoding the same
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Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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QY      1  MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db      160 ATGGCCAGGTGCTTCAAGCTGGTGTCTCTCACTTCCATCTGGACCAAGAGGCTCTG 219
QY      21  ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db      220 GTCCAAAGGCTCTTGGTGCAGAAAGAGCTTTCATCCAGTGTGTCATGCAATATATGGGG 279
QY      41  IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPhenThrGluAlaLysGluAla 60
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Db      280 ATCACCCCTGTGAGCAAAAAGCGAACCGAGCTGAATTCACAGAACCTAAGAGGCC 339
QY      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db      340 TGTAGCGCTGCTGGGACTAAGTTTGGCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399
QY      81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db      400 ACCTTTGAACCTTGACGCTATGGCTGGGTGGAGATGGATTCGTGCTCATCTCTAGGATT 459
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QY      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db      520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTGGACTAACTCGTGCAAT 579
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Db      640 GAATTTATGTGAGTGACAGTACTACTCGGTGGATCCCTTACTCTACATATCTGCC 699
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QY      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
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QY      261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
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LOCUS   BD175383
DEFINITION Secretory and transmembrane polypeptide and nucleic acid encoding
the same.
ACCESSION BD175383
VERSION   BD175383.1 GI:29121079
KEYWORDS JP 200253280-A/165.
SOURCE    Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
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Yuan,J.
Secretory and transmembrane polypeptide and nucleic acid encoding
the same
Patent: JP 200253280-A 165 10-SEP-2002;
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24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR
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WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI
JIAN ZHENG,
PI JEAN YUAN
PC C12N15/09,A61K45/00,A61P1/00,A61P13/12,A61P17/00,A61P17/06, PC
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QY      61  CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
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QY      101  SerProAsnProIysCysGlyLysAsnGlyValGlyValLeuIleTyrIysValProVal 120
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QY      121  SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTyrThrAsnSerCysIle 140
Db      520  AGCCGACAGTTTGCAGCTTATTTGTACAACTCATCTGATCTGGACTAAGTCTGTCATT 579
QY      141  ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db      580  CCAGAAATTTATCACCACCAAGATCCCATATTCACACACTCAAACTGCAACACAAACA 639
QY      161  GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
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QY      181  ProThrThrThrProProAlaProAlaSerThrSerIleProArgLysLysLeuIle 200
Db      700  CCTACTACTACTCTCTCTGCTCCAGCTTCCATCTTATTTCCACGGAGAAAAATTTGAT 759
QY      201  CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db      760  TGTGTACAGAAAGTTTTTATGGAACTAGCACCATGTCTACAGAACTGAACCATTTGTT 819
QY      221  GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db      820  GAAATAAAGCAGCATTCAGAAATGAAGTGTCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879
QY      241  LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
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QY      261  ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
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QY      281  LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db      1000  AAAGTAGTAAGGAGGAGGAGCCCAATGATAGCAACCCCTAATGAGGAATCAAGAGAACT 1059
QY      301  AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
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## RESULT 18

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LOCUS      AY358925
DEFINITION Homo sapiens clone DNA34431 XLK01 (UNQ230) mRNA, complete cds.
ACCESSION  AY358925
VERSION     AY358925.1 GI:37182967
KEYWORDS   FLI CDNA.
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 2372)  
 Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,  
 Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,  
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 Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,  
 Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,  
 Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,  
 Stinson,J., Vagts,A., Vandien,K., Watanabe,C., Wileand,D., Woods,K.,  
 Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,  
 Goddard,A., Wood,W.I. and Godowski,P.  
 The Secreted Protein Discovery Initiative (SPDI), a Large-Scale  
 Effort to Identify Novel Human Secreted and Transmembrane Proteins:  
 A Bioinformatics Assessment  
 Genome Res. 13 (10), 2265-2270 (2003)

JOURNAL  
 PUBMED  
 12975309  
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 Clark,H.F.  
 TITLE  
 Direct Submission  
 Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,  
 Inc., 1 DNA Way, South San Francisco, CA 94080, USA  
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Alignment Scores:  
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 Score: 322.00 Matches: 322  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
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 QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40  
 Db 220 GTCCAAGGCTCTTTGCGTGCAGAGAGCTTTCCATCCAGGTGTCATGAGAAATTATGGG 279  
 QY 41 IleThrLeuValSerLysIysAlaAenGlnLeuAsnPheThrGluAlaLysGluAla 60  
 Db 280 ATCAACCTTGTGAGCAAAAGCGCAACACGAGCTGGAATTCACAGAAGCTAAGGAGGCC 339  
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Qy	21	ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	106	GTCCAAAGGCTCTTTGGGTGCAGAGAGCTTTCATCCAGGTGTCTATCGAGAATATGSGG	165
Qy	41	IleThrIleuValSerLysLysAlaAsnGlnIleuAsnPheThrGluAlaLysGluAla	60
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Qy	220	lGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLe	240
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QY      180  AlaProThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeu 199
Db      628  GCCCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTG 687
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VERSION    AX136529.1 GI:14272933
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
TITLE      Secretory protein or membrane protein
JOURNAL    Patent: EP 1067182-A 451 10-JAN-2001;
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Db      441  ACCTTTGAAACTTGCAGCTATGCTGGGTGGGTGGATTCGTGTCATCTCTAGGATT 500
QY      101  SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
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QY      121  SerArgGlnPheAla 125
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ACCESSION BD123769
VERSION    BD123769.1 GI:23218714
KEYWORDS   JP 2002017376-A/278.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 716)
AUTHORS    Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
TITLE      Secretory protein or membrane protein
JOURNAL    Patent: JP 2002017376-A 278 22-JAN-2002;
           HELIX RESEARCH INSTITUTE
COMMENT     OS Homo sapiens (human)
           PN JP 2002017376-A/278
           PD 22-JAN-2002
           PF 07-JUL-2000 JP 2000253173
           PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,YURI KAWAI,TOMOYASU
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           PI KOJI HAYASHI
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QY 121 SerArgGlnPheAla 125
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ACCESSION  BD076146
VERSION     BD076146.1  GI:22621749
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ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE  1 (bases 1 to 451)
AUTHORS   Edwards,J.B.D.M., Duclert,A. and Lacroix,B.
TITLE     5' EST of tissue-nonspecific secretory protein
JOURNAL   Patent: JP 2001512011-A 94 21-AUG-2001;
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COMMENT    OS Homo sapiens (human)
          PN JP 2001512011-A/94
          PD 21-AUG-2001
          PF 31-JUL-1998 JP 2000505289
          PR 01-AUG-1997 US 08/905135
          PI JEAN BAPTISTE DUMAS MILNE EDWARDS, AYMERIC DUCLERT, BRUNO PI
            LACROIX
          PC C12N15/09,C12N15/09,C07K14/47,C12Q1/68,C12N15/00,C12N15/00 CC
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CC Von Heijne matrix
CC score 6.7
CC seq CFSILVLLTSLWT/TR
FH Key Location/Qualifiers
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FT misc feature 289..396
FT misc feature 422..453
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FT misc feature 222..289
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  Best Local Similarity: 100.00% Mismatches: 0
  Query Match:     36.02%       Indels:     0
  DB:              6           Gaps:       0
US-10-079-111-1 (1-322) x BD076146 (1-451)
QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 104 ATGGCCAGGTCTTCAGCTGGTGGTTCCTCCTCCATCCAGGACGAGGCTCCCTG 163
QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 164 GTCCAGAGCTCTTTGGTGCAGAGAGCTTCCATCCAGGTGTGATGCAGATTATGGGG 223
QY 41 IleThrLeuValSerIlyslsAlaAsnGlnGlnLeuAsnPhetrGluAlalysGluAla 60
Db 224 ATCACCCTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTCACAGAGCTAAGGAGGCC 283
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLeuAspGlnValGluThrAlaLeuLysAla 80
Db 284 TGTAGCTGTGGGACTAAGTTTGGCCGAGGACCAAGTTGAACACGCTTGAAGCT 343
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 344 AGCTTTGAACCTTGCAGCTATGCTGGTGGATGGATTCGTGTCATCTAGGATT 403
QY 101 SerProAsnProIlyslsCysGlyIlyslsGlyValGlyValLeuIleTrp 116
Db 404 AGCCCAACCCCAAGTGTGGGAAAATGGGGTGGTGTCTGATTTGG 451

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## RESULT 24

AC009532/c  
 LOCUS AC009532 165698 bp DNA linear PRI 07-SEP-2001  
 DEFINITION Homo sapiens chromosome , clone RP11-58H20, complete sequence.  
 ACCESSION AC009532  
 VERSION AC009532.9 GI:15487414  
 KEYWORDS HTG.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 JOURNAL 1 (bases 1 to 165698)  
 REFERENCE Birren,B., Linton,L., Nusbaum,C. and Lander,E.

REFERENCE  
 AUTHORS Homo sapiens chromosome, clone RP11-58H20  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 165698)

REFERENCE  
 AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,  
 Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A.,  
 Castle,A., Cerny,J., Collangelo,M., Collins,S., Collymore,A.,  
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 Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.  
 Direct Submission

TITLE Submitted (26-AUG-1999) Whitehead Institute/MIT Center for Genome  
 JOURNAL Research, 320 Charles Street, Cambridge, MA 02141, USA  
 REFERENCE 3 (bases 1 to 165698)

REFERENCE  
 AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,  
 Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B.,  
 Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,  
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 Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,  
 Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R.,  
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 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,  
 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.  
 Direct Submission

TITLE Submitted (07-SEP-2001) Whitehead Institute/MIT Center for Genome  
 JOURNAL Research, 320 Charles Street, Cambridge, MA 02141, USA  
 COMMENT On Sep 7, 2001 this sequence version replaced gi:14627146.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WBR  
 Web site: <http://www-seq.wi.mit.edu>  
 Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
 ----- Project Information  
 Center project name: L1647  
 Center clone name: 58\_H\_20

FEATURES  
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 /db\_xref="taxon:9606"  
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 19646..19769

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Score: 103.00 Matches: 103  
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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 31.99% Indels: 0  
DB: 9 Gaps: 0

US-10-079-111-1 (1-322) x AC009532 (1-165698)

QY 133 AspThrTrrPThrAsnSerCysIleProGluIleIleThrThrLysAspProIlePheAsn 152  
Db 12427 GATACCTGGACTACTCGTCGATTCAGAAATATCACCACCAAGATCCCATATTCAC 12369  
QY 153 ThrGlnThrAlaThrGlnThrThrGluPheIleValSerAspSerThrTyrSerValAla 172

Db 12367 ACTCAAACTGCACACAAACAGAAATTTATGTGAGTGACAGTACTACTCGTGGCA 12308  
QY 173 SerProTyrSerThrIleProAlaProThrThrThrProProAlaProAlaSerThrSer 192  
Db 12307 TCCCTTACTCTACAATACCTGCCCTACTACTACTCTCTCTCCAGCTTCCACTTCT 12248  
QY 193 IleProArgArgLysLysLeuIleCysValThrGluValPheMetGluThrSerThrMet 212  
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QY 213 SerThrGluThrGluProPheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGly 232  
Db 12187 TCTACAGAACTGACACCATTTGTTGAAAAATAAAGCAGCATTCAGAAATGAAGCTGCTGG 12128  
QY 233 PheGlyGly 235  
Db 12127 TTTGGAGGT 12119  
RESULT 25  
BD077623  
LOCUS 363 bp DNA linear PAT 27-AUG-2002  
DEFINITION 5'EST of secreted protein expressed in muscles and other mesodermal tissues.  
ACCESSION BD077623  
VERSION BD077623.1 GI:22623226  
KEYWORDS JP 2001512016-A/209.  
SOURCE Homo sapiens (human).  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 363)  
AUTHORS Edwards,J.B.D.M., Duclert,A. and Lacroix,B.  
TITLE 5'EST of secreted protein expressed in muscles and other mesodermal tissues  
JOURNAL Patent: JP 2001512016-A 209 21-AUG-2001;  
COMMENT GENSET  
OS Homo sapiens (human)  
PN JP 2001512016-A/209  
PD 21-AUG-2001  
PF 31-JUL-1998 JP 2000505295  
PR 01-AUG-1997 US 08/905134  
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, AYMERIC DUCLERT, BRUNO PI LACROIX  
PC C12N15/09,C12N15/09,C07K14/47,C12M1/00,C12N15/00,C12N15/00 CC  
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CC identity 97  
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CC id AA081350  
CC est  
CC blastn  
CC identity 97  
CC region 3..50  
CC id AA046671  
CC est  
CC Von Heijne matrix  
CC score 6.7  
CC seq CFSLLVLLTSIWT/TR  
CC n=a, g, c or t  
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 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 12.11% Indels: 0  
 DB: 6 Gaps: 0

US-10-079-111-1 (1-322) x BD077623 (1-363)

Qy 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu 20  
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 Db 157 ATGCCAGGCTCTTCAGCCTGGTGTCTTCACCTTCATCGACACGAGGCTCTG 216  
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 Qy 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMet 39  
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 Db 217 GTCCAGGCTCTTCGCGTCAGAGAGCTTTCATCCAGGCTGTCATGCAGAAATTATG 273  
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RESULT 26  
 BD073800 373 bp DNA linear PAT 27-AUG-2002  
 LOCUS 5'EST of secreted protein expressing in testis and other tissues.  
 DEFINITION  
 BD073800  
 ACCESSION  
 BD073800.1 GI:22619403  
 VERSION  
 JP 2001512012-A/204.  
 KEYWORDS  
 Homo sapiens (human)  
 SOURCE  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 1 (bases 1 to 373)  
 Bapatist,D.M.B.J., Eimeric,D. and Bruno,L.  
 5'EST of secreted protein expressing in testis and other tissues  
 Patent: JP 2001512012-A 204 21-AUG-2001;  
 JOURNAL  
 GENSET

OS Homo sapiens (human)  
 PN JP 2001512012-A/204  
 PD 31-AUG-2001  
 PF 31-JUL-1998 JP 2000505290  
 PR 01-AUG-1997 US 08/905279  
 PI DUMAS MILNE EDWARDS JEAN BAPUTIST,DUCLAIR EIMERIC,LACROIX PI  
 BRUNO  
 PC C12N15/09,A61K38/00,A61K48/00,C07K14/435,C07K19/00,C12P21/02,  
 C12Q1/68,  
 PC G01N33/50,G01N33/53,G01N33/53,G01N33/566,C12N15/00,A61K37/02  
 CC Strandedness: Double;  
 CC Topology: Linear;  
 CC Identity 98  
 CC region 1..124  
 CC id AA081350  
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 CC id AA046671  
 CC est  
 CC score 6.7  
 CC seq CFSLVLLLSIWT/TR  
 FT sig\_peptide 200..247.  
 Key Location/Qualifiers

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 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 11.49% Indels: 0  
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US-10-079-111-1 (1-322) x BD073800 (1-373)

Qy 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu 20  
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 Qy 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArg 37  
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 Db 260 GTCCAGGCTCTTCGCGTCAGAGAGCTTTCATCCAGGCTGTCATGCAGA 310  
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RESULT 27  
 AY372937 1613 bp mRNA linear MAM 27-OCT-2003  
 LOCUS Bos taurus cell surface retention sequence binding protein-1 mRNA,  
 DEFINITION complete cds.  
 ACCESSION  
 AY372937  
 VERSION  
 AY372937.1 GI:36304137  
 KEYWORDS  
 Bos taurus (cow)  
 SOURCE  
 ORGANISM  
 Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovidae; Bovinae; Bos.  
 REFERENCE  
 1 (bases 1 to 1613)  
 Huang,S.S., Tang,F.M., Huang,Y.H., Liu,I.H., Hsu,S.C., Chen,S.T.  
 and Huang,J.S.  
 Cloning, expression, characterization and role in autocrine cell  
 growth of cell surface retention sequence binding protein-1  
 J. Biol. Chem. 278 (44), 43855-43869 (2003)  
 PUBMED  
 12912978  
 JOURNAL

REFERENCE  
 2 (bases 1 to 1613)  
 Huang,S.S. and Huang,J.S.  
 Direct Submission  
 TITLE  
 Submitted (22-AUG-2003) Biochemistry & Molecular Biology, St. Louis  
 University School of Medicine, 1402 S. Grand Blvd., St. Louis, MO  
 63104, USA

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CDS

34..1002  
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 KLVSDSTHSELSTGDPYVTVTTVAPPLASTSTPRKRLICITEAFMDTSATATRES  
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ORIGIN

Alignment Scores:  
 Pred. No.: 9.51e-24 Length: 1613  
 Score: 32.00 Matches: 32  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 9.94% Indels: 0  
 DB: 4 Gaps: 0

US-10-079-111-1 (1-322) x AY372937 (1-1613)

Qy 257 CysTyrValIysArgTyrValIysAlaPheProPheThrAsnLysAsnGlnGlnLysGlu 276  
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 Db 802 TGTACGTCAAAGGTATGTGAGGCATTCCCTTTTACAAATAGAACACGAGAGGAA 861  
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 Qy 277 MetIleGluThrLysValIysValIysGluGluLysAla 288  
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 Db 862 ATGATAGAAACTAAAGTAGTAAAGAGGAGGAGGCC 897  
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RESULT 28
MMU3111501      1516 bp      mRNA      linear      ROD 01-JUN-2001
LOCUS
DEFINITION      Mus musculus mRNA for lymphatic endothelial hyaluronan receptor
                  (LYVE-1 gene).
ACCESSION      AJ3111501
VERSION        GI:13162222
KEYWORDS       hyaluronan receptor; LYVE-1 gene.
SOURCE         Mus musculus (house mouse)
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      Banerji,S., Ni,J., Wang,S.X., Clasper,S., Su,J., Tammi,R., Jones,M.
AUTHORS        and Jackson,D.G.
TITLE          LYVE-1, a new homologue of the CD44 glycoprotein, is a
JOURNAL        LYVE-1, a new homologue of the CD44 glycoprotein, is a
MEDLINE        LYVE-1, a new homologue of the CD44 glycoprotein, is a
PUBMED         99156989
REFERENCE      J. Cell Biol. 144 (4), 789-801 (1999)
AUTHORS        2
TITLE          Prevo,R., Banerji,S., Ferguson,D.J., Clasper,S. and Jackson,D.G.
JOURNAL        Mouse LYVE-1 is an endocytic receptor for hyaluronan in lymphatic
MEDLINE        endothelium
PUBMED         10037799
REFERENCE      J. Biol. Chem. 276 (22), 19420-19430 (2001)
AUTHORS        3
TITLE          (bases 1 to 1516)
JOURNAL        Direct Submission
MEDLINE        Submitted (16-FEB-2001) Jackson D.G., Institute of Molecular
PUBMED         Medicine, MRC Human Immunology Unit, John Radcliffe Hospital,
REFERENCE      Headington, Oxford, OX3 9DS, UNITED KINGDOM
AUTHORS        Location/Qualifiers
TITLE          1. .1516
JOURNAL        /organism="Mus musculus"
MEDLINE        /mol_type="mRNA"
PUBMED         /strain="Balb/c"
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AUTHORS        /tissue_type="digestive tract"
TITLE          /dev_stage="Adult"
JOURNAL        /country="United Kingdom:Oxford"
MEDLINE        1. .1516
PUBMED         /gene="LYVE-1"
REFERENCE      241. .1197
AUTHORS        /gene="LYVE-1"
TITLE          /function="lymphatic endothelial hyaluronan receptor for
JOURNAL        hyaluronan uptake"
MEDLINE        /codon_start=1
PUBMED         /evidence=experimental
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AUTHORS        /protein_id="CAC33082.1"
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AUTHORS        PRCKNGKGVLIWAPSKFKAYCHNSDWTWNSCIPETVTFYPLVDTQTPATEFS
TITLE          VSSAYLASSPDSITPVSAWTRAPPLTSMARKTKICITEYTFEITWATEAFVAS
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AUTHORS        /evidence=experimental
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Score:          29.00         Matches:    29

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Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%    Mismatches: 0
Query Match: 9.01%               Indels: 0
DB: 10                           Gaps: 0

US-10-079-111-1 (1-322) x MMU3111501 (1-1516)

Qy      224 AlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeuValLeu 243
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Db      898 GCACGATTCAGAACGAAGCAGCTGGTGTGGAGGTGTCCCCACGCCCTGCTGCTG 957
      |||||

Qy      244 AlaLeuLeuPheGlyAlaAlaAla 252
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Db      958 GCTCTCCTCTTCTTTTGTGCTGCCGCT 984
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RESULT 29
BC038653      2027 bp      mRNA      linear      ROD 07-OCT-2003
LOCUS
DEFINITION      Mus musculus extra cellular link domain-containing 1, mRNA (cdna
                  clone MGC:48237 IMAGE:2936961), complete cds.
ACCESSION      BC038653
VERSION        BC038653.1
KEYWORDS       MGC.
SOURCE         Mus musculus (house mouse)
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      Klausner,R.D., Collins,F.S., Wagner,L., Shemen,C.M., Schuler,G.D.,
AUTHORS        Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
                Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
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                Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
                Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalilus,D.E.,
                Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
                Generation and initial analysis of more than 15,000 full-length
                human and mouse cDNA sequences
                Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                22388257
                12477932
                2 (bases 1 to 2027)
                Direct Submission
                Strausberg,R.
                Submitted (15-OCT-2002) National Institutes of Health, Mammalian
                Gene Collection (MGC), Cancer Genomics Office, National Cancer
                Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                USA
                NIH-MGC Project URL: http://mgc.nci.nih.gov
                Contact: MGC help desk
                Email: cgapbs-r@mail.nih.gov
                Tissue Procurement: Gilbert Smith, Ph.D.
                cDNA Library Preparation: M. Bento Soares, University of Iowa
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
                DNA Sequencing by: Institute for Systems Biology
                http://www.systemsbio.org
                contact: amadan@systemsbiology.org
                Anup Madan, Jessica Fahey, Erin Helton, Mark Ketterman, Anuradha
                Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILLNL at: http://image.llnl.gov
Series: IRAK Plate: 83 Row: m Column: 14

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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

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    Percent Similarity: 100.00%
    Conservative: 29
    Best Local Similarity: 100.00%
    Mismatches: 0
    Indels: 0
    Gaps: 0
    DB: 10

US-10-079-111-1 (1-322) x BC038653 (1-2027)
QY 224 AlaAlaPheGlyAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeuValLeu 243
Db 849 GCAGCATTCAGAACAGACGCTGGTTGGAGGTGTCCTCCACCGCTGCTGGTCTG 908

QY 244 AlaLeuLeuPheGlyAlaAla 252
Db 909 GCTCTCTCTCTCTTGTGTCGCGCT 935

RESULT 30
BC038892 2027 bp mRNA linear ROD 07-OCT-2003
LOCUS Mus musculus extra cellular link domain-containing 1, mRNA (cDNA
DEFINITION clone MGC:48275 IMAGE:3372151), complete cds.
ACCESSION BC038892
VERSION BC038892.1 GI:24416482
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2027)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
  
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TITLE human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE 22388257
PUBMED 12477932
REFERENCE 2 (bases 1 to 2027)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (25-OCT-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbb-re@mail.nih.gov
Tissue Procurement: Marcello Bento Soares, Ph.D.
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbio.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
  
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAC Plate: 83 Row: 0 Column: 17.

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##### ORIGIN

Alignment Scores:  
 Pred. No.:  
 Length: 1.9e-20  
 Matches: 29  
 Score: 29.00  
 Percent Similarity: 100.00%  
 Conservative: 29  
 Best Local Similarity: 100.00%  
 Mismatches: 0  
 Indels: 0  
 Gaps: 0  
 DB: 10

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Score: 29.00 Matches: 29
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.01% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x BC038892 (1-2027)

QY 224 AlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeuValLeu 243
|||||
Db 849 GCAGCATTACAGACGAGACGCTGGTGTGGAGGTGTCCACCCGCCCTGCTGGTGC 908
|||||

QY 244 AlaLeuLeuPhePheGlyAlaAlaAla 252
|||||
Db 909 GCTCTCTCTCTTTTGGTGTCTGCGCT 935
|||||

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Sequence split into 4 fragments LOCUS AC110451 Accession AC110451
Fragment Name Begin End
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AC110451_2 100001 210000
AC110451_3 200001 310000
AC110451_4 300001 359529
Continuation (4 of 4) of AC110451 from base 300001 (AC110451 Rattus norvegicus clone CH2)

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Best Local Similarity: 100.00% Mismatches: 0
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US-10-079-111-1 (1-322) x AC110451_3 (1-59529)

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ACCESSION AC130104
VERSION AC130104.3 GI:30578716
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
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Muzny,D,Marle., Metzker,M, Lee., Abranzon,S., Adams,C., Alder,J.,
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Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 235382)
Worley,K.C.
Direct Submission
Submitted (08-AUG-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 235382)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (13-MAY-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On May 13, 2003 this sequence version replaced gi:23119636.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GJNK
Center clone name: CH230-226A9
----- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 214760 bases at least Q40
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Consensus quality: 218876 bases at least Q30
Consensus quality: 220968 bases at least Q20
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Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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* NOTE: Estimated insert size may differ from sequence length
  (see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.html).
* NOTE: This is a 'working draft' sequence. It currently
  * consists of 2 contigs. The true order of the pieces
  * is not known and their order in this sequence record is
  * arbitrary. Gaps between the contigs are represented as
  * runs of N, but the exact sizes of the gaps are unknown.
  * This record will be updated with the finished sequence
  * as soon as it is available and the accession number will
  * be preserved.
*
* 1 231554: contig of 231554 bp in length
*
* 231555 231654: gap of unknown length
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* 231655 235382: contig of 3728 bp in length.
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ORIGIN
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Pred. No.:          Length:      235382
Score:             Matches:      28
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:       Indels:       8.70%
DB:                Gaps:         2
US-10-079-111-1 (1-322) x AC130104 (1-235382)
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QY 281 LysValValIysGluGluIysAla 288
Db 197747 AAGGTTGTAAGGAGAGAAAGCT 197724
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AC129402
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Rattus norvegicus clone CH230-39G8, WORKING DRAFT SEQUENCE, 2
unordered pieces.
ACCESSION
AC129402
VERSION
AC129402.3 GI:25073370
KEYWORDS
HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Rattus norvegicus

```

REFERENCE  
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

1 (bases 1 to 239307)

Muzny,D.,Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Angiano,D., Anvalbechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Cesar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Lavan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensuhewa,L., Louised,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Mundaya,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Parks,K., Nwackelme,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkuch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rizzo,N., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.O., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wlezyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

TITLE  
JOURNAL

Direct Submission

Unpublished

2 (bases 1 to 239307)

Worley,K.C.

REFERENCE  
AUTHORS

Direct Submission

Submitted (30-JUL-2002)

Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 239307)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (19-NOV-2002)

Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

On Nov 19, 2002 this sequence version replaced gi:23196012.

The sequence in this assembly is a combination of BAC based reads

and whole genome shotgun sequencing reads assembled using Atlas

(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described

in the feature table below represents a scaffold in the Atlas

assembly (a 'contig-scaffold'). Within each contig-scaffold,





BD172396 50 bp DNA linear PAT 18-FEB-2003  
LOCUS  
DEFINITION  
Secreted and transmembrane polypeptides and nucleic acids encoding  
the same.  
ACCESSION  
BD172396  
VERSION  
BD172396.1 GI:28413596





FT /organism='Artificial Sequence'.  
source Location/Qualifiers  
1. .50  
/organism="synthetic construct"  
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## ORIGIN

Alignment Scores: 4.52e-08 Length: 50  
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US-10-079-111-1 (1-322) x BD173353 (1-50)

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3 GAGGCGCTGAGGCTGCTGGGACTAAGTTGGCGGCGGACGACCAAGTT 50

## RESULT 42

BD175387

LOCUS

DEFINITION

Secretory and transmembrane polypeptide and nucleic acid encoding

the same.

ACCESSION

BD175387

VERSION

BD175387.1 GI:29121083

KEYWORDS

JP 2002253280-A/169.

synthetic construct

synthetic construct

artificial sequences.

1 (bases 1 to 50)

REFERENCE

WOOD, W.I., GURNEY, A.L., GODDARD, A., PENNICA, D., ZHENG, J. and

YUAN, J.

Secretory and transmembrane polypeptide and nucleic acid encoding

the same

JOURNAL

Patent: JP 2002253280-A 169 10-SEP-2002;

GENENTECH INC

OS Artificial Sequence

PN JP 2002253280-A/169

PD 10-SEP-2002

PF 18-DEC-2001 JP 2001385319

PR 17-SEP-1997 US 60/059115, 17-SEP-1997 US 60/059184 PR

17-SEP-1997 US 60/059122, 17-SEP-1997 US 60/059117 PR

17-SEP-1997 US 60/059113, 17-SEP-1997 US 60/059121 PR

17-SEP-1997 US 60/059119, 18-SEP-1997 US 60/059263 PR

18-SEP-1997 US 60/059266, 15-OCT-1997 US 60/062125 PR

17-OCT-1997 US 60/062287, 17-OCT-1997 US 60/062816 PR

21-OCT-1997 US 60/063486, 24-OCT-1997 US 60/063127 PR

24-OCT-1997 US 60/062814, 24-OCT-1997 US 60/063121 PR

24-OCT-1997 US 60/063120, 24-OCT-1997 US 60/063128 PR

27-OCT-1997 US 60/063045, 24-OCT-1997 US 60/063327 PR

28-OCT-1997 US 60/063329, 27-OCT-1997 US 60/063541 PR

28-OCT-1997 US 60/063549, 28-OCT-1997 US 60/063542 PR

28-OCT-1997 US 60/063550, 28-OCT-1997 US 60/063564 PR

29-OCT-1997 US 60/063544, 28-OCT-1997 US 60/063564 PR

29-OCT-1997 US 60/063734, 29-OCT-1997 US 60/063738 PR

29-OCT-1997 US 60/063704, 29-OCT-1997 US 60/063735 PR

29-OCT-1997 US 60/064215, 29-OCT-1997 US 60/063735 PR

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31-OCT-1997 US 60/063870, 03-NOV-1997 US 60/064248 PR

07-NOV-1997 US 60/064809, 12-NOV-1997 US 60/065186 PR

17-NOV-1997 US 60/065846, 18-NOV-1997 US 60/065693 PR

21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066364 PR

24-NOV-1997 US 60/066772, 24-NOV-1997 US 60/066466 PR

24-NOV-1997 US 60/066770, 24-NOV-1997 US 60/066511 PR

24-NOV-1997 US 60/066453, 25-NOV-1997 US 60/066840 PR

WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI

JIAN ZHENG,

PI JEAN YUAN

PC C12N15/09, A61K45/00, A61P1/00, A61P13/12, A61P17/00, A61P17/06, PC

PC A61P25/00,  
PC A61P25/16, A61P25/28, A61P31/12, A61P35/00, C07K14/47, C07K16/18,  
PC C07K19/00,  
PC C12N1/19, C12N1/21, C12N5/10//A61K38/00, A61K39/395, A61K39/395,  
PC A61P43/00,  
PC C12P21/08, (C12N1/19, C12R1:645), (C12N1/21, C12R1:19), (C12N5/10,  
C12R1:91),  
PC C12N15/00, C12N5/00, A61K37/02, (C12N5/00, C12R1:91) CC  
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Location/Qualifiers  
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source Location/Qualifiers  
1. .50  
/organism="synthetic construct"  
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## ORIGIN

Alignment Scores: 4.52e-08 Length: 50  
Pred. No.: 16.00 Matches: 16  
Score: 100.00% Conservatative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 4.97% Gaps: 0  
DB: 6

US-10-079-111-1 (1-322) x BD175387 (1-50)

QY 59 GluAlaCysArgLeuGlyLeuSerLeuAlaGlyLysAspGlnVal 74

|||||

3 GAGGCGCTGAGGCTGCTGGGACTAAGTTGGCGGCGGACGACCAAGTT 50

## RESULT 43

SCBARP1/c

LOCUS

DEFINITION

SCBARP1

Accession

X77949

Version

X77949.1 GI:1263905

Keywords

B alpha pheromone; B alpha pheromone-receptor; bap1 gene; bap1

gene.

SOURCE

Schizophyllum commune

ORGANISM

Schizophyllum commune

Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;

Agaricales; Schizophyllaceae; Schizophyllum.

REFERENCE

1 (bases 460 to 5883)

Wendland, J., Vaillancourt, L.J., Hegner, J., Lengeler, K.B.,

Laddison, K.J., Specht, C.A., Raper, C.A. and Kothé, E.

The mating-type locus B alpha 1 of Schizophyllum commune contains a

pheromone receptor gene and putative pheromone genes

EMBO J. 14 (21), 5271-5278 (1995)

MEDLINE

96080162

PUBMED

7489716

REFERENCE

2

Wendland, J.

Direct Submission

AUTHORS

Submitted (02-MAR-1994) J. Wendland, Philipps-Universitaet Marburg,

Karl-von-Frisch Strasse, 35032 Marburg, FRG

revised by author 05-JUL-95 & 20-SEP-95. Revised by [4]

3 (bases 1 to 5883)

Wendland, J.

Direct Submission

AUTHORS

Submitted (16-APR-1996) J. Wendland, Philipps-Universitaet Marburg,

Karl-von-Frisch Strasse, 35032 Marburg, FRG

On Apr 17, 1996 this sequence version replaced gi:1246904.

COMMENT

Location/Qualifiers

1. .5883

/organism="Schizophyllum commune"

/mol\_type="genomic DNA"

/strain="4-40"

/db\_xref="taxon:5334"

/chromosome="XI"

/clone="Btr 2-2"

source

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1026b frag.

SCBARP1 5883 bp DNA linear PLN 25-OCT-1996  
S. commune bap1 and bap1 genes.  
X77949  
X77949.1 GI:1263905  
B alpha pheromone; B alpha pheromone-receptor; bap1 gene; bap1  
gene.

Schizophyllum commune  
Schizophyllum commune  
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
Agaricales; Schizophyllaceae; Schizophyllum.

1 (bases 460 to 5883)  
Wendland, J., Vaillancourt, L.J., Hegner, J., Lengeler, K.B.,  
Laddison, K.J., Specht, C.A., Raper, C.A. and Kothé, E.  
The mating-type locus B alpha 1 of Schizophyllum commune contains a  
pheromone receptor gene and putative pheromone genes

EMBO J. 14 (21), 5271-5278 (1995)

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96080162

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2

Wendland, J.

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AUTHORS

Submitted (02-MAR-1994) J. Wendland, Philipps-Universitaet Marburg,

Karl-von-Frisch Strasse, 35032 Marburg, FRG

revised by author 05-JUL-95 & 20-SEP-95. Revised by [4]

3 (bases 1 to 5883)

Wendland, J.

Direct Submission

AUTHORS

Submitted (16-APR-1996) J. Wendland, Philipps-Universitaet Marburg,

Karl-von-Frisch Strasse, 35032 Marburg, FRG

On Apr 17, 1996 this sequence version replaced gi:1246904.

COMMENT

Location/Qualifiers

1. .5883

/organism="Schizophyllum commune"

/mol\_type="genomic DNA"

/strain="4-40"

/db\_xref="taxon:5334"

/chromosome="XI"

/clone="Btr 2-2"

source



B/gvk

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 15, 2004, 06:39:21 ; Search time 156 Seconds  
(without alignments)  
7217.919 Million cell updates/sec

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Perfect score: 2029  
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Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	1994	98.3	2372	4	US-09-907-794A-200
5	1994	98.3	2372	4	US-09-905-125A-200
6	1994	98.3	2372	4	US-09-902-775A-200
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9	334	16.5	339	2	US-08-892-880-11
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13	239	11.8	241	4	US-09-433-826B-324
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32	46.6	2.3	3207	2	US-08-478-882-1	Sequence 1, Appli
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43	41.8	2.1	20674	4	US-09-641-638-651	Sequence 651, App
44	41.4	2.0	6113	4	US-10-204-708-13	Sequence 13, Appl
45	41	2.0	1559	4	US-09-489-847-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1  
US-09-232-160-13  
; Sequence 13, Application US/09232160  
; Patent No. 6368794  
; GENERAL INFORMATION:  
; APPLICANT: Steve Daniel  
; APPLICANT: James Gilmore  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Laura Stuve  
; TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL  
; FILE OF INVENTION: PROLIFERATION  
; FILE REFERENCE: PA-0003 US  
; CURRENT APPLICATION NUMBER: US/09/232,160  
; CURRENT FILING DATE: 1999-01-15  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PERL Program  
; SEQ ID NO 13  
; LENGTH: 2029  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: 3044710  
US-09-232-160-13

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Best Local Similarity	100.0%	Pred. No. 0;		
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QY	121	CTGCTCTCATATCAGCAGTGGCCATCTCAGGTGTTTCCCTGCTCTGAAGGGGTAGGCA	180	
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Db 1021 CCAAAAGTATGAAGGAGAGAGGCGCAATGATGACCACTTATGAGGAATCAAGAA 1080  
QY 1081 CTGATAAAACCCAGAGAGTCCAAAGAGTCCAAAGCAAACTACCGTGGCATGCCCTGGAAG 1140  
Db 1081 CTGATAAAACCCAGAGAGTCCAAAGAGTCCAAAGCAAACTACCGTGGCATGCCCTGGAAG 1140  
QY 1141 CTGAAGTTTATGATGACAGAAATAGGAGAGACACCTGAGCTGGTTTCTTTCATGCTC 1200  
Db 1141 CTGAAGTTTATGATGACAGAAATAGGAGAGACACCTGAGCTGGTTTCTTTCATGCTC 1200  
QY 1201 CTTACCTGCCCCAGCTGGGAAATCAAAAGGCGCAAGAACCAAGAGAAAGTCCACC 1260  
Db 1201 CTTACCTGCCCCAGCTGGGAAATCAAAAGGCGCAAGAACCAAGAGAAAGTCCACC 1260  
QY 1261 CTTGGTTCCTAACTGGAATCAGCTCAGGACTGCCATTTGAGTATGGAGTGACCAAGAG 1320  
Db 1261 CTTGGTTCCTAACTGGAATCAGCTCAGGACTGCCATTTGAGTATGGAGTGACCAAGAG 1320  
QY 1321 AATGCCCTTCTCTTATTTGAACCTGTCTGGATCCTATCTCTTACCTCCAAAGCTCC 1380  
Db 1321 AATGCCCTTCTCTTATTTGAACCTGTCTGGATCCTATCTCTTACCTCCAAAGCTCC 1380  
QY 1381 CACGCGCTTTCTAGCCTGGCTATGCTCTAATAATATCCACTGGGAGAAAGGATTTGC 1440  
Db 1381 CACGCGCTTTCTAGCCTGGCTATGCTCTAATAATATCCACTGGGAGAAAGGATTTGC 1440

QY 1441 AAAGTGCAAGGACCTTAAACATCTCATCTCATGATTCAGATGTTGTAAGAGCCCTCTGGTGT 1500  
Db 1441 AAAGTGCAAGGACCTTAAACATCTCATCTCATGATTCAGATGTTGTAAGAGCCCTCTGGTGT 1500  
QY 1501 CTGAGGCTAGCTGGGTTGAAAGCCAGGAGTCTACTGAGACCAAGGCTTTCTTACTGATT 1560  
Db 1501 CTGAGGCTAGCTGGGTTGAAAGCCAGGAGTCTACTGAGACCAAGGCTTTCTTACTGATT 1560  
QY 1561 CCGCAGCTCAGACCCCTTTCTTTCAGCTCTGAAAGAGAAACACGATATCCACTGACATGTC 1620  
Db 1561 CCGCAGCTCAGACCCCTTTCTTTCAGCTCTGAAAGAGAAACACGATATCCACTGACATGTC 1620  
QY 1621 CTTTCTGAGCCCGGTAGAGCAAAAGAAATGCGACAAAGATTTAGCCCTGAAAGCCATGGA 1680  
Db 1621 CTTTCTGAGCCCGGTAGAGCAAAAGAAATGCGACAAAGATTTAGCCCTGAAAGCCATGGA 1680  
QY 1681 GATTCTCATAACTTGTAGACCTTAATCTCTGTAAAGCTTAAATAAAGAAATAGAACAGGCT 1740  
Db 1681 GATTCTCATAACTTGTAGACCTTAATCTCTGTAAAGCTTAAATAAAGAAATAGAACAGGCT 1740  
QY 1741 GAGGATACGACAGTACACTGTCTCAGAGGAGTCTGTAACACAGACAGGCTCAAAAGTGT 1800  
Db 1741 GAGGATACGACAGTACACTGTCTCAGAGGAGTCTGTAACACAGACAGGCTCAAAAGTGT 1800  
QY 1801 CTTTGAACATTTGAGTGTGGAATCAGTCTGTTTGAACACACACACTTCTTTTCTGGTCT 1860  
Db 1801 CTTTGAACATTTGAGTGTGGAATCAGTCTGTTTGAACACACACACTTCTTTTCTGGTCT 1860  
QY 1861 CTACCACTGCTGATATTTTCTCTAGGAAATATATCTTTTACAGTAACAAATAAATAACT 1920  
Db 1861 CTACCACTGCTGATATTTTCTCTAGGAAATATATCTTTTACAGTAACAAATAAATAACT 1920  
QY 1921 CTTATAAATTTCTATTTTATCTGAGTTTACAGAAATGATTTCTAAGAGAAATTTACTCAGT 1980  
Db 1921 CTTATAAATTTCTATTTTATCTGAGTTTACAGAAATGATTTCTAAGAGAAATTTACTCAGT 1980  
QY 1981 AATTGTTTTAAAGTAATAAATTTCAACAAACATTTTAAAAA 2029  
Db 1981 AATTGTTTTAAAGTAATAAATTTCAACAAACATTTTAAAAA 2029

RESULT 2

US-09-833-381-849  
; Sequence 849, Application US/09833381  
; Patent No. 6672186  
; GENERAL INFORMATION:  
; APPLICANT: Robison, Keith E.  
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs  
; FILE REFERENCE: 5800-119  
; CURRENT APPLICATION NUMBER: US/09/833,381  
; PRIOR FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: 09/516,448  
; NUMBER OF SEQ ID NOS: 2050  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 849  
; LENGTH: 2404  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-833-381-849

Query Match 98.8%; Score 2005; DB 4; Length 2404;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2019; Conservative 0; Mismatches 5; Indels 1; Gaps 1;  
QY 2 CTTGACAAGTCAGAA-GCTTGAAGACAGGAAATCCGATGCTCGGTTATGAAGTGAG 60  
Db 8 CTTGACAAGTCAGAACGCTTGAAGACAGGAAATCCGATGCTCGGTTATGAAGTGAG 67  
QY 61 CAGTGAGTGTGAGCTCAACATAGTTCAGAACTCTCCATCCGACTAGTTATTGAGCAT 120  
Db 68 CAGTGAGTGTGAGCTCAACATAGTTCAGAACTCTCCATCCGACTAGTTATTGAGCAT 127





; TYPE: DNA									
; ORGANISM: Homo sapiens									
US-09-833-381-853									
Query Match 98.8%; Score 2005; DB 4; Length 2404;									
Best Local Similarity 99.7%; Pred. No. 0;									
Matches 2019; Conservative 0; Mismatches 5; Indels 1; Gaps 1;									
QY	2	CTTGACAAGTCAGAA-GCTTGAAAGCAGGGAATCCGGATGTCCTCGGTTATGAAGTGGAG	60						
DB	8	CTTGACAAGTCAGAACGCTTGAAAGCAGGGAATCCGGATGTCCTCGGTTATGAAGTGGAG	67						
QY	61	CAGTGAAGTGAAGCCTCAACATAGTTCAGAACTCTCCATCCGAGCTAGTTATTTAGACAT	120						
DB	68	CAGTGAAGTGAAGCCTCAACATAGTTCAGAACTCTCCATCCGAGCTAGTTATTTAGACAT	127						
QY	121	CTGCCCTCTCATATCACCAAGTGGCCATCTGAGGTGTTTTCCCTGGCTCTGAAGGGGTAGGCA	180						
DB	128	CTGCCCTCTCATATCACCAAGTGGCCATCTGAGGTGTTTTCCCTGGCTCTGAAGGGGTAGGCA	187						
QY	181	CGATGGCCAGGTGCTTCAGCGTGGTGTGTTGCTTCTCACTTCCATCTCGACCAAGAGCTCC	240						
DB	188	CGATGGCCAGGTGCTTCAGCGTGGTGTGTTGCTTCTCACTTCCATCTCGACCAAGAGCTCC	247						
QY	241	TGCTCCAAAGCCTCTTTGGCGTGAGAGAGCTTTCCATCCAGGTGTCATGCAGAAATATGG	300						
DB	248	TGCTCCAAAGCCTCTTTGGCGTGAGAGAGCTTTCCATCCAGGTGTCATGCAGAAATATGG	307						
QY	301	GGATCACCTTGTGAGCAAAAAGGCGAACAGCAGCTGAATTTCAAGAACTTAAGGAGG	360						
DB	308	GGATCACCTTGTGAGCAAAAAGGCGAACAGCAGCTGAATTTCAAGAACTTAAGGAGG	367						
QY	361	CTGTAGGCTGTGGGACTAAGTTTGGCGGAGGAGCAAGTTGAAAAGCTTCAAAG	420						
DB	368	CTGTAGGCTGTGGGACTAAGTTTGGCGGAGGAGCAAGTTGAAAAGCTTCAAAG	427						
QY	421	CTAGCTTTGAAACTTCAGCTATGGCTGGGTTGGAGATGGATTCGGTGCATCTCTAGGA	480						
DB	428	CTAGCTTTGAAACTTCAGCTATGGCTGGGTTGGAGATGGATTCGGTGCATCTCTAGGA	487						
QY	481	TTAGCCCAAAACCCCAAGTGTGGGAAAAATGGGTTGGGTTGCTTGAATTTGGAAAGTTCCAG	540						
DB	488	TTAGCCCAAAACCCCAAGTGTGGGAAAAATGGGTTGGGTTGCTTGAATTTGGAAAGTTCCAG	547						
QY	541	TTAGCCCGACAGTTTGAGCCTATTTGTTACATCATCTGATCTGAGCTTGGACTTCACTGCA	600						
DB	548	TTAGCCCGACAGTTTGAGCCTATTTGTTACATCATCTGATCTGAGCTTGGACTTCACTGCA	607						
QY	601	TTCCAGAAATTTATCACCAAGATCCCATATTTCAACACTCAAACTGCAACACAAACAA	660						
DB	608	TTCCAGAAATTTATCACCAAGATCCCATATTTCAACACTCAAACTGCAACACAAACAA	667						
QY	661	CAGAAATTTATGTCAGTGACGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTG	720						
DB	668	CAGAAATTTATGTCAGTGACGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTG	727						
QY	721	CCCCCTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGA	780						
DB	728	CCCCCTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGA	787						
QY	781	TTTGTGTCAAGAAATTTTATGGAAACTAGCACCATGTCATCAGAAACTGAAACCAATTTG	840						
DB	788	TTTGTGTCAAGAAATTTTATGGAAACTAGCACCATGTCATCAGAAACTGAAACCAATTTG	847						
QY	841	TTGAAAATTAAGCAGCATTTCAAGATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTC	900						
DB	848	TTGAAAATTAAGCAGCATTTCAAGATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTC	907						
QY	901	TGCTAGTGCTGTCTCTCTCTCTTCTTGGTGTGCTGCTGCTGCTTGGATTTTGTATGTCA	960						
DB	908	TGCTAGTGCTGTCTCTCTCTCTTCTTGGTGTGCTGCTGCTGCTTGGATTTTGTATGTCA	967						
QY	961	AAAGGTATGTGAAGGCTTCCCTTTTACAAACAAGAAATCAGCAGAAAGGAAATGATCGAAA	1020						

US-09-907-794A-200  
; Sequence 200, Application US/09907794A  
; Patent No. 6635466  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gottard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/907,794A  
; CURRENT FILING DATE: 2001-07-17  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 200  
; LENGTH: 2372  
; TYPE: DNA  
; ORGANISM: Homo sapiens

US-09-907-794A-200  
Query Match 98.3%; Score 1994; DB 4; Length 2372;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 24 AGCAGGAAATCCGGATGTCCTGGTTATGAAAGTGGAGCAGTGTGAGCCTCAACATA 83  
Db 1 AGCAGGAAATCCGGATGTCCTGGTTATGAAAGTGGAGCAGTGTGAGCCTCAACATA 60  
QY 84 GTTCCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATACCAAGTGGC 143  
Db 61 GTTCCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATACCAAGTGGC 120  
QY 144 CATCTGAGGTGTTTCCCTGGCTCTGAAAGGGTAGGCAGATGCCAGGTGCTTCAGCCTG 203  
Db 121 CATCTGAGGTGTTTCCCTGGCTCTGAAAGGGTAGGCAGATGCCAGGTGCTTCAGCCTG 180  
QY 204 GTGTTGCTTCTCATTCCATCTGGACACGAGGCTCTGGTCCAGGCTCTTTGGGTGCA 263  
Db 181 GTGTTGCTTCTCATTCCATCTGGACACGAGGCTCTGGTCCAGGCTCTTTGGGTGCA 240  
QY 264 GAAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGGGATCACCTCTGTGAGCAAAAG 323  
Db 241 GAAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGGGATCACCTCTGTGAGCAAAAG 300  
QY 324 GCGAACCAAGCAGCTGAAATTTTCAAGAAGCTAAGAGGCTGTAGGCTGTGGAGCTAAGT 383  
Db 301 GCGAACCAAGCAGCTGAAATTTTCAAGAAGCTAAGAGGCTGTAGGCTGTGGAGCTAAGT 360  
QY 384 TTGGCCGGCAAGGACCAAGTTGAAACAGCTTGAAGCTAGCTTTGAACCTTTGACGCTAT 443  
Db 361 TTGGCCGGCAAGGACCAAGTTGAAACAGCTTGAAGCTAGCTTTGAAACCTTTGACGCTAT 420  
QY 444 GGCTGGTTGGAGATGGATTCGTGCTCATCTAGAGATTAGCCAAACCCCAAGTGTGGG 503  
Db 421 GGCTGGTTGGAGATGGATTCGTGCTCATCTAGAGATTAGCCAAACCCCAAGTGTGGG 480  
QY 504 AAAAATGGGGTGGGTGCTCTGATTTTGAAGGTTCCAGTGAGCCGACAGTTTGAGCCTAT 563  
Db 481 AAAAATGGGGTGGGTGCTCTGATTTTGAAGGTTCCAGTGAGCCGACAGTTTGAGCCTAT 540  
QY 564 TGTTACAATCATCTGATCTTGGACTAACTCGTCGATTCGAGAAATATACCAACCA 623  
Db 541 TGTTACAATCATCTGATCTTGGACTAACTCGTCGATTCGAGAAATATACCAACCA 600  
QY 624 GATCCATATTCACACACTCAAACTGCAACACAAACACAGAAATTTATTCTCAGTGACAGT 683  
Db 601 GATCCATATTCACACACTCAAACTGCAACACAAACACAGAAATTTATTCTCAGTGACAGT 660  
QY 684 ACCTACTCGTGGCATCCCTTTACTCTCAATACCTGGCCCTACTACTCTCTCTGCT 743  
Db 661 ACCTACTCGTGGCATCCCTTTACTCTCAATACCTGGCCCTACTACTCTCTCTGCT 720  
QY 744 CCAGCTTCCACTTCTATTCCAGGAGAAAATTTGATTGTGTGTCACAGAACTTTTATG 803  
Db 721 CCAGCTTCCACTTCTATTCCAGGAGAAAATTTGATTGTGTGTCACAGAACTTTTATG 780  
QY 804 GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAATAAAGCAGCATTCAG 863  
Db 781 GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAATAAAGCAGCATTCAG 840  
QY 864 AATGAAGCTGTGGGTTTGGAGGTGTCGCCACGCTGTGCTAGTGTGCTCTCTCTTC 923  
Db 841 AATGAAGCTGTGGGTTTGGAGGTGTCGCCACGCTGTGCTAGTGTGCTCTCTCTTC 900  
QY 924 TTTGCTGTGAGCTGTCTTTGGATTTTGTATGTCAAAAGTATGTGAAGCCTTCCT 983  
Db 901 TTTGCTGTGAGCTGTCTTTGGATTTTGTATGTCAAAAGTATGTGAAGCCTTCCT 960  
QY 984 TTTACAAAACAAGATCAGCAGAAAGAAATGATCGAAACCAAAAGTAGTAAGAGGAGAG 1043  
Db 961 TTTACAAAACAAGATCAGCAGAAAGAAATGATCGAAACCAAAAGTAGTAAGAGGAGAG 1020



Query Match 98.3%; Score 1994; DB 4; Length 2372; Best Local Similarity 99.8%; Pred. No. 0; Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;									
QY	24	AGCAGGAAATCCGGATGTCCTGGTATTAAGAGTGGAGCAGTGAAGTGTGAGCCTCAACATA	83						
Db	1	AGCAGGAAATCCGGATGTCCTGGTATTAAGAGTGGAGCAGTGAAGTGTGAGCCTCAACATA	60						
QY	84	GTTCAGAACTCTCATCCGGACTAGTTATAGAGATCTGGCTCTCATATACCAAGTGGC	143						
Db	61	GTTCAGAACTCTCATCCGGACTAGTTATAGAGATCTGGCTCTCATATACCAAGTGGC	120						
QY	144	CATCTGAGGTGTTCCCTGGCTCTGAAGGGTAGCAGCATGCCAGGTCTTTGCGTGCA	203						
Db	121	CATCTGAGGTGTTCCCTGGCTCTGAAGGGTAGCAGCATGCCAGGTCTTTGAGCCTG	180						
QY	204	GTGTTGCTTCTCACTTCCATCTGGACACAGAGCTCTGGTCCAAAGCTCTTTGGTGCA	263						
Db	181	GTGTTGCTTCTCACTTCCATCTGGACACAGAGCTCTGGTCCAAAGCTCTTTGGTGCA	240						
QY	264	GAAAGCTTTCATCCAGGTGTCATGCAAGATTTAGGGATCACCCCTGTGAGCAAAAG	323						
Db	241	GAAAGCTTTCATCCAGGTGTCATGCAAGATTTAGGGATCACCCCTGTGAGCAAAAG	300						
QY	324	GGAAACAGCAGCTGAATTTACAGAGCTAAGAGGCTGTAGGCTGTGGACTAAGT	383						
Db	301	GGAAACAGCAGCTGAATTTACAGAGCTAAGAGGCTGTAGGCTGTGGACTAAGT	360						
QY	384	TTGGCCGGCAAGGACCAAGTTGAAACAGCTTTGAAAGCTAGCTTTGAACTTTGCAGCTAT	443						
Db	361	TTGGCCGGCAAGGACCAAGTTGAAACAGCTTTGAAAGCTAGCTTTGAACTTTGCAGCTAT	420						
QY	444	GGCTGGGTGGAGATGGATTCGTGGTCACTCTAGATTTAGGCCAAAACCCCAAGTGTGGG	503						
Db	421	GGCTGGGTGGAGATGGATTCGTGGTCACTCTAGATTTAGGCCAAAACCCCAAGTGTGGG	480						
QY	504	AAAAATGGGGTGGGTGCTGATTTGGAAGGTTCCAGTGAGCGCAGTTTCAGCCTAT	563						
Db	481	AAAAATGGGGTGGGTGCTGATTTGGAAGGTTCCAGTGAGCGCAGTTTCAGCCTAT	540						
QY	564	TGTTAACTCATCTGATCTTGGACTAACTCGTGCAATTCAGAAATTTATCAACCACAA	623						
Db	541	TGTTAACTCATCTGATCTTGGACTAACTCGTGCAATTCAGAAATTTATCAACCACAA	600						
QY	624	GATCCCATTTCAACACTCAAACTGCAACACAAACAGAAATTTATGTCAGTGACAGT	683						
Db	601	GATCCCATTTCAACACTCAAACTGCAACACAAACAGAAATTTATGTCAGTGACAGT	660						
QY	684	ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTACTACTCTCTCTGCT	743						
Db	661	ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTACTACTCTCTCTGCT	720						
QY	744	CCAGTTCCTACTTCTTATCCAGGAGAAAAAATTAATTTGTTGTCACAGAAATTTTATG	803						
Db	721	CCAGTTCCTACTTCTTATCCAGGAGAAAAAATTAATTTGTTGTCACAGAAATTTTATG	780						
QY	804	GAACTAGCACATGTCATAGAACTGAACATTTGTTGAAAAAATAGAGCAGATTCAG	863						
Db	781	GAACTAGCACATGTCATAGAACTGAACATTTGTTGAAAAAATAGAGCAGATTCAG	840						
QY	864	AATGAAGCTGTGGGTGAGGTGCCCGCTCTGCTAGTGTGCTGCTCTCTCTCTC	923						
Db	841	AATGAAGCTGTGGGTGAGGTGCTCCCGCTCTGCTAGTGTGCTGCTCTCTCTCTC	900						
QY	924	TTTGTGCTGACGTGCTTGGATTTTGTCTATGTCAAAAGGTATGTGAAGGCTTCCCT	983						
Db	901	TTTGTGCTGACGTGCTTGGATTTTGTCTATGTCAAAAGGTATGTGAAGGCTTCCCT	960						
QY	984	TTTACAAACAAGATCAGCAGAAAGGAATGATCGAAACCAAAGTAGTAAGGAGGAG	1043						
Db	961	TTTACAAACAAGATCAGCAGAAAGGAATGATCGAAACCAAAGTAGTAAGGAGGAG	1020						
QY	1044	GCCAAATGATGCAACCTTAATGAGGAATCAAGAAAACTGATAAAAAACCCAGAGTCC	1103						

RESULT 6  
US-09-902-775A-200  
; Sequence 200, Application US/09902775A  
; Patent No. 6686451  
; GENERAL INFORMATION:

Db	1021	GCCAATGATAGCAACCTTAATGAGGAATCAAGAAAACTGATAAAAAACCCAGAGAGTCC	1080						
QY	1104	AAGAGTCCAAGCAAAACTACCGTGCATGCCCTGGAAGCTGAAAGTTTAGTAGAGACAGAAA	1163						
Db	1081	AAGAGTCCAAGCAAAACTACCGTGCATGCCCTGGAAGCTGAAAGTTTAGTAGAGACAGAAA	1140						
QY	1164	TAAGGAGACACACTGAGGCTGGTTTCTTTATGCTCCTTACCTGCCAGCTGGGGAA	1223						
Db	1141	TAAGGAGACACACTGAGGCTGGTTTCTTTATGCTCCTTACCTGCCAGCTGGGGAA	1200						
QY	1224	ATCAAAAGGGCCAAAGAAACCAAGAGAAAGTCCACCTTGGTTCCTAACTGGAATCAGC	1283						
Db	1201	ATCAAAAGGGCCAAAGAAACCAAGAGAAAGTCCACCTTGGTTCCTAACTGGAATCAGC	1260						
QY	1284	TCAGGACTGCCATTGGACTATGGAGTGCAACAAAGAAATGCCCTTCTCTTATTTGTAAC	1343						
Db	1261	TCAGGACTGCCATTGGACTATGGAGTGCAACAAAGAAATGCCCTTCTCTTATTTGTAAC	1320						
QY	1344	CCTGTCTGATCCTATCCTCTACCTCCAAAGCTTCCACGGCCTTTCTAGCCTGGCTAT	1403						
Db	1321	CCTGTCTGATCCTATCCTCTACCTCCAAAGCTTCCACGGCCTTTCTAGCCTGGCTAT	1380						
QY	1404	GTCTCTAAATAATATCCACTGGGAGAAAGAGTTTTCGAAAGTGCAAGGACCTAAACATC	1463						
Db	1381	GTCTCTAAATAATATCCACTGGGAGAAAGAGTTTTCGAAAGTGCAAGGACCTAAACATC	1440						
QY	1464	TCATCAGTATCAGTGGTAAAGGCCCTCTGGCTGTCTGAGGCTAGTGGGTGAAAGC	1523						
Db	1441	TCATCAGTATCAGTGGTAAAGGCCCTCTGGCTGTCTGAGGCTAGTGGGTGAAAGC	1500						
QY	1524	CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGGAGCTCAGACCTTTCTTCA	1583						
Db	1501	CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGGAGCTCAGACCTTTCTTCA	1560						
QY	1584	GCTCTGAAAGAGAAACAGTATCCACCTGACATGCTCTTCTGAGCCGGTAAGAGCAAA	1643						
Db	1561	GCTCTGAAAGAGAAACAGTATCCACCTGACATGCTCTTCTGAGCCGGTAAGAGCAAA	1620						
QY	1644	AGAATGGCAGAAAAGTTTAGCCCTGAAAGCCATCGAGATTCTCATAACTTGAGACCTAA	1703						
Db	1621	AGAATGGCAGAAAAGTTTAGCCCTGAAAGCCATCGAGATTCTCATAACTTGAGACCTAA	1680						
QY	1704	TCTCTGTAAGCTAAATTAAGAAATAGAAACAGGCTGAGGATAGACAGTACACTGTCA	1763						
Db	1681	TCTCTGTAAGCTAAATTAAGAAATAGAAACAGGCTGAGGATAGACAGTACACTGTCA	1740						
QY	1764	GCAGGACTGTAAACACACAGAGGGTCAAGGTGTTTCTCTGAACACATTTGAGTTGGAT	1823						
Db	1741	GCAGGACTGTAAACACACAGAGGGTCAAGGTGTTTCTCTGAACACATTTGAGTTGGAT	1800						
QY	1824	CACGTTTGAACACACACACTTACTTTTCTGGTCTCTACACCTGCTGATATTTCTCT	1883						
Db	1801	CACGTTTGAACACACACACTTACTTTTCTGGTCTCTACACCTGCTGATATTTCTCT	1860						
QY	1884	AGGAAATATCTTTTACAGTTAAACAAAATAAAACTCTTATAAATTTCTATTTTATCT	1943						
Db	1861	AGGAAATATCTTTTACAGTTAAACAAAATAAAACTCTTATAAATTTCTATTTTATCT	1920						
QY	1944	GAGTTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAA	2003						
Db	1921	GAGTTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAA	1980						
QY	2004	TTCAACAAACATTTTAAAAAAA	2025						
Db	1981	TTCAACAAACATTTTCTGTAATA	2002						

APPLICANT: Genentech, Inc.  
 APPLICANT: Ashkenazi, Avi  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, A.  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, Christopher J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Hillan, Kenneth, J.  
 APPLICANT: Kljavin, Ivar J.  
 APPLICANT: Mather, Jennie P.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William, I.  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: 10466-14  
 CURRENT APPLICATION NUMBER: US/09/902,775A  
 PRIORITY FILING DATE: 2001-07-10  
 PRIOR APPLICATION NUMBER: PCT/US00/04414  
 PRIOR FILING DATE: 2000-02-22  
 PRIOR APPLICATION NUMBER: US 60/143,048  
 PRIOR FILING DATE: 1999-07-07  
 PRIOR APPLICATION NUMBER: US 60/145,698  
 PRIOR FILING DATE: 1999-07-26  
 PRIOR APPLICATION NUMBER: US 60/146,222  
 PRIOR FILING DATE: 1999-07-28  
 PRIOR APPLICATION NUMBER: PCT/US99/20594  
 PRIOR FILING DATE: 1999-09-08  
 PRIOR APPLICATION NUMBER: PCT/US99/20944  
 PRIOR FILING DATE: 1999-09-13  
 PRIOR APPLICATION NUMBER: PCT/US99/21090  
 PRIOR FILING DATE: 1999-09-15  
 PRIOR APPLICATION NUMBER: PCT/US99/21547  
 PRIOR FILING DATE: 1999-09-15  
 PRIOR APPLICATION NUMBER: PCT/US99/23089  
 PRIOR FILING DATE: 1999-10-05  
 PRIOR APPLICATION NUMBER: PCT/US99/28214  
 PRIOR FILING DATE: 1999-11-29  
 PRIOR APPLICATION NUMBER: PCT/US99/28313  
 PRIOR FILING DATE: 1999-11-30  
 PRIOR APPLICATION NUMBER: PCT/US99/28564  
 PRIOR FILING DATE: 1999-12-02  
 PRIOR APPLICATION NUMBER: PCT/US99/28565  
 PRIOR FILING DATE: 1999-12-02  
 PRIOR APPLICATION NUMBER: PCT/US99/30095  
 PRIOR FILING DATE: 1999-12-16  
 PRIOR APPLICATION NUMBER: PCT/US99/30911  
 PRIOR FILING DATE: 1999-12-20  
 PRIOR APPLICATION NUMBER: PCT/US99/30999  
 PRIOR FILING DATE: 1999-12-20  
 PRIOR APPLICATION NUMBER: PCT/US00/00219  
 PRIOR FILING DATE: 2000-01-05  
 NUMBER OF SEQ ID NOS: 423  
 SEQ ID NO 200  
 LENGTH: 2372  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-902-775A-200

Query Match 98.3%; Score 1994; DB 4; Length 2372;  
 Best Local Similarity 99.8%; Pred. No. 0;

	Matches 1997;	Conservative	0;	Mismatches	5;	Indels	0;	Gaps	0;
QY	24	AGCAGGAAATCGGATGTCGTTATGAAGTGAGCAGTGAAGTGAGCCTCAACATA	83						
DB	1	AGCAGGAAATCGGATGTCGTTATGAAGTGAGCAGTGAAGTGAGCCTCAACATA	60						
QY	84	GTTCCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCTCTCATATCACCAGTGGC	143						
DB	61	GTTCCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCTCTCATATCACCAGTGGC	120						
QY	144	CATCTGAGGTGTTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGCTTTCAGCCTG	203						
DB	121	CATCTGAGGTGTTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGCTTTCAGCCTG	180						
QY	204	GTTGTTGCTTCTCACTTCATCTGGACACGAGGCTCTGCTCAAGGCTCTTTGGCTGCA	263						
DB	181	GTTGTTGCTTCTCACTTCATCTGGACACGAGGCTCTGCTCAAGGCTCTTTGGCTGCA	240						
QY	264	GAAGAGCTTTCATCCAGGTGTCAGAAATTTATGGGATCACCTTCTGAGCAAAAAG	323						
DB	241	GAAGAGCTTTCATCCAGGTGTCAGAAATTTATGGGATCACCTTCTGAGCAAAAAG	300						
QY	324	GCGAACACGACGTGAATTTCAAGAAGCTAAGGAGGCTGTAGGCTGCTGGACTAAGT	383						
DB	301	GCGAACACGACGTGAATTTCAAGAAGCTAAGGAGGCTGTAGGCTGCTGGACTAAGT	360						
QY	384	TTGGCCGGCAAGCCAAAGTTGAAACAGCCTTGAAGCTAGCTTTGAAACTTGCAGCTAT	443						
DB	361	TTGGCCGGCAAGCCAAAGTTGAAACAGCCTTGAAGCTAGCTTTGAAACTTGCAGCTAT	420						
QY	444	GGCTGGTTGGAGATGGATTTCGTGTCATCTAGGATAGCCCAAAACCCCAAGTGGG	503						
DB	421	GGCTGGTTGGAGATGGATTTCGTGTCATCTAGGATAGCCCAAAACCCCAAGTGGG	480						
QY	504	AAAAATGGGGTGGCTGCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTCAGCCTAT	563						
DB	481	AAAAATGGGGTGGCTGCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTCAGCCTAT	540						
QY	564	TGTTAACTCATCTGATCTTGGACTAATCGTGCTTCCAGAAATTTATTCAGTGACAGT	623						
DB	541	TGTTAACTCATCTGATCTTGGACTAATCGTGCTTCCAGAAATTTATTCAGTGACAGT	600						
QY	624	GATCCCATATTCACACACTCAACACAAACAAAGAAATTTATTCAGTGACAGT	683						
DB	601	GATCCCATATTCACACACTCAACACAAACAAAGAAATTTATTCAGTGACAGT	660						
QY	684	ACCTACTGGTGCCATGCCCTTACTCTACAATCCCTGCCCTACTACTCTCTCTGCT	743						
DB	661	ACCTACTGGTGCCATGCCCTTACTCTACAATCCCTGCCCTACTACTCTCTCTGCT	720						
QY	744	CCAGCTTCCACTTCTATTCCAGGAGAAAAATTTGATTTGTGCACAGAGTTTATG	803						
DB	721	CCAGCTTCCACTTCTATTCCAGGAGAAAAATTTGATTTGTGCACAGAGTTTATG	780						
QY	804	GAACCTAGCACCCTCTACAGAACTGAACCAATTTGTTGAAAAATAAGCAGCATCAAG	863						
DB	781	GAACCTAGCACCCTCTACAGAACTGAACCAATTTGTTGAAAAATAAGCAGCATCAAG	840						
QY	864	AATGAAGTGTGGGTTGGAGGTGTCCCAAGGCTCTGCTAGTGTGCTCTCTCTTC	923						
DB	841	AATGAAGTGTGGGTTGGAGGTGTCCCAAGGCTCTGCTAGTGTGCTCTCTCTTC	900						
QY	924	TTTGGTGTGCAGCTGGCTTGGATTTTGCTATGTCAAAAGTATGTGAAGCCTTCCCT	983						
DB	901	TTTGGTGTGCAGCTGGCTTGGATTTTGCTATGTCAAAAGTATGTGAAGCCTTCCCT	960						
QY	984	TTTCAAAACAGAACTCAGCAGAAAGAAATGATCGAAACCAAAAGTAGTAAAGGAGAGAG	1043						
DB	961	TTTCAAAACAGAACTCAGCAGAAAGAAATGATCGAAACCAAAAGTAGTAAAGGAGAGAG	1020						
QY	1044	GCCAAATGATAGCAACCTTAATCAGAAATCAAGAAAACTGATAAAAAACCAGAGAGTCC	1103						
DB	1021	GCCAAATGATAGCAACCTTAATCAGAAATCAAGAAAACTGATAAAAAACCAGAGAGTCC	1080						

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QY 1104 AAGAGTCCAGCAAACTACCGTGGATGCTGGAAGCTGAACTTAGATGACAGAAA 1163
Db 1081 AAGAGTCCAGCAAACTACCGTGGATGCTGGAAGCTGAACTTAGATGACAGAAA 1140
QY 1164 TGAGGAGACACACTGAGGCTGTTCTTTTCATGCTCTTACCTGCCCCAGCTGGGAA 1223
Db 1141 TGAGGAGACACACTGAGGCTGTTCTTTTCATGCTCTTACCTGCCCCAGCTGGGAA 1200
QY 1224 ATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCTTGGTTCTTAATCGAATCAGC 1283
Db 1201 ATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCTTGGTTCTTAATCGAATCAGC 1260
QY 1284 TCAGGACTGCTATGACTATGAGTGCCACCAAGAGATGCCCTTCTCTTATTTGTAAC 1343
Db 1261 TCAGGACTGCTATGACTATGAGTGCCACCAAGAGATGCCCTTCTCTTATTTGTAAC 1320
QY 1344 CTGTCTGGATCTATCTCTCTACCTCCAAAGCTTCCACGGCTTTCTAGCCTGGCTAT 1403
Db 1321 CTGTCTGGATCTATCTCTCTACCTCCAAAGCTTCCACGGCTTTCTAGCCTGGCTAT 1380
QY 1404 GTCCTAATATATCCCACTGGGAGAAAGGATTTTGCAAAGTGCAGGACCTTAAACATC 1463
Db 1381 GTCCTAATATATCCCACTGGGAGAAAGGATTTTGCAAAGTGCAGGACCTTAAACATC 1440
QY 1464 TCATCAGTATCCAGTGGTAAAGGCTCTCTGGCTGTCTGAGGCTAGGTGGTTGAAGC 1523
Db 1441 TCATCAGTATCCAGTGGTAAAGGCTCTCTGGCTGTCTGAGGCTAGGTGGTTGAAGC 1500
QY 1524 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1583
Db 1501 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1560
QY 1584 GCTCTGAAAGAGAAACAGTATCCCACTGACATGTCTTCTGAGCCCGGTGAAGCAAA 1643
Db 1561 GCTCTGAAAGAGAAACAGTATCCCACTGACATGTCTTCTGAGCCCGGTGAAGCAAA 1620
QY 1644 AGAATGGCAGAAAAGTTTAGCCCTCAAAGCCATGGAGATTCTCATACTTGAGACCTAA 1703
Db 1621 AGAATGGCAGAAAAGTTTAGCCCTCAAAGCCATGGAGATTCTCATACTTGAGACCTAA 1680
QY 1704 TCTCTGTAAGCTAAAATAAGAAATAGAAACAGGCTGAGGATACGACAGTACACTGTCA 1763
Db 1681 TCTCTGTAAGCTAAAATAAGAAATAGAAACAGGCTGAGGATACGACAGTACACTGTCA 1740
QY 1764 GCAGGAGCTGTAACACACAGAGGTCAAAGTGTCTTCTGAAACATGAGTTGGAAT 1823
Db 1741 GCAGGAGCTGTAACACACAGAGGTCAAAGTGTCTTCTGAAACATGAGTTGGAAT 1800
QY 1824 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT 1883
Db 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT 1860
QY 1884 AGGAATATACHTTTTACAGTAAACAAAATAAAAACTCTTATAAATTTCTATTTTATCT 1943
Db 1861 AGGAATATACHTTTTACAGTAAACAAAATAAAAACTCTTATAAATTTCTATTTTATCT 1920
QY 1944 GAGTTTACAGAAATGATTACTAGGAGATTAATCTAGTAATTTGTTTAAAGATTAATAAA 2003
Db 1921 GAGTTTACAGAAATGATTACTAGGAGATTAATCTAGTAATTTGTTTAAAGATTAATAAA 1980
QY 2004 TTCAACAAACATTTTAAAAAAA 2025
Db 1981 TTCAACAAACATTTTGTGTAATA 2002

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RESULT 7

US-08-892-880-1  
; Sequence 1, Application US/08892880  
; Patent No. 5942417  
; GENERAL INFORMATION:  
; APPLICANT: NI, JIAN  
; APPLICANT: GENTZ, REINER L.

```

; APPLICANT: DILLON, PATRICK J.  

; TITLE OF INVENTION: CD44-LIKE PROTEIN  

; NUMBER OF SEQUENCES: 15  

; CORRESPONDENCE ADDRESS:  

; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  

; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600  

; CITY: WASHINGTON  

; STATE: DC  

; COUNTRY: USA  

; ZIP: 20005-3934  

; COMPUTER READABLE FORM:  

; MEDIUM TYPE: Floppy disk  

; COMPUTER: IBM PC compatible  

; OPERATING SYSTEM: PC-DOS/MS-DOS  

; SOFTWARE: PatentIn Release #1.0, Version #1.30  

; CURRENT APPLICATION DATA:  

; APPLICATION NUMBER: US/08/892,880  

; FILING DATE: HEREWITH  

; CLASSIFICATION: 435  

; PRIOR APPLICATION DATA:  

; APPLICATION NUMBER: 60/021,762  

; FILING DATE: 15-JUL-1996  

; ATTORNEY/AGENT INFORMATION:  

; NAME: STEFFE, ERIC K  

; REGISTRATION NUMBER: 36,688  

; REFERENCE/DOCKET NUMBER: 1488.0490001  

; TELECOMMUNICATION INFORMATION:  

; TELEPHONE: 202-371-2600  

; TELEFAX: 202-371-2540  

; INFORMATION FOR SEQ ID NO: 1:  

; SEQUENCE CHARACTERISTICS:  

; LENGTH: 2313 base pairs  

; TYPE: nucleic acid  

; STRANDEDNESS: single  

; TOPOLOGY: linear  

; MOLECULE TYPE: DNA (genomic)  

; FEATURE:  

; NAME/KEY: CDS  

; LOCATION: 91..1056  

; FEATURE:  

; NAME/KEY: mat_peptide  

; LOCATION: 154..1056  

; FEATURE:  

; NAME/KEY: sig_peptide  

; LOCATION: 91..153  

; US-08-892-880-1

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Query Match          94.4%; Score 1915.2; DB 2; Length 2313;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1920; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 98 CATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATCTCAGGTGTTT 157
Db 6 CATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATCTCAGGTGTTT 65
QY 158 CCCTGGCTCTGAGGGTAGGCACGATGCCAGGTGCTTACGCTGTGCTTCTCTAC 217
Db 66 CCCTGGCTCTGAGGGTAGGCACGATGCCAGGTGCTTACGCTGTGCTTCTCTAC 125
QY 218 TTCCATCTGGACCAAGAGGCTCTGCTGTCAGAGGCTCTTGGTGCAGAGAGCTTTCCAT 277
Db 126 TTCCATCTGGACCAAGAGGCTCTGCTGTCAGAGGCTCTTGGTGCAGAGAGCTTTCCAT 185
QY 278 CCAGGTGTCTATGCAGAAATTATGGGGATCACCTTTGTGAGCAAAAAGGCGAACAGCAGCT 337
Db 186 CCAGGTGTCTATGCAGAAATTATGGGGATCACCTTTGTGAGCAAAAAGGCGAACAGCAGCT 245
QY 338 GAAATTTACAGAGCTAAGGAGGCTGTAGGCTGTCTGGGACTAAGTTTGGCCGCAAGGA 397
Db 246 GAAATTTACAGAGCTAAGGAGGCTGTAGGCTGTCTGGGACTAAGTTTGGCCGCAAGGA 305
QY 398 CCAAGTTGAAACAGCCTTTGAAAGCTAGCTTTGAAACTTGACGCTATGCTGGTTGGAGA 457

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Db 306 CCAAGTTGAAACAGCCTTGAAGCTAGCTTTGGAACCTTCAGCTATGCGTGGTGGCGA 365  
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 Db 366 TGGATTGCGTGCATCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAATAATGGGTTGG 425  
 Qy 518 TGTCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTTGAGCGCTATTGTACACATC 577  
 Db 426 TGTCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTTGAGCGCTATTGTACACATC 485  
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 Qy 638 CACTCAAACTGCAACCAACCAAGAAATTTATGTGAGTGACAGTACCTACTCGGTGGC 697  
 Db 546 CACTCAAACTGCAACCAACCAAGAAATTTATGTGAGTGACAGTACCTACTCGGTGGC 605  
 Qy 698 ATCCCTTACTCTACAACTACCTGCGCTACTACTCTCTCTCTCTCTCTCTCTCTCTCT 757  
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 Db 786 GTTTCAGGCTGTCACCGCTCTGCTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 845  
 Qy 938 TGGCTTTGGATTGCTATGCTCAAAAGGTATGGAAGGCTTCCCTTTTACAAACAGAA 997  
 Db 846 TGGCTTTGGATTGCTATGCTCAAAAGGTATGGAAGGCTTCCCTTTTACAAACAGAA 905  
 Qy 998 TCAGCAGAGGAATAATGATCGAAACCAAGTAGTAAAGGAGGAGAGCCCAATGATAGCAA 1057  
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 Db 1026 AACTACCGTGCATGCTCGAAGCTGAAGTTTAGATGAGACAGAAATGAGGACACACC 1085  
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 Qy 1238 AGAACCAAGAGAAAGTCCACCTTGGTTCCTAACTGGAATCAGCTCAGGAGTCCCAT 1297  
 Db 1146 AGAACCAAGAGAAAGTCCACCTTGGTTCCTAACTGGAATCAGCTCAGGAGTCCCAT 1205  
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 Qy 1418 CCACTGGGAGAAAGGATTTTGAAGAGTGAAGGACCTAAACATCTCATCAGTATCCAG 1477  
 Db 1326 CCACTGGGAGAAAGGATTTTGAAGAGTGAAGGACCTAAACATCTCATCAGTATCCAG 1385  
 Qy 1478 TGTGTAAGAGGCTCTCTGCTGCTGAGGCTAGTGGTTGAAAGCCAGGAGTCACTGA 1537  
 Db 1386 TGTGTAAGAGGCTCTCTGCTGCTGAGGCTAGTGGTTGAAAGCCAGGAGTCACTGA 1445

RESULT 8

US-09-724-864-28  
 ; Sequence 28, Application US/09724864  
 ; Patent No. 6380362  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Watson, James D.  
 ; APPLICANT: Marison, James G.  
 ; TITLE OF INVENTION: Polynucleotides, polypeptides expressed  
 ; FILE REFERENCE: 11000.1050U1  
 ; CURRENT APPLICATION NUMBER: US/09/724,864  
 ; CURRENT FILING DATE: 2000-11-28  
 ; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678  
 ; PRIOR FILING DATE: 1999-12-23  
 ; NUMBER OF SEQ ID NOS: 72  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 28  
 ; LENGTH: 1896  
 ; TYPE: DNA  
 ; ORGANISM: Mouse  
 ; US-09-724-864-28

Query Match 29.7%; Score 603.6; DB 4; Length 1896;  
 Best Local Similarity 76.2%; Pred. No. 2.8e-167;  
 Matches 786; Conservative 0; Mismatches 234; Indels 12; Gaps 3;  
 Qy 163 GCTCTGAAGGGGTAGGACGATGCGCAGGTGCTTACGCTGCTGCTGCTGCTGCTGCTGCT 222  
 Db 42 GCGCCGAGGGATCTGCAAAATGCTCCAGCACACTAGCCTGGTGTACTCTCGCTCTA 101  
 Qy 223 TCTGGACACGAGGCTCTGCTTCAAGGCTCTTGGTGCAGAGAGCTTCCATCCAGG 282  
 Db 102 TTTGGACCACTAGGACCCAGTCCAGGTGCCACCTCGTGCAGAGCTTCCAT---TT 158  
 Qy 283 TGTATGCAAAATATGCGGATCACCTTGTGAGCAAAAGGCGAACCCAGCAGTGAAT 342



159	CTACATG	CAGAAATCAT	GGCGGTG	CCCTTGT	GGCAGAAA	CAAAAAC	CCACAGAT	GCAATT	218	
343	TCACAGA	AGCTTAAG	GAGGAG	CCCTGT	AGGCTG	CTGGGACT	TAAGTTT	TGGCCG	GCAGGACCAAG	402
219	TCACAGA	AGCCAA	CGAGCC	TGTAA	GATGCT	GGAGT	GACTCT	TGCC	CACAGGGAC	278
403	TTGAAA	CAGCCTT	GAAAGCT	AGCTTT	GAAACT	TTCAGCT	ATGCGT	TGGGT	TTGGAGATGGAT	462
279	TAGAGT	CAGCC	CAGAAAT	CTGGCT	TTGAGACT	TTCAGCT	ATGGA	TGGT	TTGGAGAACGT	338
463	TCGTGGT	CATCTCT	TAGGAT	TAGCCCA	ACCCAGT	GTGGG	AAAAAT	CGGGT	TGGGTGTC	522
339	TCTCTGT	CAUCCCT	CGGATTTT	CTCAA	ACCCAGG	GTGGG	AGAAAT	CGCA	AAAGTGTC	398
523	TGATTT	TGGAAG	GGTCC	AGTGA	GGCCG	CAGTTT	TGCAG	CCCTAT	TGTTTACA	582
399	TGATTT	TGGAAT	GTCCCT	CACG	CCAAAG	TTCAA	AGCTAT	TGCC	CAACTCAT	458
583	CTTGGAC	TAACTCG	TGCAT	TC	CAGAAAT	TATCA	CCACAA	AGATCC	CAAT	642
459	CTGGG	TTAACTCT	CTGAT	TC	CAGAAAT	CGT	TAGCA	ATTTA	CCCGT	518
643	AAACTG	CAACA	AAACAG	AATTTAT	TGTCA	GTGAC	GTAC	TACT	ACGTG	702
519	A-----	AA	CA	CCGCA	ACAGAG	TTTCT	GT	CAG	CGCCCT	572
703	CTTACT	CTCAAT	ACTG	CGCCCT	ACTACT	CTCT	CTCT	GTCT	CCAGCT	762
573	CTGACT	TC	CAACAC	CTG--	-TTTCT	GC	CAAC	CCCGG	CTCCAC	629
763	CACGGA	AAAAAAT	TGAT	TGTGC	ACAGAG	TTTTAT	TG	AAACT	TAGCA	822
630	CACGGA	AGACAAA	AGATTT	TGTAT	CA	CGGAAG	TTTTAT	PAC	AGA	689
823	CAGAA	ACTGA	ACCAT	TTTGT	TGAAA	ATAAG	CAG	CATTCA	AGAA	882
690	CAGAA	CAGA	AGCAT	TTGTT	GCAAG	TGG	AGCAG	CATTCA	GAA	749
883	GAGGT	TCCC	ACGGCT	CTCGT	AGTGT	CTCT	CTCT	CTTT	TGGT	942
750	GAGGT	TCCC	ACCGCC	CTCGT	GGTGGT	CTCT	CTCT	CTTT	TGGT	809
943	TTGGA	TTTTC	TATGT	CAAA	AGGTAT	GTGA	AGGCTT	CCCTTT	TAC	1002
810	TGCTG	TTTTC	TAGTGA	AAAG	TATGTGA	AGGCTT	CCCTTT	TAC	AA	869
1003	AGA	GAAAT	TGAT	CGAA	ACCA	AAAGT	AGTAA	GAGG	AGAA	1062
870	AGA	GAAAT	TGAT	CGAA	ACCA	AAAGT	AGTAA	GAGG	AGAA	929
1063	ATG	GAAAT	CA	AGAA	AACTG	ATATA	AAAC	CCG	AGAGT	1122
930	ATG	A	GAAAT	CA	AGAA	AAAC	CA	TTTAA	AAAC	989
1123	CCGT	GC	GAT	CGCT	TGGA	AGCT	GAA	GT	TAGAT	1182
990	CGGT	GC	GAT	CGCT	TGGA	AGCT	GAA	GT	TAGAT	1182
1183	CTG	GT	TTCT	TTTC	1194					
1050	CAAG	TTT	TCAT	GC	1061					

RESULT 9  
US-88-892-880-11/c  
: Sequence 11, Application US/08892880  
: Patent No. 5942417  
: GENERAL INFORMATION:  
: APPLICANT: NI, JIAN  
: APPLICANT: GENTZ, REINER L.  
: APPLICANT: DILLON, PATRICK J.  
: TITLE OF INVENTION: CD44-LIKE PRO

NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/892,880  
FILING DATE: HEREWITH  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/021,762  
FILING DATE: 15-JUL-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: STEFF, ERIC K  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.0490001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 339 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-892-880-11

Query Match 16.5%; Score 334; DB 2; Length 339;  
Best Local Similarity 98.5%; Pred. No. 2.3e-88;  
Matches 334; Conservative 0; Mismatches 5; Indels

Qy	1489	CCTCTGGCTGTC	TGAGGCT	TAGTGGGTT	GAAAGCCAA	GAGTCACT	GTAGACCAAGGC	TT	1548
Db	339	CCTCTGGCTGTC	TGAGGCT	TAGTGGGTT	GAAAGCCAA	GAGTCACT	GTAGACCAAGGC	TT	280
Qy	1549	TCTCTACTGAT	TCGGCAGCT	CAGACCC	TTTCTT	CAGCTG	TAAAGAAAC	ACGTATCCC	1608
Db	279	NCTCTACTGAT	TCGGCAGCT	CAGACCC	TTTCTT	CAGCTG	TAAAGAAAC	ACGTATCCC	220
Qy	1609	ACCTGCATGTC	CTCTGAGCCCG	GTAAGGCAAA	AGAAATG	GCAGAAA	AGTTTAG	CCCCCT	1668
Db	219	ACCTGCATGTC	CTCTGAGCCCG	GTAAGGCAAA	AGAAATG	GCAGAAA	AGTTTAG	CCCCCT	160
Qy	1669	GAAAGCCATGG	AGATTCT	CATAACT	TGAGACCT	TAATCT	CTGTAAAGCT	AAAAATAAAGAA	1728
Db	159	GAAAGCCATGG	AGANTCT	CATAACT	TGAGACCT	TAATCT	CTGTAAAGCT	AAAAATAAAGAA	100
Qy	1729	TAGAACAGGCT	GAGGATAC	GACAGTAC	ACTGT	TCAGCAGG	CACTGT	TAAACACAGACAGGG	1788
Db	99	TAGAACAGGCT	GAGGATAC	GACAGTAC	ACTGT	TCAGCAGG	CACTGT	TAAACACAGACAGGG	40
Qy	1789	TCAAAGTGT	TTTTCT	CTGAACAC	ATTG	AGTTGGA	ATCACT		1827
Db	39	TCAAAGTGT	TTTTCT	CTGAACAC	ATTG	AGTTGGA	ATCACT		1

RESULT 10  
US-08-892-880-12  
; Sequence 12, Application US/08892880  
; Patent No. 5942417  
; GENERAL INFORMATION:  
; APPLICANT: NI, JIAN  
; APPLICANT: GENTZ, REINER L.  
; APPLICANT: GENTZ, PATRICK J.  
; APPLICANT: DILLON, PATRICK J.

```
; TITLE OF INVENTION: CD44-LIKE PROTEIN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/892,880
; FILING DATE: HERewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/021,762
; FILING DATE: 15-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0490001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 492 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-892-880-12

Query Match 14.6%; Score 296.8; DB 2; Length 492;
Best Local Similarity 98.3%; Pred. No. 2.6e-77;
Matches 298; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 98 CATCCGACTAGTTATTGAGCATCTGCTCTCATATCACAGTGGCCATCTCAGGTGTTT 157
Db 14 CATCCGACTAGTTATTGAGCATCTGCTCTCATATCACAGTGGCCATCTCAGGTGTTT 73

QY 158 CCTCGCTCTGAAGGGTAGGCACGATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCAC 217
Db 74 CCTCGCTCTGAAGGGTAGGCACGATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCAC 133

QY 218 TTCCATCTGACACAGAGCTCTGCTGCAAGGCTCTTGGTGCAAGAGCTTCCAT 277
Db 134 TTCCATCTGACACAGAGCTCTGCTGCAAGGCTCTTGGTGCAAGAGCTTCCAT 193

QY 278 CCAGGTGTCTGAGCAATATGGGATCACCCCTTGTGAGCAAAAAGGCGAACCCAGCAGCT 337
Db 194 CCAGGTGTCTGAGCAATATGGGATCACCCCTTGTGAGCAAAAAGGCGAACCCAGCAGCT 253

QY 338 GAATTTACAGAGCTTAAGAGGCTGTAGGCTGTGGGACTTAAGTTTGGCCCGGAAGGA 397
Db 254 GAATTTACAGAGCTTAAGAGGCTGTAGGCTGTGGGACTTAAGTTTGGCCCGGAAGGC 313

Query Match 11.8%; Score 239; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.7e-60;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1518 GAAAGCCAAAGGAGTCACTGAGACCAAGGCTTTCTTACTGATTCGCGAGCTCAGACCCCTT 1577
Db 241 GAAAGCCAAAGGAGTCACTGAGACCAAGGCTTTCTTACTGATTCGCGAGCTCAGACCCCTT 182

QY 1578 TCTTCAGCTCTGAAAGAGAAACACGATATCCCACTTGACATGTCTTCTGAGCCCGTAAG 1637
Db 181 TCTTCAGCTCTGAAAGAGAAACACGATATCCCACTTGACATGTCTTCTGAGCCCGTAAG 122

QY 1638 AGCAAAAGAAATGCGAGAAAGTTTAGCCCCCTGAAAGCCATGGAGATTCTCATAACTTGAG 1756
Db 61 ACCTAATCTCTGTAAGCTAAATAAAGAAATAGAAATAGAACAGGCTGAGGATACGACAGTAC 3

RESULT 12
US-09-620-405B-324/c
; Sequence 324, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 324
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-620-405B-324

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Best Local Similarity 100.0%; Pred. No. 1.7e-60;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1518 GAAAGCCAAAGGAGTCACTGAGACCAAGGCTTTCTTACTGATTCGCGAGCTCAGACCCCTT 1577
Db 241 GAAAGCCAAAGGAGTCACTGAGACCAAGGCTTTCTTACTGATTCGCGAGCTCAGACCCCTT 182

QY 1578 TCTTCAGCTCTGAAAGAGAAACACGATATCCCACTTGACATGTCTTCTGAGCCCGTAAG 1637
Db 181 TCTTCAGCTCTGAAAGAGAAACACGATATCCCACTTGACATGTCTTCTGAGCCCGTAAG 122

QY 1638 AGCAAAAGAAATGCGAGAAAGTTTAGCCCCCTGAAAGCCATGGAGATTCTCATAACTTGAG 1697
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Db 121 ACACAAAGATGGCAGAAAAGTTTACCCCTGAAAGCCATGGAGATTCATCAACTTTGAG 62  
QY 1698 ACCTAATCTCTGTAAGCTTAAAGCTAAATAAGAAATAGAACAAAGGCTGGAGATACGACAGTAC 1756  
Db 61 ACCTAATCTCTGTAAGCTTAAAGCTTAAATAAGAAATAGAACAAAGGCTGGAGATACGACAGTAC 3

RESULT 13  
US-09-433-826B-324/c  
; Sequence 324, Application US/09433826B  
; Patent No. 6579973  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; TITLE OF INVENTION: COMPOSITIONS OF BREAST CANCER AND METHODS FOR THEIR USE  
; FILE REFERENCE: 210121.470C4  
; CURRENT APPLICATION NUMBER: US/09/433,826B  
; CURRENT FILING DATE: 1999-11-03  
; NUMBER OF SEQ ID NOS: 474  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 324  
; LENGTH: 241  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-433-826B-324

Query Match 11.8%; Score 239; DB 4; Length 241;  
Best Local Similarity 100.0%; Pred. No. 1.7e-60;  
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1518 GAAAGCCAAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTT 1577  
Db 241 GAAAGCCAAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTT 182  
QY 1578 TCTTCAGCTCTGAAAGAGAAACACATATCCACCTGACATGTCCTTCTGAGCCCGGTAAG 1637  
Db 181 TCTTCAGCTCTGAAAGAGAAACACATATCCACCTGACATGTCCTTCTGAGCCCGGTAAG 122  
QY 1638 AGCAAAAGAAATGGCAGAAAAGTTTACCCCTGAAAGCCATGGAGATTCATCAACTTTGAG 1697  
Db 121 AGCAAAAGAAATGGCAGAAAAGTTTACCCCTGAAAGCCATGGAGATTCATCAACTTTGAG 62  
QY 1698 ACCTAATCTCTGTAAGCTTAAAGCTTAAATAAGAAATAGAACAAAGGCTGGAGATACGACAGTAC 1756  
Db 61 ACCTAATCTCTGTAAGCTTAAAGCTTAAATAAGAAATAGAACAAAGGCTGGAGATACGACAGTAC 3

RESULT 14  
US-09-604-287A-324/c  
; Sequence 324, Application US/09604287A  
; Patent No. 6586572  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Hepler, William T.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.470C7  
; CURRENT APPLICATION NUMBER: US/09/604,287A  
; CURRENT FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 489  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 324  
; LENGTH: 241  
; TYPE: DNA

; ORGANISM: Homo sapiens  
US-09-604-287A-324  
Query Match 11.8%; Score 239; DB 4; Length 241;  
Best Local Similarity 100.0%; Pred. No. 1.7e-60;  
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1518 GAAAGCCAAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTT 1577  
Db 241 GAAAGCCAAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTT 182  
QY 1578 TCTTCAGCTCTGAAAGAGAAACACATATCCACCTGACATGTCCTTCTGAGCCCGGTAAG 1637  
Db 181 TCTTCAGCTCTGAAAGAGAAACACATATCCACCTGACATGTCCTTCTGAGCCCGGTAAG 122  
QY 1638 AGCAAAAGAAATGGCAGAAAAGTTTACCCCTGAAAGCCATGGAGATTCATCAACTTTGAG 1697  
Db 121 AGCAAAAGAAATGGCAGAAAAGTTTACCCCTGAAAGCCATGGAGATTCATCAACTTTGAG 62  
QY 1698 ACCTAATCTCTGTAAGCTTAAAGCTTAAATAAGAAATAGAACAAAGGCTGGAGATACGACAGTAC 1756  
Db 61 ACCTAATCTCTGTAAGCTTAAAGCTTAAATAAGAAATAGAACAAAGGCTGGAGATACGACAGTAC 3

RESULT 15  
US-09-834-759-324/c  
; Sequence 324, Application US/09834759  
; Patent No. 6680197  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Henderson, Robert A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.470C9  
; CURRENT APPLICATION NUMBER: US/09/834,759  
; CURRENT FILING DATE: 2001-04-13  
; NUMBER OF SEQ ID NOS: 547  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 324  
; LENGTH: 241  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-834-759-324

Query Match 11.8%; Score 239; DB 4; Length 241;  
Best Local Similarity 100.0%; Pred. No. 1.7e-60;  
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1518 GAAAGCCAAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTT 1577  
Db 241 GAAAGCCAAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGACCCCTT 182  
QY 1578 TCTTCAGCTCTGAAAGAGAAACACATATCCACCTGACATGTCCTTCTGAGCCCGGTAAG 1637  
Db 181 TCTTCAGCTCTGAAAGAGAAACACATATCCACCTGACATGTCCTTCTGAGCCCGGTAAG 122  
QY 1638 AGCAAAAGAAATGGCAGAAAAGTTTACCCCTGAAAGCCATGGAGATTCATCAACTTTGAG 1697  
Db 121 AGCAAAAGAAATGGCAGAAAAGTTTACCCCTGAAAGCCATGGAGATTCATCAACTTTGAG 62  
QY 1698 ACCTAATCTCTGTAAGCTTAAAGCTTAAATAAGAAATAGAACAAAGGCTGGAGATACGACAGTAC 1756  
Db 61 ACCTAATCTCTGTAAGCTTAAAGCTTAAATAAGAAATAGAACAAAGGCTGGAGATACGACAGTAC 3

Search completed: September 15, 2004, 11:26:46  
Job time : 163 secs

B/awk

Checked

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 15, 2004, 16:29:45 ; Search time 493 Seconds  
(without alignments)  
2774.685 Million cell updates/sec

Title: US-10-079-111-1

Perfect score: 322

Sequence: 1 MARCFSLVLLTSITWTRLL.....NPESKSPKTTVRCLEAEV 322

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Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Word size: 12

Total number of hits satisfying chosen parameters: 174

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

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-NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

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6: geneseqn2002as.\*  
7: geneseqn2003as.\*  
8: geneseqn2003bs.\*  
9: geneseqn2003cs.\*  
10: geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	322	100.0	1755	5	AAF93818 Human CDN
2	322	100.0	2027	10	ADE71449 Human CDN
3	322	100.0	2029	3	AZ98172 Human sig
4	322	100.0	2029	10	ADE71445 Human CDN
5	322	100.0	2372	2	AX52250 Protein P
6	322	100.0	2372	3	ADC78520 Human PRO
7	322	100.0	2372	4	AAF72408 Human PRO
8	322	100.0	2372	4	AAF92060 Human PRO

9	322	100.0	2372	6	ABS74380 Human CDN
10	322	100.0	2372	6	ABL88087 Human PRO
11	322	100.0	2372	6	ABL95576 Human ang
12	322	100.0	2372	7	ACA59060 Human PRO
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17	322	100.0	2372	7	ACD81543
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22	322	100.0	2372	7	ACA63988
23	322	100.0	2372	7	ACA91252
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83	322	100.0	2372	9	ADD03581	Add03581 Human sec
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86	322	100.0	2372	9	ADR34833	ADR34833 Human sec
87	322	100.0	2372	10	ADC52143	ADC52143 Novel hum
88	322	100.0	2372	10	ADG79278	ADG79278 Human sec
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91	322	100.0	2372	10	ADG73378	ADG73378 Human sec
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93	322	100.0	2372	10	ADG73913	ADG73913 Human sec
94	314	97.5	2324	4	ABA09223	ABA09223 Human PRO
95	287	89.1	1680	9	ADD04999	ADD04999 Human sec
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98	239	74.2	2369	6	ABL90698	ABL90698 Human pol
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ALIGNMENTS						
RESULT 1						
ID	AAF93818 standard; cDNA; 1755 BP.					
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XX	AC					
DT	23-MAY-2001 (first entry)					
XX	Humar cDNA encoding a membrane or secretory protein clone PSEC0135.					
DE	Human; secretory protein; membrane protein; vaccine; gene therapy;					
XX	rheumatoid arthritis; diabetes; ss.					
KW	Homo sapiens.					
XX	EP1067182-A2.					
PN	10-JAN-2001.					
PD	07-JUL-2000; 2000EP-00114090.					
XX	08-JUL-1999; 99JP-00194179.					
PR	11-JAN-2000; 2000JP-00118775.					
PR	02-MAY-2000; 2000JP-00183766.					
XX	(HELI-) HELIX RES INST.					
PA	Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;					
PI	WPI; 2001-093989/11.					
XX	P-PSDB; AAB88391.					
DR	Nucleic acids encoding secretory proteins/membrane proteins, useful in					
XX	gene therapy or as candidate target molecules in drug development.					
PT	Claim 1; SEQ ID NO 149; 609pp + Sequence Listing; English.					
XX	This invention relates to nucleic acid sequences AAF93744 - AAF93916					
CC	which encode human secretory or membrane proteins represented by AAB88317					
CC	- AAB88419. Included in the invention are primers AAF93917 - AAF94295 and					
CC	AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the					
CC	invention. The invention also includes methods for the production of					
CC	antibodies directed against the proteins, and cDNA sequences, which can					
CC	be used in vaccines. The polynucleotide sequences can be used in gene					
CC	therapy. The polynucleotide sequences and the proteins they encode may be					
CC	used in the prevention, treatment and diagnosis of diseases associated					
CC	with inappropriate secretory protein/membrane protein expression. The					
CC	nucleic acids and complementary sequences may also be used as DNA probes					
CC	in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect					
CC	and quantitate the presence of similar nucleic acid sequences in samples.					

CC	They may also be used to study the expression and function of secretory					
CC	proteins/membrane polypeptides and their role in metabolism. The					
CC	polypeptides may be used as antigens in the production of antibodies					
CC	against them and in assays to identify modulators (agonists and					
CC	antagonists) of expression and activity. The antibodies and antagonists					
CC	may also be used as therapeutic agents to down regulate expression and					
CC	activity. The antibodies may also be used as diagnostic agents for					
CC	detecting the presence of the polypeptides in samples (e.g. by enzyme					
CC	linked immunosorbent assay (ELISA). Examples of diseases which may be					
CC	treated include rheumatoid arthritis and diabetes					
XX	Sequence 1755 BP; 502 A; 422 C; 406 G; 425 T; 0 U; 0 Other;					
SQ	Alignment Scores:					
	Pred. No.:	1,12e-304	Length:	1755		
	Score:	322.00	Matches:	322		
	Percent Similarity:	100.00%	Conservative:	0		
	Best Local Similarity:	100.00%	Mismatches:	0		
	Query Match:	100.00%	Indels:	0		
DB:		5	Gaps:	0		
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QY	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60			
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QY	61	CysArgLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80			
Db	381	TGTAGGCTGCTGGGACTAAGTTTGGCGCGCAAGGCCAAGTTGAAACAGCCTTGAAGCT	440			
QY	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100			
Db	441	AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGGTCATCTTAGAAT	500			
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120			
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QY	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140			
Db	561	AGCCGACAGTTTGCAGCCTATTGTTACACTCATCTGATACTTGGACTAATCTGTCATT	620			
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160			
Db	621	CCAGAAATATATCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA	680			
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180			
Db	681	GAATTTATTGTCAGTGACAGTACTACTCGGTGGATCCCTTACTCTCAATACCTGCC	740			
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200			
Db	741	CCTACTACTACTCTCTCTCTCCAGCTTCCACTTCTATTCCAGCGAGAAAAAATTGATT	800			
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220			
Db	801	TGTGTACAGAAGTTTTTATGGAACATAGCACCATGTCTACAGAACTGAACTTTGTT	860			
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240			
Db	861	GAATAATAAGCAGCATTCAAGATGAAGCTGCTGGGTTTGGAGGTGCTCCACCGCTCTG	920			
QY	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260			

```

Db      921 CTAGTGCTGCTCTCTCTCTTGGTGTGCTGAGCTGGCTTGGATTGTGCTATGTCAAA 980
QY      261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db      981 AGGTATGTGAAGCCCTTCCCTTTTACAAACAAGAATCAGCAGAAGAAATGATCGAAACC 1040
QY      281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db      1041 AAAGTAGTAAAGGAGAGAGAGCCCAATGATGCAACCCCTTAATGAGGAATCAAGAAGAACT 1100
QY      301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db      1101 GATAAAACCCAGAGAGTCCAAAGAGTCCAAAGCAAACTACCGTGGATGCTTGGAGCT 1160
QY      321 GluVal 322
Db      1161 GAAAGTT 1166

RESULT 2
ADE71449
ID ADE71449 standard; cDNA; 2027 BP.
AC ADE71449;
DT 29-JAN-2004 (first entry)
DE Human cDNA encoding PDEBC #2.
XX
XX
KW breast cancer; PDEBC; metastatic; human; ss; gene.
XX
OS Homo sapiens.
XX
PN US2003124543-A1.
XX
PD 03-JUL-2003.
XX
PF 20-FEB-2002; 2002US-00079111.
XX
PR 15-JAN-1999; 99US-00232160.
XX
PA (STUA/) STUART S G.
XX
PA (STRE/) STREETER D G.
XX
PI Stuart SG, Streeter DG;
XX
XX WPI; 2004-009141/01.
DR P-PSDB; ADE71444.
XX
XX A new cDNA encoding a protein differentially expressed in breast cancer
PT designated PCBC is useful to stage, treat, and monitor progression or
PT treatment of breast cancer, particularly an invasive, metastatic stage of
PT the disease.
XX
XX Claim 2; Fig 1; 31pp; English.
XX
XX The invention relates to an isolated cDNA encoding a protein that is
CC differentially expressed in breast cancer, designated PDEBC. The
CC invention is useful to diagnose breast cancer. The invention is also
CC useful to stage, treat, and monitor progression or treatment of breast
CC cancer, particularly an invasive, metastatic stage of the disease. The
CC present sequence represents cDNA encoding human PDEBC Incyte 3044710CBI.
CC Note: There are two sequences that have been assigned SEQ ID 2 in the
CC specification, the present sequence represents the sequence given in
CC figure 1.
XX
SQ Sequence 2027 BP; 612 A; 461 C; 445 G; 509 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.28e-304 Length: 2027
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

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RESULT 3

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DB:      10      Gaps:      0
US-10-079-111-1 (1-322) x ADE71449 (1-2027)
QY      1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTyrThrThrArgLeuLeu 20
Db      181 ATGGCCAGGTGCTTCAGCTGGTGTGCTTCTCACTTCCATCTGGACCAAGGCTCCCTG 240
QY      21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db      241 GTCCAAAGGCTCTTTCGCTGCAGAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGGG 300
QY      41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db      301 ATCACCCCTGTGTAGCAAAAGCGCAACAGCAGCTGAATTTCCACAGAAAGTCAAGGAGCC 360
QY      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db      361 TGTAGGCTGTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 420
QY      81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db      421 AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTGCTGTCATCTCTAGGATT 480
QY      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTyrLysValProVal 120
Db      481 AGCCCAAAACCCCAAGTGTGGGAAATGGGGTGGTGTCTGATTGGAAAGTTCCAGTG 540
QY      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTyrThrAsnSerCysIle 140
Db      541 AGCCGACAGTTTGGAGCTTATTTACAACTCATCTGATCTTGGACTAACTTCGTGCATT 600
QY      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db      601 CCAGAAATTATCACCAACCAAGATCCCATATTTCAACACTCAAACTGCAACACAAACA 660
QY      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db      661 GAAITTTATTGTGAGTGACAGTACCTACTCGGTGGCATCCCTTACTTACATACTCTGCC 720
QY      181 ProThrThrThrProAlaProAlaSerThrSerIleProAlaArgLysLysLeuIle 200
Db      721 CCTACTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
QY      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db      781 TGTGTACAGAAAGTTTTTATGAAACTAGCACCATGTCTACAGAACTGAACCAATTTGTT 840
QY      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db      841 GAAATAAAGCAGCAGCATTCAGAAATGAAGCTGTGGGTTTGGAGGTGTCCCAACGGCTCTG 900
QY      241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db      901 CTAGTGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
QY      261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db      961 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAATGATCGAAACC 1020
QY      281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db      1021 AAAGTAGTAAAGGAGAGAGCCCAATGATGAGCAACCCCTAATAGGAATCAAGAAGAACT 1080
QY      301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db      1081 GATAAAACCCAGAGAGTCCAAAGAGTCCAAAGTCCAAAGTCCAAAGTCCAAAGTCCAAAG 1140
QY      321 GluVal 322
Db      1141 GAAAGTT 1146

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Db 1083 GATAAAACCCAGAGAGTCCAGAGTCCAAGAGTCCAAGCAAACTACCGTGCATCGCTGGAAGCT 1142
QY 321 GluVal 322
Db 1143 GAAGTT 1148

RESULT 4
ADE71445
ID ADE71445 standard; cDNA; 2029 BP.
XX ADE71445;
XX 29-JAN-2004 (first entry)
XX Human cDNA encoding PDEBC Incyte 3044710CB1.
XX breast cancer; PDEBC; metastatic; human; ss; gene.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 183..1151
XX FT /*tag= a
XX FT /product= "PDEBC"
XX US2003124543-A1.
XX 03-JUL-2003.
XX 20-FEB-2002; 2002US-00079111.
XX 15-JAN-1999; 99US-00232160.
XX (STUA/) STUART S G.
XX (STRE/) STREETER D G.
XX Stuart SG, Streeter DG;
XX WPI: 2004-009141/01.
XX P-PSDB; ADE71444.
XX A new cDNA encoding a protein differentially expressed in breast cancer
XX designated PCBC is useful to stage, treat, and monitor progression or
XX treatment of breast cancer, particularly an invasive, metastatic stage of
XX the disease.
XX Claim 2; SEQ ID NO 2; 31pp; English.
XX The invention relates to an isolated cDNA encoding a protein that is
XX differentially expressed in breast cancer, designated PDEBC. The
XX invention is useful to diagnose breast cancer. The invention is also
XX useful to stage, treat, and monitor progression or treatment of breast
XX cancer, particularly an invasive, metastatic stage of the disease. The
XX present sequence represents cDNA encoding human PDEBC Incyte 3044710CB1.
XX Note: There are two sequences that have been assigned SEQ ID 2 in the
XX specification, the present sequence represents the sequence given in the
XX sequence listing.
XX Sequence 2029 BP; 612 A; 463 C; 445 G; 509 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.28e-304 Length: 2029
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x ADE71445 (1-2029)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 183 ATGGCCAGGTGCTTCAGCGCTGGTGTGCTTCTCACTTCATCTGCACCAAGGCTCTG 242
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QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
DB 640 GAATTTATTGTCAGTGACAGTACCTACTCGTGGCATCCCTTACTCTTCAATACCTGCC 699
QY 181 ProThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
DB 700 CCTACTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
DB 760 TGTGTCCACAGAAGTTTTTATGGAAGTACAGCACCATGCTTACAGAAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
DB 820 GAAATTAAGCAGCATTCAGATGAGCTGTGGGTTTGGAGGTGCCCCAGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
DB 880 CTAGTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
DB 940 AGTATGTGAAGGCCCTCTCTCTTTTACAAACAAGAATCAGCAGAAGAAATGATCGAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluLysSerLysThr 300
DB 1000 AAAGTAGTAAAGAGAGAGAGGCCAATGATAGCAACCTTAATGAGGAATCAAGAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
DB 1060 GATAAAACCAGAGAGTCCCAAGAGTCCCAAGCAAAACTACCGTGGATCGCTGGAGCT 1119
QY 321 GluVal 322
DB 1120 GAAATT 1125
RESULT 6
ADC78520
ID ADC78520 standard; cDNA; 2372 BP.
XX
AC ADC78520;
XX
DT 01-JAN-2004 (first entry)
DE Human PRO263 cDNA.
XX
KW antinflammatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian;
KW neurotropic; neuroprotective; vasotropic; chemotactic; angiogenic;
KW neurotrophic; osteopathic; antiasthmatic; antiarthritic; antirheumatic;
KW antiarteriosclerotic; cardiant; antidiabetic; cerebroprotective;
KW thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome;
KW gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease;
KW Alzheimer's; ALS; neuropathy; dermal scarring; wound healing;
KW nerve repair; thrombosis; bone; cartilage formation; angiogenesis;
KW asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder;
KW atherosclerosis; cardiac injury; infertility; premature aging; AIDS;
KW diabetes; stroke; gene therapy; transgenic; PRO; human; ss; gene.
XX
OS Homo sapiens.
XX
PN WO200015796-A2.
XX
XX 23-MAR-2000.
XX
PF 15-SEP-1999; 99WO-US021090.
XX
PR 16-SEP-1998; 98WO-US019330.
XX
BA (GETH ) GENENTECH INC.
XX
PI Chen J, Goddard A, Gurney AL, Hillan K, Pennica D, Wood WI;
PI Yuan J;
XX
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DR WPI; 2000-271434/23.
DR P-PSDB; ADC78521.
XX
PT Novel nucleic acids encoding secreted and transmembrane polypeptides with
XX homology, e.g. to growth and cancer-associated antigens.
PS Claim 2; SEQ ID NO 200; 355pp; English.
XX
CC The invention relates to a novel nucleic acid encoding a PRO polypeptide.
CC The polypeptides and polynucleotides of the invention may be useful as
CC research tools and as therapeutics for treating enterocolitis, Zollinger-
CC Ellison syndrome, gastrointestinal ulceration, psoriasis, cancer,
CC Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal
CC scarring and wound healing, nerve repair, thrombosis, bone and/or
CC cartilage formation, angiogenesis, asthma, rheumatoid arthritis, multiple
CC sclerosis, inflammatory disorders, atherosclerosis, cardiac injury,
CC infertility, premature aging, AIDS, diabetes complications and stroke.
CC The molecules may also be utilised during gene therapy procedures and
CC transgenic animal production. The current sequence is that of the human
CC PRO cDNA of the invention.
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.49e-304 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-10-079-111-1 (1-322) x ADC78520 (1-2372)
QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleThrThrArgLeuLeu 20
DB 160 ATGGCCAGGTGCTTCAGCCTGGTGTGTTCTTCTCACTTCCATTCGACACGAGGCTCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
DB 220 GTCCAAGGCTTTTGGTGCAGAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
DB 280 ATCACCCTTGTGAGCAAAAGGCAACCCAGCAGCTGAATTTCCAGAAAGCTAAGGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
DB 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
DB 400 AGCTTTGAAACTTGAGCTATGCGTGGGTGGAGATGGATTTCGTGTCATCTTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleThrLysValProVal 120
DB 460 AGCCCAAAACCCCAAGTGGGAAAAATGGGTGGGTGTCCTGATTGGAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrThrThrAsnSerCysIle 140
DB 520 AGCCGACAGTTTGCAGCCTATTGTTACAACATCATCTGATACTTGGACATACTCGTCGATT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
DB 580 CCAGAAATATTACCAACCAAGATCCCATATTCAACACTCAAACTGCAACCAACAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
DB 640 GAATTTATTGTCAGTGACAGTACCTACTCGTGGGATCCCTTACTCTACAACTACTGCC 699
QY 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
DB 700 CCTACTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 759
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QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
 Db 760 TGTGTCACAGAGTTTATGGAAGTACCATGCTACAGAACTGAACCATTTGTT 819  
 QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240  
 Db 820 GAAATTAAGCAGCAATCAAGATGAAGCTGCTGGGTTGGAGGTGTCGCCAGGCTCTG 879  
 QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
 Db 880 CTAGTCTTGGCTCTCTCTCTTTTGGTGTGCAGCTGGTCTTGGATTTTGTATGTCAAA 939  
 QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
 Db 940 AGGTATGTGAGGCCCTTCCTTTTACAAACAGAAATCAGCAGGAAGAAATGATCGAAACC 999  
 QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysThr 300  
 Db 1000 AAAGTAGTAAAGGAGGAGGAGGCAATGATAGCAACCTTAATGAGGAATCAAAAGAAACT 1059  
 QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrValArgCysLeuGluAla 320  
 Db 1060 GATAAAACCCAGAGAGTCCAGAGTCCAGCAAAACTACCGTGCATGCCCTGGAAGCT 1119  
 QY 321 GluVal 322  
 Db 1120 GAAGTT 1125

RESULT 7  
 AAF72408  
 ID AAF72408 standard; cDNA; 2372 BP.  
 XX  
 AC AAF72408;  
 XX  
 DT 24-APR-2001 (first entry)  
 XX  
 DE Human PRO263 cDNA.  
 XX  
 KW Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;  
 KW antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant;  
 KW antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;  
 KW antiarthritic; antifertility; antidiabetic; antiviral; diabetes;  
 KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;  
 KW ischaemia; inflammation; ss.  
 XX Homo sapiens.  
 OS  
 XX WO200104311-A1.  
 XX  
 PN 18-JAN-2001.  
 XX  
 PD 22-FEB-2000; 2000WO-US004414.  
 XX  
 PP 07-JUL-1999; 99US-0143048P.  
 XX 26-JUL-1999; 99US-0145698P.  
 PR 28-JUL-1999; 99US-0146222P.  
 PR 08-SEP-1999; 99WO-US020594.  
 PR 13-SEP-1999; 99WO-US020944.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 15-SEP-1999; 99WO-US021547.  
 PR 05-OCT-1999; 99WO-US023089.  
 PR 29-NOV-1999; 99WO-US028214.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 02-DEC-1999; 99WO-US028564.  
 PR 02-DEC-1999; 99WO-US028565.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 20-DEC-1999; 99WO-US030911.  
 PR 20-DEC-1999; 99WO-US030999.  
 PR 05-JAN-2000; 2000WO-US000219.  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX Ashkenazi AU, Botstein D, Desnoyers L, Eaton DL, Ferrara N;  
 PI

PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;  
 PI Godowski PV, Grimaldi CJ, Gurney AL, Hillan KJ, Kijavlin IJ;  
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;  
 PI Williams PM, Wood WI;  
 XX WPI: 2001-081051/09.  
 DR P-PSDB; AAB80247.  
 XX  
 PT Sixty one nucleic acids encoding PRO polypeptides which are useful in the  
 PT treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous  
 PT cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's  
 PT disease).  
 XX  
 PS Claim 2; Fig 73; 393pp; English.  
 XX  
 CC The present sequence is one of sixty one nucleic acids encoding novel  
 CC secreted and transmembrane PRO polypeptides. The PRO polypeptides are  
 CC useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung  
 CC squamous cell carcinoma), gastrointestinal disorders (e.g.  
 CC enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,  
 CC Parkinson's disease), wound repair, cardiovascular disorders (e.g.  
 CC endometrial bleeding angiogenesis, ischaemias such as coronary ischaemia,  
 CC atherosclerosis), inflammatory disorders (e.g. asthma, rheumatoid  
 CC arthritis, multiple sclerosis), infertility, AIDS and diabetes and  
 CC retinal disorders such as retinitis pigmentosum. The PRO nucleic acids  
 CC have applications in molecular biology, including use as hybridization  
 CC probes, and in chromosome and gene mapping  
 XX  
 SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1 49e-304 Length: 2372  
 Score: 322.00 Matches: 322  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 4 Gaps: 0  
 US-10-079-111-1 (1-322) x AAF72408 (1-2372)  
 QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20  
 Db 160 ATGGCCAGGTGCTTCAGCTGGTGTCTTCTCCTCCATCTGGACCAAGAGCTCTG 219  
 QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40  
 Db 220 GTCCAAAGGCTCTTTCGTCGAGAAGAGCTTTCATCCAGGTGTCTATGCAATATATGGGG 279  
 QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
 Db 280 ATCACCCTTGTGACCAAAAGGCGAACAGCAGAGCTGAATTCACAGAAGCTAAGGAGGCC 339  
 QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
 Db 340 TGTAGGCTCTGGGACTAAGTTTGGCCGCAAGACCAAGTTGAAACAGCCTTGAAGCT 399  
 QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100  
 Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTCTCTAGGATT 459  
 QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
 Db 460 AGCCCAACCCCAAGTGTGGGAAATGGGGTGGGTGCTCTGATTTGGAAGGTTCCAGTG 519  
 QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
 Db 520 AGCCGACAGCTTTCAGCCTTATTTGTACAACTCATCTGACTTGGACTTAACCTCGTCATT 579  
 QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
 Db 580 CCAGAAATATCACCACCAAGATCCCATATTCACACTCAAACTGACACACACACACACA 639  
 QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180





extracellular domain of the proteins with their associated signal peptide or lacking its associated signal peptide. Also included are the nucleic acids encoding the proteins, vectors, host cells, fusion proteins and antibodies which specifically bind to the proteins. The proteins are useful for detecting a polypeptide designated as A, B, C or D in a sample suspected of containing an A, B, C or D polypeptide, by contacting the sample with a polypeptide designated as E, F, G, H or I (or vice versa) and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide conjugate in the sample, where the formation of the conjugate is indicative of the presence of an A, B, C or D polypeptide in the sample, where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801 polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G, H or I polypeptide is labeled with a detectable label or is attached to a solid support. The proteins are useful for linking a bioactive molecule to a cell expressing a polypeptide designated as A, B, C or D or E, F, G, H or I. The bioactive molecule is a toxin, a radiolabel or an antibody. The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H, or I, or antibodies against them are useful for modulating a biological activity of a cell expressing a polypeptide designated as A, B, C or D or E, F, G, H, or I. The cell is killed. The proteins are useful for identifying agonists or antagonists, for the preparation of a medicament useful in the treatment of a condition which is responsive to the proteins, as molecular weight markers for protein electrophoresis purposes, and as therapeutic agents for treating sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis. Nucleic acids encoding the proteins are useful as hybridisation probes, in chromosome and gene mapping, in the generation of anti-sense RNA and DNA, for the preparation of the proteins, to generate transgenic or knockout animals which are useful in the development and screening of therapeutic useful reagents, for chromosome identification, and in gene therapy. The antibody is useful as a therapeutic agent, in a diagnostic assay and for affinity purification of the protein from recombinant cell culture natural sources. The present sequence encodes a novel secreted or transmembrane protein of the invention

SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1 49e-304 Length: 2372  
Score: 322.00 Matches: 322  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-079-111-1 (1-322) x ABS74380 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20  
Db 160 ATGGCCAGGTGCTTCAGCCCTGGTGTGTTCTTCTCATTCCATCTGGACACGAGGCTCTGT 219  
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
Db 220 GTCCAGAGCTCTTGGGTGAGAAGAGCTTTCATCCAGGTGTCAGCAATATGCGG 279  
QY 41 IleThrLeuValSerIleLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
Db 280 ATCACCTTGTGAGCAAAAAGGCGAACAGCAGCTGAATTCACAGAAGCTAAGAGGCC 339  
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
Db 340 TGTAGGCTGTGGACTAAAGTTGGCCGCGCAGGACCAAGTTGAAACAGCTTGAAGCT 399  
QY 81 SerPheGluThrCysSerIleGlyTrpValGlyAspGlyPheValValIleSerArgIle 100  
Db 400 AGCTTTGAACATTGCAGCTATGCTGGGTGGAGATGGATTCGTGTCATCTCTAGATT 459  
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120

Db 460 AGCCCAAAACCCCAAGTGGGGAAAAATGGGTGGGTCTCTGATTTGGAGGTTCCAGTG 519  
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
Db 520 AGCCGACAGTGTGGAGCCCTATTGTTACAACTCATCTGATACCTTGGACTTAACCTGTCATT 579  
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
Db 580 CCAGAAATATATCACCAACCAAGATCCCATATTCAAACTCAAACTGCAACACAAACAACA 639  
QY 161 GluPheIleValSerAspSerThrTrpSerValAlaSerProTyrSerThrIleProAla 180  
Db 640 GAATTTATTTGTCAGTGACAGTACTACTCGGTGGCATCCCTTACTCTACATACCTGCC 699  
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200  
Db 700 CCTACTACTACT 759  
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
Db 760 TGTGTACAGAAAGTTTTTATGAAACTAGCACCATGTCTACAGAACTGAACCATTTGTT 819  
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
Db 820 GAAATTAAGCAGCATTCAGATTCAGCTGCTGGTTGGAGGTGTCCTCCACGGCTCTG 879  
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260  
Db 880 CTAGTGTCT 939  
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnGlnGlnMetIleGluThr 280  
Db 940 AGGTATGTGAAGGCTTCTCTTTTCAACAACAAGATCAGCAAGAAATGATCGAAACC 999  
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluLysSerLysThr 300  
Db 1000 AAAGTAGTAAAGGAGGAGGAGGCCAATGATACACCTTAATGAGGAATCAAGAAACT 1059  
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
Db 1060 GATAAAACCCAGAGAGTCCAGAGTCCAGCAAACTACCGTGCATGCTCGTGAAGCT 1119  
QY 321 GluVal 322  
Db 1120 GAAGTT 1125  
RESULT 10  
ABL88087  
ID ABL88087 standard; cDNA; 2372 BP.  
XX ABL88087;  
AC ABL88087;  
XX  
XX 16-MAY-2002 (first entry)  
XX  
XX Human PRO263 cDNA sequence SEQ ID NO:31.  
DE  
XX Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;  
KW vulnary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
KW age-related macular degeneration; arterial restenosis; angina;  
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
KW wound healing; chromosome mapping; gene mapping; gene; ss.  
OS Homo sapiens.  
XX  
XX WO200200690-A2.  
XX  
XX 03-JAN-2002.  
PD  
XX 20-JUN-2001; 2001WO-US019692.  
PF





```

RESULT 11
ABL95576
ID ABL95576 standard; cDNA; 2372 BP.
XX
AC ABL95576;
XX
DT
XX
DE 19-JUL-2002 (first entry)
XX
DE Human angiogenesis related cDNA PRO263 SEQ ID NO: 31.
XX
KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
XX atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
XX cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;
XX antiarteriosclerotic; gene; ss.
XX
OS Homo sapiens.
XX
XX WO200208284-A2.
XX
PD 31-JAN-2002.
XX
XX
PF 09-JUL-2001; 2001WO-US021735.
XX
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
XX
(GETH ) GENENTECH INC.
PA (BAKE ) BAKER K P.
PA (FERR ) FERRARA N.
PA (GERB ) GERBER H.
PA (GERR ) GERRITSEN M E.
PA (GODO ) GODDARD A.
PA (GODO ) GODDARD A.
PA (GODI ) GODOWSKI P J.
PA (GURN ) GURNEY A L.
PA (HILL ) HILLAN K J.
PA (MARS ) MARSTERS S A.
PA (PANU ) PAN J.
PA (PAON ) PAONI N F.
PA (STEP ) STEPHAN J F.
PA (WATA ) WATANABE C K.

```

```

PA (WILL ) WILLIAMS P M.
PA (WOOD ) WOOD W I.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
XX Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2002-171999/22.
DR P-PSDB; ABB95438.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX infarction), endothelial or angiogenic disorders in a mammal.
XX
PS Claim 1; Fig 31; 567pp; English.
XX
XX The present invention provides the protein and coding sequences of human
XX PRO proteins. These are useful for treating or diagnosing a
XX cardiovascular, endothelial or angiogenic disorder, including cardiac
XX hypertrophy, trauma, cancer, age-related macular degeneration,
XX atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
XX angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
XX angiogenesis (such as breast carcinoma and liver carcinoma) and wound
XX healing. The present sequence is a coding sequence of the invention
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.49e-304 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-079-111-1 (1-322) x ABL95576 (1-2372)
QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
DB 160 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCAGTTCATCTGCACCCAGGCTCTTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
DB 220 GTCCAAAGGCTCTTTCGCTGCAGAAAGCTTTCATCCAGGTGTCATGCAGAAATTATGGG 279
QY 41 IleThrLeuValSerLysLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
DB 280 ATCACCCCTTGTGAGCAAAAAGCGCAACCCAGCAGCTGAATTTCCACAGAGCTAAGGAGGC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
DB 340 TGTAGGCTGTGGGACTAAGTTTGGCCGCAAGGCAAGATTGAAACAGCCCTGAAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
DB 400 AGCTTTGAAACTTGAGCTATGCGCTGGGTGGAGATGGATTGCTGGTCATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
DB 460 AGCCCAAAACCCCAAGTGGGAAAAATGGGTGGGTGCTCTGATTGGGAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
DB 520 AGCCGACAGATTTCAGCCCTATTGTTACAACTCATCTGATCTGGACTTAACCTCGGCATT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
DB 580 CCAGAAATTAATCACCACCAAGATCCCATATTCAACTCAAACTCAAACTCAACAAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
DB 640 GAATTTATTGTCAGTGACAGTACTACTTCGGTGGCATCCCTTACTCTTACTACATACTGCC 699

```



DR WPI; 2003-328338/31.  
DR P-PSDB; ABU71625.  
XX  
PT Isolated nucleic acid useful for e.g., treating pathological disorders  
PT encodes a secreted or transmembrane protein.  
XX  
PS Claim 2; Fig 73; 473pp; English.  
XX  
CC The invention relates to human PRO polypeptides (secreted or  
CC transmembrane polypeptides) and the polynucleotides encoding them. The  
CC PRO polypeptides and polynucleotides can be used in treating pathological  
CC disorders and tumours, in therapeutic treatment of cardiac insufficiency  
CC disorders and in therapeutic treatment of disorders involving protein  
CC secretion by the pancreas, including diabetes. They can also be used in  
CC treating disorders associated with the preservation and maintenance of  
CC gastrointestinal mucosa and the repair of acute and chronic mucosal  
CC lesions, and skin diseases associated with abnormal keratinocyte  
CC differentiation (e.g., psoriasis, epithelial cancers such as lung  
CC squamous cell carcinoma, epidermoid carcinoma of the vulva and gliomas).  
CC The sequences can be used as molecular markers for protein  
CC electrophoresis purposes and can be utilised in protein-protein binding  
CC assays, biochemical screening assays, immunoassays and cell-based assays.  
CC This sequence represents a human PRO polynucleotide of the invention  
XX  
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1.49e-304 Length: 2372  
Score: 322.00 Matches: 322  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 7 Gaps: 0

US-10-079-111-1 (1-322) x ACA59060 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20  
DB 160 ATGGCCAGGTGCTTCAGCTGTGTGTCTTCATCTTCATCTGCACGAGGTCCTGT 219  
QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40  
DB 220 GTCCAGGCTCTTGGTGCAGAGAGCTTTCATCCAGTGTGCATGCAGATTATGGG 279  
QY 41 IleThrLeuValSerIlyslsAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
DB 280 ATCACCCCTGTGAGCAAAAGGCGAACACAGCAGCTGAATTCACAGAACTTAAGAGGCC 339  
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
DB 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAACAGCCTTGAAGCT 399  
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100  
DB 400 AGCTTTGAACCTTGACGATATGGCTGGGTGGATGGATTGGTGTATCTCTAGGATT 459  
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
DB 460 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCTGATTTGGAAAGGTTCAGTG 519  
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
DB 520 AGCCGACATTTGACGCTTATTGTTTCAACTCATCTGATCTTGGACTTAACCTGTCGATT 579  
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
DB 580 CCAGAAATTTATCACCAAGATCCCATATTCACACTCAAACTGCACACAAACAACA 639  
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
DB 640 GAATTTATTGTGAGTGACAGTACCTACTCGTGGCATCCCTTACTCTACAAATACCTGCC 699  
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLeuIle 200

DB 700 CCTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAATGATT 759  
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
DB 760 TGTGTCACAGAAGTTTTTATGGAACCTAGCACCATTGTCTACAGAAACTGAACCAITTTGTT 819  
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
DB 820 GAAATAAAGCAGCATTCAGAATGAAGCTGTGGGTTTGGAGGTGTCCCCACGGCTCTG 879  
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
DB 880 CTAGTGCTGTCTCTCTCTCTTCTTGGTGTGCGAGCTGTCTTGGAITTTGCTATGTCAAA 939  
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
DB 940 AGGTATGTGAAGCCCTTCCCTTTTACAAACAAGATCAGCAGAGAAATGATCGAAACC 999  
QY 281 LysValValLysGluGluLysAlaAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
DB 1000 AAAGTAGTAAAGGAGGAGAGGCCCAATGATAGCAACCTTAATGAGGAATCAAAAGAAACT 1059  
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
DB 1060 GATAAAAACCCAGAAGAGTCCAGAGTCCAGCAAAACTACCGTGGATGCTCGAAGCT 1119  
QY 321 GluVal 322  
DB 1120 GAAGTT 1125  
RESULT 13  
ACA58457  
ID ACA58457 standard; cDNA; 2372 BP.  
XX  
AC ACA58457;  
XX  
DT 10-JUN-2003 (first entry)  
XX  
DE cDNA encoding human PRO polypeptide #36.  
XX  
KW Human; secreted and transmembrane protein; PRO polypeptide; cancer;  
KW Alzheimer's disease; ischaemia; cytostatic; nootropic; vasotropic;  
KW neuroprotective; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN US2002192659-A1.  
XX  
PD 19-DEC-2002.  
XX  
PF 10-JUL-2001; 2001US-00902853.  
XX  
PR 17-SEP-1997; 97US-0059113P.  
PR 17-SEP-1997; 97US-0059115P.  
PR 17-SEP-1997; 97US-0059117P.  
PR 17-SEP-1997; 97US-0059119P.  
PR 17-SEP-1997; 97US-0059121P.  
PR 17-SEP-1997; 97US-0059122P.  
PR 17-SEP-1997; 97US-0059184P.  
PR 18-SEP-1997; 97US-0059263P.  
PR 18-SEP-1997; 97US-0059266P.  
PR 15-OCT-1997; 97US-0062125P.  
PR 17-OCT-1997; 97US-0062285P.  
PR 21-OCT-1997; 97US-0062287P.  
PR 21-OCT-1997; 97US-0063486P.  
PR 24-OCT-1997; 97US-0062814P.  
PR 24-OCT-1997; 97US-0062816P.  
PR 24-OCT-1997; 97US-0063045P.  
PR 24-OCT-1997; 97US-0063120P.  
PR 24-OCT-1997; 97US-0063121P.  
PR 24-OCT-1997; 97US-0063127P.  
PR 24-OCT-1997; 97US-0063128P.

27-OCT-1997; 97US-0063327P.  
 27-OCT-1997; 97US-0063329P.  
 28-OCT-1997; 97US-0063341P.  
 28-OCT-1997; 97US-0063342P.  
 28-OCT-1997; 97US-0063344P.  
 28-OCT-1997; 97US-0063349P.  
 28-OCT-1997; 97US-0063350P.  
 28-OCT-1997; 97US-0063356P.  
 29-OCT-1997; 97US-0063343P.  
 29-OCT-1997; 97US-0063370P.  
 29-OCT-1997; 97US-0063372P.  
 29-OCT-1997; 97US-0063373P.  
 29-OCT-1997; 97US-0063378P.  
 29-OCT-1997; 97US-0064215P.  
 31-OCT-1997; 97US-0063870P.  
 31-OCT-1997; 97US-0064103P.  
 03-NOV-1997; 97US-0064248P.  
 07-NOV-1997; 97US-0064809P.  
 12-NOV-1997; 97US-0065186P.  
 17-NOV-1997; 97US-0065846P.  
 18-NOV-1997; 97US-0065693P.  
 21-NOV-1997; 97US-0066120P.  
 21-NOV-1997; 97US-0066364P.  
 24-NOV-1997; 97US-0066453P.  
 24-NOV-1997; 97US-0066466P.  
 24-NOV-1997; 97US-0066511P.  
 24-NOV-1997; 97US-0066770P.  
 24-NOV-1997; 97US-0066772P.  
 10-SEP-1998; 98WO-US018824.  
 14-SEP-1998; 98WO-US019177.  
 16-SEP-1998; 98WO-US019330.  
 17-SEP-1998; 98WO-US019437.  
 01-DEC-1998; 98WO-US025108.  
 08-SEP-1999; 99WO-US020594.  
 13-SEP-1999; 99WO-US020944.  
 15-SEP-1999; 99WO-US021090.  
 15-SEP-1999; 99WO-US021547.  
 05-OCT-1999; 99WO-US023089.  
 30-NOV-1999; 99WO-US028214.  
 30-NOV-1999; 99WO-US028313.  
 01-DEC-1999; 99WO-US028301.  
 02-DEC-1999; 99WO-US028564.  
 02-DEC-1999; 99WO-US028565.  
 16-DEC-1999; 99WO-US030095.  
 20-DEC-1999; 99WO-US030911.  
 20-DEC-1999; 99WO-US030999.  
 05-JAN-2000; 2000WO-US000219.  
 11-FEB-2000; 2000WO-US003565.  
 22-FEB-2000; 2000WO-US004414.  
 24-FEB-2000; 2000WO-US005004.  
 02-MAR-2000; 2000WO-US005841.  
 20-MAR-2000; 2000WO-US007377.  
 30-MAR-2000; 2000WO-US008439.  
 22-MAY-2000; 2000WO-US014042.  
 02-JUN-2000; 2000WO-US015264.  
 28-JUL-2000; 2000WO-US020710.  
 24-AUG-2000; 2000WO-US023328.  
 18-SEP-2000; 2000US-00665350.  
 (GETH ) GENENTECH INC.  
 Ashkenazi A, Botstein D, Desnovers L, Eaton DL, Ferrara N;  
 Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;  
 Godowski PJ, Grimaldi JC, Gurney AL, Hillian KJ, KJavin IJ;  
 Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;  
 Williams PM, Wood WI;  
 WPI; 2003-361832/34.  
 P-PSDB; ABU71480.  
 New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or  
 PRO1868, useful in molecular biology, chromosome and gene mapping, in

PT generating antisense RNA and DNA, and in gene therapy.  
 XX Claim 2; Fig 73; 474pp; English.  
 XX The present invention relates to the isolation of novel human secreted  
 CC and transmembrane proteins (PRO polypeptides), and the polynucleotide  
 CC sequences encoding them. The polynucleotide sequences are useful in  
 CC molecular biology, as hybridisation probes, in chromosome and gene  
 CC mapping, in generating antisense RNA and DNA, and in gene therapy. The  
 CC polynucleotide sequences may also be used in preparing PRO polypeptides  
 CC by recombinant techniques, and in generating either transgenic animals or  
 CC knock-out animals which, in turn, are useful in the development and  
 CC screening of therapeutically useful reagents. The PRO polypeptides or  
 CC their antibodies are useful in preparing a medicament for treating a  
 CC condition responsive to the polypeptide or antibody, such as cancer,  
 CC Alzheimer's disease or ischaemia, and in various diagnostic assays. The  
 CC present sequence encodes a human PRO polypeptide of the invention  
 XX  
 SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;  
  
 Alignment Scores:  
 Pred. No.: 1.49e-304 Length: 2372  
 Score: 322.00 Matches: 322  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 7 Gaps: 0  
  
 US-10-079-111-1 (1-322) x ACA58457 (1-2372)  
  
 QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20  
 Db 160 ATGGCCAGGTGCTTCAGCTGGTGTCTTCACCTTCATCTGGACCAAGGCTCCG 219  
 QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
 Db 220 GTCCAAGGCTCTTTGGTGCAGAGAGCTTCCATCCAGTGTGTCAGAGATTATGGG 279  
 QY 41 IleThrLeuValSerIlyslsAlaAsnGlnGlnLeuAsnPhetThrGluAlaLysGluAla 60  
 Db 280 ATCACCCTTGAGCAAAAGCGAAACCCAGCAGCTGAATTTCCACAGAGCTAAGGAGCC 339  
 QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
 Db 340 TGTAGCTGTGGAGTAAAGTTTGGCCGCAAGGACCAAGTTGAACACAGCTTGAAGCT 399  
 QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100  
 Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGTGGAGATGGATTCTGTCATCTAGGATT 459  
 QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
 Db 460 AGCCCAAAACCCCAAGTGGGAAAAATGGGTGGGTGGTCTCTGATTGGAAGGTTCCAGTG 519  
 QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
 Db 520 AGCCCAAGTGTGACGCTATTTGTACCACTCATCTGTACTTGGACTTAACCTCTGCATT 579  
 QY 141 ProGluIlelleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
 Db 580 CCAGAAATTTATCACCAACCAAGATCCCATATTTCAACACTCAAACTGCAACACAAACA 639  
 QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
 Db 640 GAAATTTATGTGACGACAGTACCTACTCGGGTGGCATCCCTTACTCTACAAATCTCGCC 699  
 QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeu 200  
 Db 700 CCTACTACTACTCTCTCTCTCTCCAGCTTCCACTTCTATTCCACGCGAGAAAAAATGATT 759  
 QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
 Db 760 TGTGTACAGAAAGTTTTTTATGAAACTAGCACCATTGTCTACAGAAACTGAACCATTTGTT 819



CC PRO protein extracellular domain. Also included are a vector comprising  
 CC the PRO nucleic acid, a host cell comprising the vector, producing a PRO  
 CC polypeptide (by culturing the host cell for the expression of the PRO  
 CC polypeptide, and recovering the PRO polypeptide from the cell culture),  
 CC an isolated PRO polypeptide (having at least 80% sequence identity to:  
 CC a) an amino acid sequence selected from the 61 PRO proteins; (b) an amino  
 CC acid sequence encoded by a nucleic acid molecule deposited with an ATCC  
 CC number (detailed in the specification); or (c) an extracellular domain of  
 CC a PRO polypeptide or to a PRO polypeptide lacking its associated signal  
 CC peptide), a chimaeric molecule comprising a PRO polypeptide of fused to a  
 CC heterologous amino acid sequence, an anti-PRO antibody, detecting a  
 CC PRO245 or PRO1868 in a sample suspected of containing the polypeptide,  
 CC linking a bioactive molecule to a cell expressing a PRO245 or PRO1868 and  
 CC modulating at least one biological activity of a cell expressing a PRO245  
 CC or PRO1868. Nucleic acids which encode PRO can be used to generate either  
 CC transgenic animals or knock-out animals which may be used in the  
 CC development and screening of therapeutically useful reagents. The nucleic  
 CC acids may also be used in gene therapy. In chromosome identification, as  
 CC chromosome markers, or in generating probes. The PRO polypeptides are  
 CC useful as molecular markers for protein electrophoresis, and the isolated  
 CC nucleic acids may be used for recombinantly expressing those markers. The  
 CC PRO polypeptides and nucleic acids may also be used in tissue typing.  
 CC Anti-PRO antibodies are useful in diagnostic assays for PRO, and in  
 CC affinity purification of PRO from recombinant cell culture or natural  
 CC sources. The present sequence encodes a PRO protein

XX Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.49e-304 Length: 2372  
 Score: 322.00 Matches: 322  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 7 Gaps: 0

US-10-079-111-1 (1-322) x ACA60164 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20  
 Db 160 ATGGCCAGGTGCTTACGCTGGTGTGCTTCTCCTCCATCTGGACACGAGGCTCCG 219  
 QY 21 ValGlnGlySerLeuArgAlaGluLeuLeuSerIleGlnValSerCysArgIleMetGly 40  
 Db 220 GTCCAAAGGCTCTTCCGTGCAGAGAGCTTCCATCCAGGTGTGATGACAGATTATGGGG 279  
 QY 41 IleThrLeuValSerIleValAsnGlnGlnLeuAsnPheThrGluAlaValGluAla 60  
 Db 280 ATCAACCTTGTGAGCAAAAGCGAACCCAGCAGCTGAATTTCCACAGAGCTAAGGAGGCC 339  
 QY 61 CysArgLeuLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
 Db 340 TGATAGCTGCTGGGACTAAGTTTGGCCGCGCAGAGCCAAAGTTGAACACGCTTGAAGCT 399  
 QY 81 SerPheGluThrCysSerTyrglyTrpValGlyAspGlyPheValValIleSerArgIle 100  
 Db 400 AGCTTTGAAACTTGCAGCTATGCTGGTGTGGAGATGATTCGTGTCATCTCTAGGATT 459  
 QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
 Db 460 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGTGTCTGATTTGGAAGGTTCCAGTG 519  
 QY 121 SerArgGlnPheAlaAlaTyrcysTyrcysAsnSerSerAspThrTrpThrAsnSerCysIle 140  
 Db 520 AGCCGACAGTTTGCAGCTATTTGTTACAACTCATCTGATCTTGGACTTAACCTCTGTCATT 579  
 QY 141 ProGluIleIleThrThrIleAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
 Db 580 CCAGAAATTTATCACCACCAAGATCCCATATTTCAACACTCAAACTGCAACACAAACA 639  
 QY 161 GluPheIleValSerAspSerThrTyrcysSerValAlaSerProTyrcysThrIleProAla 180  
 Db 640 GAATTTATTTGTCAGTGACAGTACCTACTCTGGTGGCATCCCCCTTACTTACAAATACCTGCC 699

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200  
 Db 700 CCTACTACTACT 759  
 QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
 Db 760 TGTGTACAGAGAGTTTATGGAATACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819  
 QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240  
 Db 820 GAAATAAAGCAGCATTCAGAAATGAAGCTGTCTGGGTTTGGAGGTCTCCCCACGGCTCTG 879  
 QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLysCysTyrcysValLys 260  
 Db 880 CTAGTGTCT 939  
 QY 261 ArgTyrcysValValPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
 Db 940 AGGTATGTGAAGGCT 999  
 QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysThr 300  
 Db 1000 AAAGTAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1059  
 QY 301 AspLysAsnProGluLysSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
 Db 1060 GATAAAACCCAGAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGT 1119  
 QY 321 GluVal 322  
 Db 1120 GAAGTT 1125  
 RESULT 15  
 ACD07564  
 ID ACD07564 standard; cDNA; 2372 BP.  
 XX  
 AC ACD07564;  
 DT 07-AUG-2003 (first entry)  
 XX  
 DE Novel human secreted and transmembrane protein PRO263 cDNA.  
 KW Human; secreted and transmembrane protein; PRO; pharmaceutical;  
 KW diagnostic; biosensor; bioreactor; Parkinson's disease;  
 KW Alzheimer's disease; inflammation; nephritis; wound healing;  
 KW nerve repair; collateral blood vessel formation; cancer;  
 KW colorectal cancer; haemorrhage; rheumatoid arthritis; diabetes;  
 KW cirrhosis; fibrosis; restenosis; dermal fibrotic condition; keloid;  
 KW scarring; ischaemia; stroke; hypertension; heart attack; atherosclerosis;  
 KW infertility; gene therapy; gene; ss.  
 XX Homo sapiens.  
 OS  
 XX  
 PN US2002197671-A1.  
 XX  
 PD 26-DEC-2002.  
 XX  
 PF 17-JUL-2001; 2001US-00907824.  
 XX  
 PR 17-SEP-1997; 97US-0059113P.  
 PR 17-SEP-1997; 97US-0059115P.  
 PR 17-SEP-1997; 97US-0059117P.  
 PR 17-SEP-1997; 97US-0059119P.  
 PR 17-SEP-1997; 97US-0059121P.  
 PR 17-SEP-1997; 97US-0059122P.  
 PR 17-SEP-1997; 97US-0059184P.  
 PR 18-SEP-1997; 97US-0059263P.  
 PR 18-SEP-1997; 97US-0059266P.  
 PR 15-OCT-1997; 97US-0062125P.  
 PR 17-OCT-1997; 97US-0062285P.  
 PR 17-OCT-1997; 97US-0062287P.  
 PR 21-OCT-1997; 97US-0063486P.

PR	24-OCT-1997;	97US-0062814P.	PI	Williams PM, Wood WI;
PR	24-OCT-1997;	97US-0062816P.	XX	
PR	24-OCT-1997;	97US-0063045P.	DR	WPI; 2003-370793/35.
PR	24-OCT-1997;	97US-0063120P.	P-PSDB; ABO01809.	
PR	24-OCT-1997;	97US-0063121P.	XX	
PR	24-OCT-1997;	97US-0063121P.	XX	
PR	24-OCT-1997;	97US-0063127P.	PT	New genes and secreted and transmembrane polypeptides (e.g. PRO245 or
PR	24-OCT-1997;	97US-0063128P.	PT	PRO335), useful for treating or diagnosing e.g. Alzheimer's disease,
PR	27-OCT-1997;	97US-0063327P.	PT	cancers, hemorrhage, rheumatoid arthritis, diabetes, cirrhosis, ischemia
PR	27-OCT-1997;	97US-0063329P.	PT	or strokes.
PR	28-OCT-1997;	97US-0063541P.	XX	
PR	28-OCT-1997;	97US-0063542P.	PS	Claim 2; Fig 73; 482pp; English.
PR	28-OCT-1997;	97US-0063544P.	XX	
PR	28-OCT-1997;	97US-0063549P.	XX	
PR	28-OCT-1997;	97US-0063550P.	CC	The invention describes a new isolated nucleic acid molecule comprising
PR	28-OCT-1997;	97US-0063564P.	CC	the full length coding sequence of the DNA deposited with the American
PR	28-OCT-1997;	97US-0063435P.	CC	Type Culture Collection (e.g. ATCC Deposit No. 209258), or a sequence
PR	29-OCT-1997;	97US-0063704P.	CC	with at least 80% identity to a DNA encoding a PRO polypeptide comprising
PR	29-OCT-1997;	97US-0063732P.	CC	any of 61 sequences having 164-1119 amino acids fully defined in the
PR	29-OCT-1997;	97US-0063732P.	CC	specification. The PRO polypeptides or polynucleotides are useful as
PR	29-OCT-1997;	97US-0063734P.	CC	pharmaceuticals, diagnostics, biosensors or bioreactors. These are
PR	29-OCT-1997;	97US-0063735P.	CC	particularly useful for detecting or treating e.g. Parkinson's disease,
PR	29-OCT-1997;	97US-0063738P.	CC	Alzheimer's disease, inflammations, nephritis, wound healing, nerve
PR	29-OCT-1997;	97US-0064215P.	CC	repair, collateral blood vessel formation, cancers (e.g. colorectal
PR	31-OCT-1997;	97US-0063870P.	CC	cancer), haemorrhage (or reduce risk for haemorrhage), rheumatoid
PR	31-OCT-1997;	97US-0064103P.	CC	arthritis, diabetes, cirrhosis of the liver, fibrosis of the lungs,
PR	03-NOV-1997;	97US-0064248P.	CC	restenosis, dermal fibrotic conditions (e.g. keloids or scarring),
PR	07-NOV-1997;	97US-0064809P.	CC	ischaemia, strokes, hypertension, heart attacks, atherosclerosis, or
PR	12-NOV-1997;	97US-0065186P.	CC	infertility in mammals (e.g. humans, dogs, cats, cattle, horses, sheep,
PR	17-NOV-1997;	97US-0065846P.	CC	pigs, goats, or rabbits) The PRO polypeptides are useful as targets for
PR	18-NOV-1997;	97US-0065693P.	CC	therapeutic intervention in these diseases, and diagnostic determination
PR	21-NOV-1997;	97US-0066120P.	CC	of the presence of these diseases. The PRO polypeptides are also useful
PR	21-NOV-1997;	97US-0066364P.	CC	as molecular weight markers, or for chromosome identification. The PRO
PR	24-NOV-1997;	97US-0066453P.	CC	genes are useful as hybridisation probes, or for screening libraries of
PR	24-NOV-1997;	97US-0066466P.	CC	human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene
PR	24-NOV-1997;	97US-0066511P.	CC	therapy, particularly for replacing a defective gene. This sequence
PR	24-NOV-1997;	97US-0066770P.	CC	encodes a novel human secreted and transmembrane PRO polypeptide
PR	24-NOV-1997;	97US-0066772P.	XX	
PR	10-SEP-1998;	98WO-US018824.	SQ	Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;
PR	14-SEP-1998;	98WO-US019177.		
PR	16-SEP-1998;	98WO-US019330.		
PR	17-SEP-1998;	98WO-US019437.		
PR	01-DEC-1998;	98WO-US025108.		
PR	08-SEP-1999;	98WO-US020594.		
PR	13-SEP-1999;	99WO-US020944.		
PR	15-SEP-1999;	99WO-US021090.		
PR	15-SEP-1999;	99WO-US021547.		
PR	05-OCT-1999;	99WO-US023089.		
PR	29-NOV-1999;	99WO-US028214.		
PR	30-NOV-1999;	99WO-US028313.		
PR	01-DEC-1999;	99WO-US028301.		
PR	02-DEC-1999;	99WO-US028564.		
PR	16-DEC-1999;	99WO-US028565.		
PR	20-DEC-1999;	99WO-US030095.		
PR	20-DEC-1999;	99WO-US030911.		
PR	20-DEC-1999;	99WO-US030999.		
PR	05-JAN-2000;	2000WO-US000219.		
PR	11-FEB-2000;	2000WO-US003565.		
PR	22-FEB-2000;	2000WO-US004414.		
PR	24-FEB-2000;	2000WO-US005004.		
PR	02-MAR-2000;	2000WO-US005841.		
PR	20-MAR-2000;	2000WO-US007377.		
PR	30-MAR-2000;	2000WO-US008439.		
PR	22-MAY-2000;	2000WO-US014042.		
PR	02-JUN-2000;	2000WO-US015264.		
PR	28-JUL-2000;	2000WO-US020710.		
PR	14-AUG-2000;	2000WO-US023328.		
PR	18-SEP-2000;	2000US-00665350.		
XX				
PA	(GETH ) GENENTECH INC.			
XX				
PI	Ashkenazi A, Desnoyers L, Eaton DL, Ferrara N;			
PI	Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;			
PI	Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Klijn JI;			
PI	Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;			

Db 520 AGCCGACAGTTTGCAGCTATTGTTACAACTCATCTGATCTTGGACTAATCGTGCAAT 579  
 QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
 Db 580 CCAGAAATTTATCACCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA 639  
 QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
 Db 640 GAATTTATGTCAGTGACAGTACTCTCGTGGCATCCCTTACTCTCAATACCTGACC 699  
 QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200  
 Db 700 CCTACTACTACTCTCTCTCTCCAGCTTCCACTTCTTATCCACGGAGAAAATTTGATT 759  
 QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
 Db 760 TGTGTACAGAAAGTTTTATGGAACTTAGCACCATGCTACAGAAACTGAACCATTTGTT 819  
 QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
 Db 820 GAAAATAAACACAGCATTTCAAGATGAAGCTGCTGGGTTGGAGGTGTCCCCACGGCTCTG 879  
 QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
 Db 880 CTAGTGTCTCTCTCTCTCTCTTGTGTCTGTCAGCTGGTCTTGGAATTTTGCTATGCAAA 939  
 QY 261 AtgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280  
 Db 940 AGGTATGTGAGGCCCTTCCCTTTTACAAACAAAGATCAGCAGAGGAATGATCGAAACC 999  
 QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
 Db 1000 AAAGTAGTAAAGGAGGAGGAGGCAATGATAGCAACCTTAATGAGGATCAAGAAACT 1059  
 QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
 Db 1060 GATAAAACCCAGAGAGTCCAGAGTCCAAAGTCCAAAGCAAAACTACCGTGGATGGCAAGCT 1119  
 QY 321 GluVal 322  
 Db 1120 GAAGTT 1125

## RESULT 16

ID ACA91166 standard; cDNA; 2372 BP.  
 AC ACA91166;

XX 11-JUL-2003 (first entry)  
 XX Novel human secreted and transmembrane protein PRO263 cDNA.  
 DE Human; secreted and transmembrane protein; PRO; antibody therapy;  
 KW Pharmaceutical; diagnostic; biosensor; bioreactor; gene; ss.  
 XX Homo sapiens.  
 OS US2003018173-Al.  
 PN 23-JAN-2003.  
 PD 01-MAY-2002; 2002US-00063515.  
 PF 06-DEC-2001; 2001US-00006867.  
 PR (GETH ) GENENTECH INC.  
 XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;  
 XX WPI: 2003-401702/38.  
 DR P-PSDB; AB090878.

XX New antibody useful for identifying PRO polypeptides, for affinity  
 PT purification of PRO polypeptides, and for preparing a medicament for  
 PT diagnosing or treating conditions responsive to the antibody or PRO  
 XX polypeptide.  
 PS Disclosure; Fig 5; 345pp; English.  
 XX The invention describes an antibody that specifically binds to a PRO  
 CC polypeptide having a fully defined amino acid sequence given in the  
 CC specification. The antibody is useful in identifying PRO polypeptides  
 CC useful for various industrial applications, including pharmaceuticals,  
 CC diagnostics, biosensors and bioreactors. The antibody is also used for  
 CC affinity purification of PRO polypeptides from recombinant cell culture  
 CC or natural sources. The antibody, PRO polypeptide, or its agonists or  
 CC antagonists, may be used for preparing a medicament for diagnosing or  
 CC treating a condition responsive to the antibody, PRO polypeptide, or its  
 CC agonists or antagonists. This sequence encodes a novel human secreted and  
 CC transmembrane PRO polypeptide  
 XX Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1,49e-304 Length: 2372  
 Score: 322.00 Matches: 322  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 7 Gaps: 0  
 US-10-079-111-1 (1-322) x ACA91166 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20  
 Db 160 ATGGCCAGGTGCTTCAGCCTGGTGTGTTCTTCTCATTCTCCATCTGGACACAGGCTCTCG 219  
 QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
 Db 220 GTCCAAAGGCTCTTTGGTGCAGAAAGCTTTCCATCCAGGTGTCTGCAAGAAATATGGGG 279  
 QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
 Db 280 ATCACCCTTGTGAGCAAAAGGCAACACAGCAGCTGAATTTACAGAACTAAGGAGGCC 339  
 QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
 Db 340 TGTAGGCTGTGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 399  
 QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100  
 Db 400 AGCTTTGAAACTTGACGCTATGCTGGTTGGATGGATGCTGTCATCTCTAGATT 459  
 QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
 Db 460 AGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGTGTCTCTGATTGGAAAGTTCCAGTG 519  
 QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
 Db 520 AGCCGACAGTTTGCAGCCTATTGTTTACAACCTCATCTGATCTGGAACCTAATCGTCATT 579  
 QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
 Db 580 CCAGAAATTTATCACCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA 639  
 QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
 Db 640 GAATTTATGTCAGTGACAGTACTCTCGTGGCATCCCTTACTCTCAATACCTGACC 699  
 QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200  
 Db 700 CCTACTACTCTCTCTCTCTCCAGCTTCCACTTCTTATTCACGGAGAAAAATTTGATT 759  
 QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220



```
Db 760 TGTGTACAGAGTTTATTGAACTAGCACCATTCTACAGAACTGAACCAATTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db 820 GAAATATAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGAGGTGTCCACGGCTCTG 879
QY 241 IeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTCTTGGCTCTCTCTCTTTGTTGCTGCAGCTGGTCTTGATTTGCTATGTCAAA 939
QY 261 ArgTyrValLysAlaAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGCCTTCCTTTTCAACACAGAAATCAGCAGAGAAATGATCGAAAC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysThr 300
Db 1000 AAAGTAGTAAAGCAGAGAGGCAATGATAGCAACCTAATGAGGAATCAAGAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCCCAAGAGTCCAGAGTCCAAAGCAAACTACCGTGCATGCCCTGGAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 17
ACD81543
ID ACD81543 standard; cDNA; 2372 BP.
AC ACD81543;
XX
XX
DT 18-SEP-2003 (first entry)
XX
DE Human cDNA encoding secreted/transmembrane protein PRO263.
XX
KW Human; ss; gene; secreted/transmembrane protein; PRO; tumour; cancer;
KW Cytostatic.
XX
OS Homo sapiens.
XX
PN US2003009013-A1.
XX
PD 09-JAN-2003.
XX
PF 01-MAY-2002; 2002US-00063519.
XX
PR 30-DEC-1998; 98KR-00062142.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 22-MAY-2000; 2000WO-US007532.
PR 02-JUN-2000; 2000WO-US014042.
PR 22-AUG-2000; 2000US-00615264.
PR 24-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
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PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
XX (GETH ) GENENTECH INC.
PA
XX
XX Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
XX WPI: 2003-447384/42.
DR P-PSDB; ABO33937.
XX
XX
XX New isolated antibody specifically binding a PRO polypeptide, useful for
PT the preparation of a medicament for treating disorders with the aberrant
PT expression or activity of the PRO polypeptide, such as tumor conditions
PT and cancer.
XX
XX
XX Disclosure; Fig 5; 223pp; English.
PS
XX
XX The invention relates to an antibody that binds to a secreted or
CC transmembrane protein designated PRO1446 appearing as ABO33941. The
CC protein is one of 84 PRO polypeptides which (along with their encoding
CC nucleic acids) are disclosed in the specification. The methods and
CC compositions of the present invention are useful for the preparation of a
CC medicament for the treatment of disorders associated with the aberrant
CC expression or activity of the PRO polypeptide, such as tumour conditions
CC and cancer. They can also be used to generate transgenic or knockout
CC animals useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides and encoding nucleic acids can be used as
CC molecular weight markers for protein electrophoresis, chromosome
CC identification and tissue typing. The antibodies may be used in various
CC diagnostic, competitive binding and/or immunoprecipitation assays. The
CC present sequence encodes a PRO polypeptide
XX
XX Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1,49e-304 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-079-111-1 (1-322) x ACD81543 (1-2372)
QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGGCCAGGTGCTTCCAGCTGTGTGTCTTCTCCTTCATCCAGTGTGTCAGAGTCCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAGGGCTCTTGGTGTCAAGAGCTTTCATCCAGTGTGTCAGAGATTTATGGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCCCTTGTGAGCAAAAGGCGAACCAGCAGCTGAAATTCACAGAGCTAAGGAGGC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTCTGGGACTAAGTTGGCCGCGCAAGGACCAAGTGTGAACACACCCCTGAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
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Db 400 AGCTTTGAAACTTGCAGCTATGCTGGTGGAGATGATTCGTGGTCATCTCTAGGATT 459  
 QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuLeuLeuLeuLeuLeuLeu 120  
 Db 460 AGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGTGTCTGTGATTTTGGAAAGTTCCAGTG 519  
 QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
 Db 520 AGCGCAGTTTGCAGCTATTGTTCAACTCATCTGATACCTGGACAACTCTGATGATT 579  
 QY 141 ProGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 160  
 Db 580 CCAGAAATTATCACCACCAAGATCCCATATTCAACACTCAACTGCAACACAAACACACA 639  
 QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
 Db 640 GAATTTTATTGTCAGTGACAGTACTACTCGTGGCATCCCTTACTCTACAACTACCTGCC 699  
 QY 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuLeu 200  
 Db 700 CCTACTACTACTCTCTCTCTCCAGCTTCCACTTCTATTCACGGGAAAAAATGATT 759  
 QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
 Db 760 TGTGTACAGAACTTTTATGGAACTAGCACCATGTCTACAGAACTGAACCATTTGTT 819  
 QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
 Db 820 GAAATTAAGACAGCATTCAGAAATGAAGCTGTGGGTGTGGAGGTGTCCACGGCTCTG 879  
 QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
 Db 880 CTAGTGTCT 939  
 QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
 Db 940 AGGTATGTGAAGCCCTTCCCTTTTACAAACAGAAATCAGCAGAAAGAAATGATCGAAACC 999  
 QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
 Db 1000 AAGTAGTAGGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1059  
 QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
 Db 1060 GATAAAACCCAGAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGT 1119  
 QY 321 GluVal 322  
 Db 1120 GAAGTT 1125  
 RESULT 18  
 ID ACA60365 standard; cDNA; 2372 BP.  
 AC ACA60365;  
 AC ACA60365;  
 DT 11-JUN-2003 (first entry)  
 DE Novel human secreted and transmembrane protein PRO263 cDNA.  
 KW Human; secreted and transmembrane polypeptide; gene;  
 KW ss. chromosome mapping; gene mapping; transgenic animal; knockout animal;  
 KW therapeutic agent screening; mapping; chromosome identification; tissue typing;  
 KW gene therapy.  
 OS Homo sapiens.  
 XX  
 XX US2003018183-A1.  
 XX  
 XX 23-JAN-2003.  
 XX  
 XX 01-MAY-2002; 2002US-00063512.  
 PF  
 XX

PR 06-DEC-2001; 2001US-00006867.  
 XX (GETH ) GENENTECH INC.  
 PA Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
 XX Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;  
 PI WPI; 2003-330984/31.  
 XX P-PSDB; ABU71954.  
 DR  
 DR  
 XX New secreted and transmembrane PRO polypeptides and nucleic acid  
 PT molecules encoding the polypeptides, useful in gene therapy or preparing  
 PT a medicament for treating a condition that is responsive to the PRO  
 PT polypeptide or antibody.  
 XX Disclosure; Fig 5; 409pp; English.  
 PS  
 PS  
 XX The invention describes novel isolated PRO polypeptides. The PRO  
 CC polypeptides or anti-PRO antibodies are useful in preparing a medicament  
 CC for treating a condition that is responsive to the PRO polypeptide or  
 CC antibody. The PRO nucleotide sequences may be used as hybridisation  
 CC probes in chromosome and gene mapping, or in generating antisense RNA and  
 CC DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in  
 CC assays to identify other proteins or molecules involved in binding  
 CC reaction, to generate transgenic animals or knockout animals, which in  
 CC turn are useful in the development and screening of therapeutically  
 CC useful reagents, for chromosome identification, and tissue typing. The  
 CC PRO polypeptides and nucleic acid molecules are also useful in gene  
 CC therapy, and as molecular weight markers for protein electrophoresis  
 CC purposes. The anti-PRO antibodies may be used in diagnostic assays for  
 CC PRO, or for the affinity purification of PRO from recombinant cell  
 CC culture or natural sources. This sequence encodes a novel human secreted  
 CC and transmembrane PRO polypeptide  
 XX  
 SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.49e-304 Length: 2372  
 Score: 322.00 Matches: 322  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 7 Gaps: 0  
 US-10-079-111-1 (1-322) x ACA60365 (1-2372)  
 QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 20  
 Db 160 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCCTTCATCTGGACACGAGGCTCCTG 219  
 QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
 Db 220 GTCCAAAGGCTCTTGGCTGCAGAAAGCTTCCATCCAGGTGTCTATGAGGATTTAGGGG 279  
 QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
 Db 280 ATCCACCTTGTGAGCAAAAAGGCGAACACAGAGCTGAATTTACAGAAGCTAAGAGGCC 339  
 QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
 Db 340 TGTAGCTCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGMAACAGCCTTGAAGCT 399  
 QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100  
 Db 400 AGCTTTGAAACTTGCAGCTATGCTGGGTGGAGATGGATTCTGTGCTCATCTCTAGGATT 459  
 QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuLeuLeuLeuLeuLeuLeu 120  
 Db 460 ACCCCCAACCCCAAGTGTGGGAAAAATGGGGTGGTGTCTGTGATTTGGAAAGTTCCAGTG 519  
 QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
 Db 520 AGCCGACAGTTTGCAGCTATTGTTTACAACTCATCTGATACCTGGACAACTCTGATGATT 579

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QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
|||
Db 580 CCAGAAATATCACCACCAAGATCCATATTTCAACACTCAAACTGCAACACAAACAACA 639
|||
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
|||
Db 640 GAATTTATTTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTCAATACCTGCC 699
|||
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
|||
Db 700 CCTACTACTACTCTCTCTCTCCAGCTTCCACTTCTTATTTCCAGGAGAGAAAAATTTGATT 759
|||
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
|||
Db 760 TGTGTCCACAGAGTTTTTATGGAACTAGCACCATGCTACAGAACTGAACCATTTGTT 819
|||
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
|||
Db 820 GAAATTAAGCAGCATTCAGAAATGAAGCTGTGGGTTTGGAGGTGTCCTCCACGGCTCTG 879
|||
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
|||
Db 880 CTAGTCTTGTCTCTCTCTCTTCTTGTGCTGCAGCTGCTTGGATTTTGTATGTCAAA 939
|||
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
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Db 940 AGGTATGTGAAGGCCCTTCCCTTTTACAAACAAAGAATCAGCAGAGGAAATGATCGAAACC 999
|||
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluSerLysLysThr 300
|||
Db 1000 AAGTAGTAAAGGAGGAGGAGGCCAATGATAGCAACCTATGAGGAATCAAGAAACT 1059
|||
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
|||
Db 1060 GATAAAACCCAGAGAGTCCAGAGTCCCAAGCAAAACTACCGTGGATGCTCGGAAGCT 1119
|||
QY 321 GluVal 322
|||
Db 1120 GAAGTT 1125
|||
RESULT 19
ABX71612
ID ABX71612 standard; cDNA; 2372 BP.
XX
AC ABX71612;
XX
DT 10-MAR-2003 (first entry)
XX
DE Human cDNA encoding secreted/transmembrane protein PRO263.
XX
KW Human; PRO; secreted protein; transmembrane protein; enterocolitis;
KW gastrointestinal ulceration; skin disease; ss; gene;
KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
KW squamous cell carcinoma; Alzheimer's disease; Parkinson's disease;
KW amyotrophic lateral sclerosis; inflammatory disease;
KW rheumatoid arthritis; asthma; multiple sclerosis; organ failure;
KW atherosclerosis; cardiac injury; infertility; birth defect;
KW premature aging; AIDS; acquired immunodeficiency syndrome; cancer;
XX
XX diabetetic complication; wound repair.
OS Homo sapiens.
XX
PN US2002132240-A1.
XX
PD 19-SEP-2002.
XX
PF 18-JUL-2001; 2001US-00909320.
XX
PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
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PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0068770P.
PR 24-NOV-1997; 97US-0066772P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 01-DEC-1998; 98WO-US025108.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 06-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
```

PR 24-AUG-2000; 2000WO-US023328.  
 PR 18-SEP-2000; 2000US-00665350.  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;  
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;  
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;  
 PI Mather JP, Pan J, Poni NF, Roy MA, Stewart TA, Tumas D;  
 PI Williams PM, Wood WI;  
 XX WPI; 2003-147434/14.  
 DR P-PSDB; ABUS4382.  
 DR  
 XX  
 PT New PRO polypeptides and nucleic acid molecules, useful in diagnosing or  
 PT treating inflammatory diseases, organ failure, atherosclerosis, cardiac  
 PT injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's  
 PT disease.  
 XX  
 PS Claim 2; Fig 73; 473pp; English.  
 XX  
 CC The invention relates to an isolated PRO polypeptide having at least 80%  
 CC amino acid sequence identity to: (a) any one of 61 fully defined amino  
 CC acid sequences given in the specification (appearing as ABUS4347-  
 CC ABUS4407); (b) an amino acid sequence encoded by the nucleotide sequence  
 CC deposited under American Type Culture Collection (accession numbers  
 CC listed in the specification); (c) any one of the PRO sequences which  
 CC lacks its associated signal peptide; (d) an extracellular domain of the  
 CC PRO polypeptide with its associated signal peptide; or (e) an  
 CC extracellular domain of the PRO polypeptide which lacks its associated  
 CC signal peptide. Also include are the nucleic acids encoding the PRO  
 CC polypeptides, vectors, host cells and anti-PRO antibodies. The PRO  
 CC polypeptides and nucleic acids are useful in diagnosing or treating  
 CC enterocolitis, gastrointestinal ulceration, skin diseases associated with  
 CC abnormal keratinocyte differentiation, e.g. psoriasis or epithelial  
 CC cancers such as squamous cell carcinoma, Alzheimer's disease, Parkinson's  
 CC disease, amyotrophic lateral sclerosis, inflammatory diseases, e.g.  
 CC rheumatoid arthritis, asthma or multiple sclerosis, organ failure,  
 CC atherosclerosis, cardiac injury, infertility, birth defects, premature  
 CC aging, AIDS, cancer, diabetic complications, or mutations in general. The  
 CC polypeptides are also useful for wound repair and associated therapies  
 CC concerned with re-growth of tissue. The nucleotide sequences may be used  
 CC as hybridisation probes in chromosome and gene mapping, or in generating  
 CC antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO  
 CC polypeptides, in assays to identify other proteins or molecules involved  
 CC in binding reaction, to generate transgenic animals or knockout animals,  
 CC which in turn are useful in the development and screening of  
 CC therapeutically useful reagents, for chromosome identification, and  
 CC tissue typing. The PRO polypeptides and nucleic acid molecules are also  
 CC useful in gene therapy, and as molecular weight markers for protein  
 CC electrophoresis purposes. The anti-PRO antibodies may be used in  
 CC diagnostic assays for PRO, or for the affinity purification of PRO from  
 CC recombinant cell culture or natural sources. The present sequence encodes  
 CC a PRO polypeptide  
 XX  
 SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 1.49e-304 Length: 2372  
 Score: 322.00 Matches: 322  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 7 Gaps: 0  
 US-10-079-111-1 (1-322) x ABX71612 (1-2372)  
 QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20  
 Db 160 ATGGCCAGGTGCTTCAGCGTGGTGTCTTCCTCACTTCATCTGCACACGAGGCTCCTG 219  
 QY 21 ValGlnGlySerLeuArgAlaGlnGluLeuSerIleGlnValSerCysArgIleMetGly 40

Db 220 GTCACAGGCTCTTTGGTGCAGAGAGCTTTCCATCCAGGTGTCATCCAGAAATTATGGGG 279  
 QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
 Db 280 ATCACCTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTTTCACAGAAGCTAAGGAGGCC 339  
 QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
 Db 340 TGTAGGCTGCTGGGACTTAAGTTTGGCGCGGCAAGGACCAAGTTGAAACAGAGCTTGAAGCT 399  
 QY 81 SerPheGluThrCysSerTyrGlyTyrValGlyValGlyPheValValIleSerArgIle 100  
 Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTCGTGGTCACTCTTAGGATT 459  
 QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
 Db 460 AGCCCCAACCCCAAGTGTGGGAAATGGGGTGGGTGCTCTGATTTGGAAGGTTCCAGTG 519  
 QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
 Db 520 AGCCGACAGTTTGCAGCTTATTGTTTACAATCTCATCTGATCTGAGCTAATCTGTCATT 579  
 QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
 Db 580 CCAGAAATTTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA 639  
 QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
 Db 640 GAATTTATTGTCAGTCAGCAGTACTACTCGTGGCATCCCTTACTCTCAATACCTGCC 699  
 QY 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200  
 Db 700 CCTACTACTACTCCTCCTCCTGCTCAGCTTCCACTTCTATTCCACGGAGAAAAATTTGATT 759  
 QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
 Db 760 TGTGTACAGAGAGTTTATGGAACTAGCACCATGCTTACAGAAATCGAACCATTTGTT 819  
 QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240  
 Db 820 GAAATATAAGCAGCATTCAGAAATGAAGTCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879  
 QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
 Db 880 CTAGTCTTGCTCTCCTCTCTCTTGTGTGCTGAGCTGGTCTTGGATTGCTATGTCAAA 939  
 QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
 Db 940 AGGTATGTGAGGCTTCCCTTTTACAAACAGAAATCAGCAGAGGAAATGATCGAAACC 999  
 QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
 Db 1000 AAGTAGTAGAGGAGAGAGGAGGCAATGATAGCAACCCCTTAATGAGGAATCAAGAAACT 1059  
 QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
 Db 1060 GATTAACCAACCCAGAGAGTCCAGAGAGTCCAGCAAAATACCGTGGATGCGTGGAGCT 1119  
 QY 321 GluVal 322  
 Db 1120 GAAGTT 1125  
 RESULT 20  
 ACH06944  
 ID ACH06944 standard; cDNA; 2372 BP.  
 XX  
 AC ACH06944;  
 XX  
 DT 08-OCT-2003 (first entry)  
 XX  
 DE Human secreted/transmembrane polypeptide PRO263 cDNA.  
 XX  
 KW Human; gene; ss; abnormal bleeding; gynaecological disease; asthma;

KW hysterectomy; angiogenesis; coronary ischaemic condition; skin disease;  
KW gastrointestinal mucosa disorder; acute mucosal lesion; neuropathy; AUS;  
KW chronic mucosal lesion; abnormal keratinocyte differentiation; psoriasis;  
KW Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;  
KW uncontrolled cell growth; cancer; blood coagulation cascade; thrombosis;  
KW haemorrhage; endometrial bleeding; angiogenesis; wound healing; tumour;  
KW tissue repair; rheumatoid arthritis; angiogenesis; multiple sclerosis; tissue typing.

XX

OS Homo sapiens.

XX

XX

PN US2003044839-A1.

XX

XX

PD 06-MAR-2003.

XX

PF 10-JUL-2001; 2001US-00902903.

XX

PR 17-SEP-1997; 97US-0059113P.

PR 17-SEP-1997; 97US-0059115P.

PR 17-SEP-1997; 97US-0059117P.

PR 17-SEP-1997; 97US-0059119P.

PR 17-SEP-1997; 97US-0059121P.

PR 17-SEP-1997; 97US-0059122P.

PR 17-SEP-1997; 97US-0059184P.

PR 18-SEP-1997; 97US-0059263P.

PR 18-SEP-1997; 97US-0059266P.

PR 15-OCT-1997; 97US-0062125P.

PR 17-OCT-1997; 97US-0062285P.

PR 17-OCT-1997; 97US-0062287P.

PR 21-OCT-1997; 97US-0063486P.

PR 24-OCT-1997; 97US-0062814P.

PR 24-OCT-1997; 97US-0062816P.

PR 24-OCT-1997; 97US-0063045P.

PR 24-OCT-1997; 97US-0063120P.

PR 24-OCT-1997; 97US-0063121P.

PR 24-OCT-1997; 97US-0063127P.

PR 27-OCT-1997; 97US-0063327P.

PR 27-OCT-1997; 97US-0063329P.

PR 28-OCT-1997; 97US-0063541P.

PR 28-OCT-1997; 97US-0063542P.

PR 28-OCT-1997; 97US-0063544P.

PR 28-OCT-1997; 97US-0063549P.

PR 28-OCT-1997; 97US-0063550P.

PR 28-OCT-1997; 97US-0063564P.

PR 29-OCT-1997; 97US-0063435P.

PR 29-OCT-1997; 97US-0063704P.

PR 29-OCT-1997; 97US-0063732P.

PR 29-OCT-1997; 97US-0063734P.

PR 29-OCT-1997; 97US-0063735P.

PR 29-OCT-1997; 97US-0063738P.

PR 29-OCT-1997; 97US-0064215P.

PR 31-OCT-1997; 97US-0063870P.

PR 31-OCT-1997; 97US-0064103P.

PR 03-NOV-1997; 97US-0064248P.

PR 07-NOV-1997; 97US-0064809P.

PR 12-NOV-1997; 97US-0065186P.

PR 18-NOV-1997; 97US-0065846P.

PR 18-NOV-1997; 97US-0065693P.

PR 21-NOV-1997; 97US-0066120P.

PR 21-NOV-1997; 97US-0066364P.

PR 24-NOV-1997; 97US-006453P.

PR 24-NOV-1997; 97US-0066466P.

PR 24-NOV-1997; 97US-0066511P.

PR 24-NOV-1997; 97US-0066770P.

PR 24-NOV-1997; 97US-0066772P.

PR 25-NOV-1997; 97US-0066840P.

PR 12-DEC-1997; 97US-0069425P.

PR 04-JUN-1998; 98US-0088026P.

PR 10-SEP-1998; 98US-0099803P.

PR 14-SEP-1998; 98WO-US0118824.

PR 14-SEP-1998; 98WO-US0100262P.

PR 14-SEP-1998; 98WO-US019177.

PR 14-SEP-1998; 98WO-US019330.

PR 16-SEP-1998;

PR 17-SEP-1998;

PR 17-SEP-1998;

PR 13-OCT-1998;

PR 20-NOV-1998;

PR 01-DEC-1998;

PR 22-DEC-1998;

PR 07-JUL-1999;

PR 26-JUL-1999;

PR 28-JUL-1999;

PR 08-SEP-1999;

PR 13-SEP-1999;

PR 15-SEP-1999;

PR 05-OCT-1999;

PR 29-NOV-1999;

PR 30-NOV-1999;

PR 01-DEC-1999;

PR 02-DEC-1999;

PR 16-DEC-1999;

PR 20-DEC-1999;

PR 05-JAN-2000;

PR 11-FEB-2000;

PR 22-FEB-2000;

PR 02-MAR-2000;

PR 30-MAR-2000;

PR 22-MAY-2000;

PR 02-JUN-2000;

PR 28-JUL-2000;

PR 24-AUG-2000;

PR 18-SEP-2000;

XX

XX

XX

PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;

PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;

PI Godowski PU, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin JF;

PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;

PI Williams PM, Wood WI;

XX WPI; 2003-492258/46.

DR P-PSDB; ABO47397.

XX

XX

PT Novel secreted and transmembrane polypeptides and polynucleotides

PT encoding them useful for treating abnormal bleeding involved in

PT gynecological diseases, skin diseases and neurodegenerative diseases.

XX

PS Claim 3; Fig 73; 478pp; English.

XX

CC The invention relates to an isolated PRO polypeptide. PRO317 is useful in

CC diagnosing or treating abnormal bleeding involved in gynecological

CC diseases e.g. to avoid or lessen the need for hysterectomy. PRO317 may

CC also be useful as an agent that affects angiogenesis and PRO317 is useful

CC in anti-tumour indications or in treating coronary ischaemic conditions.

CC PRO211 and PRO217 polypeptides are useful for treating disorders

CC associated with the preservation and maintenance of gastrointestinal

CC mucosa and the repair of acute and chronic mucosal lesions, skin diseases

CC associated with abnormal keratinocyte differentiation (e.g. psoriasis).

CC PRO187 polypeptide is useful for treating Parkinson's disease,

CC Alzheimer's disease, amyotrophic lateral sclerosis (ALS), neuropathies

CC and disease related to uncontrolled cell growth, e.g. cancer. PRO219

CC polypeptide plays a regulatory role in the blood coagulation cascade.

CC PRO246 polypeptides which serves as tumour specific antigens may be

CC exploited as therapeutic targets for anti-tumour drugs. PRO269

CC polypeptide is useful as an antithrombotic agent with reduced risk for

CC haemorrhage as compared with heparin. PRO317 polypeptide is useful in

CC treating endometrial bleeding angiogenesis. PRO287 polypeptides and

CC portion have therapeutic applications in wound healing and tissue repair.

CC PRO234 polypeptides are useful for treating asthma, rheumatoid arthritis,

CC psoriasis and multiple sclerosis. The polypeptide and its nucleic acid

CC

CC

CC are useful for tissue typing. PRO antibodies are useful for  
CC immunohistochemical staining and/or assay of sample fluids. Anti-PRO  
CC antibodies are useful in diagnostic assays for PRO e.g. detecting its  
CC expression in specific cells, tissues or serum and for affinity  
CC purification of PRO from recombinant cell culture or natural sources. The  
CC present sequence represents cDNA encoding a human secreted/transmembrane  
CC PRO polypeptide  
XX

SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.49e-304 Length: 2372  
Score: 322.00 Matches: 322  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 7 Gaps: 0

US-10-079-111-1 (1-322) x ACH06944 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20  
Db 160 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCAAGAGGCTCCTG 219  
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
Db 220 GTCCAGGCTCTTGGTGGCAGAGAGCTTTCATCCAGGTGTCATGCGAATATTATGGGG 279  
QY 41 IleThrLeuValSerIleLysAlaGlnGlnLeuAsnGlnPheThrGluAlaLysGluAla 60  
Db 280 ATCACCTTGTGAGCAAAAGGCGAACAGCAGCTGAATTTACAGAGCTAAGAGGCC 339  
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
Db 340 TGTAGCTCTGGGACTAGTTGGCTGGCGGACAGCAAGTTGAAACAGCTTTGAAAGCT 399  
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100  
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTCTGTGTCATCTCTAGATT 459  
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
Db 460 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTCTCTGATTTGGAAGGTTCCAGTG 519  
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
Db 520 AGCCGACAGTTTGCAGCTTATTTGTACAACTCATCTGATCTGGACTAACTCGTGCAAT 579  
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
Db 580 CCAGAAATTTATCACCAACCAAGATCCCATATTTCAACACTCAAACTGCAACACACAAACA 639  
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
Db 640 GAAATTTATGTTCAGTGACAGTACTACTCGGTGGCATCCCTTACTCTCAATACCTGCC 699  
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgGlyLysIleLeu 200  
Db 700 CCTACTACT 759  
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
Db 760 TGTGTACAGAAAGTTTTATGAAACTAGCACCATGTCTACAGAACTGAACCATTTGTT 819  
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
Db 820 GAAATAAAGCAGCATTCAGAAATGAAGTGTCTGGGTTTGGAGGTGTCCCAACGGCTCTG 879  
QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
Db 880 CTAGTGTCT 939  
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280

Db 940 AGTATGTGAAGCCTTCCCTTTTACAAACAAGAAATCAGCAGAAATGATCGAAACC 999  
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
Db 1000 AAGTAGTAGAAGAGAGAGAGAGCCCAATGATAGCAACCTTAATGAGGAATCAAGAAACT 1059  
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
Db 1060 GATAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCTGCGATCCCTTGAAGCT 1119  
QY 321 GluVal 322  
Db 1120 GAAGTT 1125  
RESULT 21  
ACA58812  
ID ACA58812 standard; cDNA; 2372 BP.  
XX  
AC ACA58812;  
XX  
DT 10-JUN-2003 (first entry)  
XX  
DE cDNA encoding human secreted polypeptide PRO263.  
XX  
KW Human; ss; gene; gene therapy; tumour; cancer.  
XX  
OS Homo sapiens.  
XX  
PN US2003013855-A1.  
XX  
PD 16-JAN-2003.  
XX  
PF 03-MAY-2002; 2002US-00063616.  
XX  
PR 30-DEC-1998; 98KR-00062142.  
PR 08-MAR-1999; 99WO-US005028.  
PR 14-MAY-1999; 99US-00311832.  
PR 14-MAY-1999; 99WO-US010733.  
PR 25-AUG-1999; 99US-00380137.  
PR 25-AUG-1999; 99US-00380138.  
PR 25-AUG-1999; 99US-00380139.  
PR 25-AUG-1999; 99US-00380142.  
PR 15-SEP-1999; 99US-00397342.  
PR 18-OCT-1999; 99US-00403297.  
PR 12-NOV-1999; 99US-00423844.  
PR 30-DEC-1999; 99WO-US031274.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 21-MAR-2000; 2000WO-US007532.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 22-AUG-2000; 2000US-00644848.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 18-SEP-2000; 2000US-0064610.  
PR 18-SEP-2000; 2000US-00665350.  
PR 08-NOV-2000; 2000US-00709238.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 22-MAR-2001; 2001US-00816744.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 30-MAY-2001; 2001US-00870574.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 05-JUN-2001; 2001US-00874503.  
PR 29-JUL-2001; 2001US-00869599.  
PR 18-JUL-2001; 2001US-00908827.  
PR 06-DEC-2001; 2001US-00068657.  
XX

PA (GBTH ) GENENTECH INC.

XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;  
XX WPI; 2003-330485/31.  
DR P-PSDB; ABU71508.

XX New isolated antibody specifically binding a PRO polypeptide, useful for  
PT the preparation of a medicament for treating disorders with the aberrant  
PT expression or activity of the PRO polypeptide, such as tumor conditions  
PT and cancer.

XX Example 4; Page 69-70; 406pp; English.

XX The invention relates to an antibody that binds to a polypeptide with a  
CC fully defined sequence given in the specification. The methods and  
CC compositions (containing antibodies that specifically bind a PRO  
CC polypeptide) of the present invention are useful for the preparation of a  
CC medicament for the treatment of disorders associated with the aberrant  
CC expression or activity of the PRO polypeptide, such as tumour conditions  
CC and cancer. They can also be used to generate transgenic or knockout  
CC animals useful in the development and screening of therapeutically useful  
CC reagents. The PRO polypeptides and encoding nucleic acids can be used as  
CC molecular weight markers for protein electrophoresis, chromosome  
CC identification and tissue typing. The PRO polypeptides are useful to  
CC induce angiogenesis e.g wound healing; in the treatment of sports-related  
CC joint problems, articular cartilage defects, osteoarthritis or rheumatoid  
CC arthritis; diabetes; hyperinsulinaemia and hypoinsulinaemia. The  
CC antibodies may be used in various diagnostic, competitive binding and/or  
CC immunoprecipitation assays. The present sequence represents a cDNA  
CC encoding a PRO polypeptide of the invention

XX Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1,498-304 Length: 2372  
Score: 322.00 Matches: 322  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 7 Gaps: 0

US-10-079-111-1 (1-322) x ACA58812 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIlePrpThrThrArgLeuLeu 20  
DB 160 ATGGCCAGGTGCTTCAGCCTGGTGTGGCTTCACATCCATCTGGACCGAGGCTCTG 219  
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
DB 220 GTCCAAGGCTCTTTGGCGTGAGAAGAGCTTTCCATCCAGGTGTTCATGGAATATATGGG 279  
QY 41 IleThrLeuValSerIleValAlaAsnGlnLeuAsnPheThrGluAlaLysGluAla 60  
DB 280 ATCACCCCTGTGAGCAAAAGGCGAACCCAGCTGAATTCACAGAGCTAAGAGGCC 339  
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
DB 340 TGTAGGCTGTGGAGCTAAGTTTGGCGGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399  
QY 81 SerPheGluThrCysSerIleGlyTrpValGlyAspGlyPheValValIleSerArgIle 100  
DB 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGGTTCATCTCTAGGATT 459  
QY 101 SerProAsnProLysCysGlyLysAspGlyValGlyValLeuIleTrpLysValProVal 120  
DB 460 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCTGATTTGGAAAGGTTCCAGTG 519  
QY 121 SerArgGlnPheAlaAlaTyCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
DB 520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTCATCTGACTTAACCTCGTGCAATT 579

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
DB 580 CCAGAAATTTATCACACCACCAAGATCCCATATTTCAACACTCAAACTGCAACACAAACA 639  
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProIla 180  
DB 640 GAATTTATTGTGAGTGACAGTACTACTCGGTGGCATCCCTTACTCTACAATAGCTGCC 699  
QY 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysIleLeu 200  
DB 700 CCTACTACTCTCTCTCTCCAGCTTCCACTTCTATTATCCACGGAGAAAAAATTGATT 759  
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
DB 760 TGTGTACACAGAAGTTTTTATGGAAACTAGCACCATTCTACAGAACTGAACCATTTGTT 819  
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
DB 820 GAAATAAAGCAGCATTCAAGAAATCAAGCTGCTGGTTTGGAGGTGTCCCAACGGCTCTG 879  
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260  
DB 880 CTAGTGCTTGTCT 939  
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280  
DB 940 AGGTATGTGAGGCTTCTCTTTTACAAACAGAAATCAGCAGAGGAAATGATCGAAACC 999  
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
DB 1000 AAAGTAGTAAAGCAGGAGAGGCAATGATAGCAACCTTAATGAGGAATCAAGAAACT 1059  
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
DB 1060 GATAAAACCCAGAGAGTCCAGAGTCCAGAGAACTACCGTGGATCGCTTGAAGCT 1119  
QY 321 GluVal 322  
DB 1120 GAAGTT 1125  
RESULT 22  
ACA63988  
ID ACA63988 standard; cDNA; 2372 BP.  
XX ACA63988;  
XX DT 16-JUN-2003 (first entry)  
XX DE cDNA encoding human PRO polypeptide #3.  
XX Human; PRO polypeptide; secreted and transmembrane protein;  
KW anti-PRO antibody; diagnostic assay; gene expression; gene; ss.  
XX Homo sapiens.  
XX PN US2002182638-A1.  
XX PD 05-DEC-2002.  
XX PF 02-MAY-2002; 2002US-00063547.  
XX PR 30-DEC-1998; 98KH-00062142.  
XX PR 08-MAR-1999; 99WO-US005028.  
XX PR 14-MAY-1999; 99US-00311832.  
XX PR 14-MAY-1999; 99WO-US010733.  
XX PR 25-AUG-1999; 99US-00380137.  
XX PR 25-AUG-1999; 99US-00380138.  
XX PR 25-AUG-1999; 99US-00380139.  
XX PR 25-AUG-1999; 99US-00380142.  
XX PR 15-SEP-1999; 99US-00397342.  
XX PR 18-OCT-1999; 99US-00403297.  
XX PR 12-NOV-1999; 99US-00423844.  
XX PR 30-DEC-1999; 99WO-US031274.

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PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
PA (GETH ) GENENTECH INC.
XX
PI Eaton DL, Filvaroff B, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-328612/04.
DR P-PSDB; ABU72289.
XX
PT An isolated secreted transmembrane polypeptide designated PRO, useful as
PT a therapeutic agent.
XX
PS Disclosure; Fig 5; 236pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a medicament
CC useful in the treatment of a condition responsive to anti-PRO antibody.
CC Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting
CC its expression in specific cells, tissues or serum, and for affinity
CC purification of PRO from recombinant cell culture or natural sources.
CC ACA63986-ACA64069 represent cDNA sequences encoding the human PRO
CC polypeptides of the invention
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1,498-304 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0
US-10-079-111-1 (1-322) x ACA63988 (1-2372)
QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu 20
Db 160 ATGGCCAGGTGCTTCAGCGTGGTGTGCTTCTCACTTCCATCTGACCAAGGCTCTCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAGAGCTCTTTCGCGTCAGAGAGAGCTTTCCATCCAGGTGTCTATGAGAAATATGGGG 279
QY 41 IleThrLeuValSerLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCTTGTGAGCAAAAAGCGGACCAAGCAGAGCTGAATTTTACAGAAAGCTAAGAGGCC 339

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QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGTGGGACTAAGTTTGGCGGCAAGCAAGTTGAAACAGACCTTGAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTTCAGCTATGCGTGGTTGGAGATGGATTCGTGGTCACTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuLeuIleTprLysValProVal 120
Db 460 AGCCCAAAACCCCAAGTGTGGAAAAATGGGTGGGTGCTCTGATTGGAAAGTTTCCAGT 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCTATTGTTACAACCTCATCTGATCTTGGACTAACTCGTGCAAT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTTATCACCAAAAGATCCCATATTCAACACTCAAACTGCAACACCAACAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTGTCAGTGACAGTACTACTCGGTGGCATCCCTTACTCTACAAATACCTGCC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCTCTCTCTCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTCACAGAAAGTTTTTATGGAACACTAGCACCATGCTACAGAAACTGAACCAATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATATAAGCAGCATTCAGAAATGAAGCTGCTGGGTTGGAGGTGTCCCCCGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGCTCTCTCTCTCTTCTTGTGCTGCAGCTGGTCTTTGGATTATGATGCAAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGCCCTTCCCTTTTACAAACAAGAAATCAGCAGAGAAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGAGGCCCAATGATAGCAACCCCTAATGAGGAATCAAGAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAAAACCCAGAGAGTCCAAAGAGTCCAAAGAGTCCAAAGAGTCCGTCGATCGCTGGAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125
RESULT 23
ACA91252
ID ACA91252 standard; cDNA; 2372 BP.
XX
AC ACA91252;
XX
DT 14-JUL-2003 (first entry)
XX
DE cDNA encoding human PRO polypeptide #3.
XX
KW Human; PRO polypeptide; secreted protein; transmembrane protein; rectal;
KW lung; stomach; oesophageal; skin; tumour; cancer; cytostatic;
KW gene therapy; gene; ss.
XX
OS Homo sapiens.
XX

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QY 321 GluVal 322  
 Db 1120 GAAGTT 1125  
 RESULT 24  
 ACD45151  
 ID ACD45151 standard; cDNA; 2372 BP.  
 XX AC ACD45151;  
 XX DT 11-SEP-2003 (first entry)  
 XX DE Human secreted/transmembrane polypeptide PRO263 cDNA.  
 XX KW Human; ss; tumour; cancer; gene therapy; tissue typing; gene.  
 XX OS Homo sapiens.  
 XX PN US2003009012-A1.  
 XX 09-JAN-2003.  
 XX 01-MAY-2002; 2002US-00063517.  
 XX 30-DEC-1998; 98KR-00062142.  
 XX 08-MAR-1999; 99WO-US005028.  
 XX 14-MAY-1999; 99US-00311832.  
 XX 14-MAY-1999; 99WO-US010733.  
 XX 25-AUG-1999; 99US-00380137.  
 XX 25-AUG-1999; 99US-00380138.  
 XX 25-AUG-1999; 99US-00380139.  
 XX 15-SEP-1999; 99US-00380142.  
 XX 15-SEP-1999; 99US-00397342.  
 XX 18-OCT-1999; 99US-00403297.  
 XX 12-NOV-1999; 99US-00423844.  
 XX 30-DEC-1999; 99WO-US031274.  
 XX 18-FEB-2000; 2000WO-US004341.  
 XX 01-MAR-2000; 2000WO-US005601.  
 XX 02-MAR-2000; 2000WO-US005841.  
 XX 21-MAR-2000; 2000WO-US007532.  
 XX 22-MAY-2000; 2000WO-US014042.  
 XX 02-JUN-2000; 2000WO-US015264.  
 XX 22-AUG-2000; 2000US-00644848.  
 XX 24-AUG-2000; 2000WO-US023328.  
 XX 18-SEP-2000; 2000US-00664610.  
 XX 18-SEP-2000; 2000US-00665350.  
 XX 08-NOV-2000; 2000US-00709238.  
 XX 10-NOV-2000; 2000WO-US030873.  
 XX 01-DEC-2000; 2000WO-US032678.  
 XX 20-DEC-2000; 2000US-00747259.  
 XX 28-FEB-2001; 2001WO-US034956.  
 XX 22-MAR-2001; 2001US-00816744.  
 XX 10-MAY-2001; 2001US-00854208.  
 XX 30-MAY-2001; 2001US-00854280.  
 XX 01-JUN-2001; 2001WO-US017800.  
 XX 05-JUN-2001; 2001US-00874503.  
 XX 29-JUN-2001; 2001US-00869599.  
 XX 18-JUL-2001; 2001US-00908827.  
 XX 06-DEC-2001; 2001US-00006867.  
 XX (GEPH) GENENTECH INC.  
 XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
 XX Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;  
 XX WPI; 2003-447383/42.  
 XX P-PSDB; ABO27283.  
 XX New isolated antibody specifically binding a PRO polypeptide, useful for  
 PT the preparation of a medicament for treating disorders with the aberrant  
 PT expression or activity of the PRO polypeptide, such as tumor conditions

PT and cancer.  
 XX  
 PS Disclosure; Fig 5; 223pp; English.  
 XX  
 CC The invention relates to an antibody that binds to a secreted and  
 CC transmembrane PRO polypeptide. The methods and compositions of the  
 CC present invention are useful for the preparation of a medicament for the  
 CC treatment of disorders associated with the aberrant expression or  
 CC activity of the PRO polypeptide, such as tumor conditions and cancer.  
 CC They can also be used to generate transgenic or knockout animals useful  
 CC in the development and screening of therapeutically useful reagents. The  
 CC PRO polypeptides and encoding nucleic acids can be used as molecular  
 CC weight markers for protein electrophoresis, chromosome identification and  
 CC tissue typing. The antibodies may be used in various diagnostic,  
 CC competitive binding and/or immunoprecipitation assays. The present  
 CC sequence represents a secreted and transmembrane PRO polypeptide cDNA  
 XX  
 SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1.49e-304 Length: 2372  
 Score: 322.00 Matches: 322  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 7 Gaps: 0

US-10-079-111-1 (1-322) x ACD45151 (1-2372)  
 QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20  
 |||||  
 Db 160 ATGCCCGAGTGTCTCAGCTGGTGTCTCTCCTTCATCTGGACCCAGAGGCTCTG 219  
 |||||  
 QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
 |||||  
 Db 220 GTCCAAAGGCTCTTGGCTGCAGAGAGCTTTCATCCAGGTGTGTCAGCAATATGGGG 279  
 |||||  
 QY 41 IleThrLeuValSerIlyslsAlaGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
 |||||  
 Db 280 ATCACCCCTTGTGAGCAAAAGGCAACAGCAGCTGATTTTCACAGAGCTAAGGAGGCC 339  
 |||||  
 QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
 |||||  
 Db 340 TGTAGGCTCTGGGACTAAGTTTGGCCGCAAGCAAGTTCAGTGAACAGCTTGAAGCT 399  
 |||||  
 QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100  
 |||||  
 Db 400 AGCTTTGAACTTGCAGCTATGGCTGGTGGAGATGGATTCTGTGTCATCTAGGATT 459  
 |||||  
 QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
 |||||  
 Db 460 AGCCCAAAACCCCAAGTGTGGGAAATGGGGTGGTCTGATTGGGAGGTTCAGTG 519  
 |||||  
 QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
 |||||  
 Db 520 AGCCGACAGTTTGCAGCTATTTGTTACACTCATCTGATCTGACTGACTGCTGCAAT 579  
 |||||  
 QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
 |||||  
 Db 580 CCAGAAATTTATCACCACCAAGATCCCATATTTCAACACTCAAACTGCAACACCAACA 639  
 |||||  
 QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
 |||||  
 Db 640 GAATTTATTTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACATACCTGCC 699  
 |||||  
 QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200  
 |||||  
 Db 700 CCTACTACTCTCTCTCTCCAGCTTCCACTTCTATTTCACCGAGAGAAAAATTTGATT 759  
 |||||  
 QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
 |||||  
 Db 760 TGTGTGCAGAGAAGTTTTTATGGAACTAGCACCATGTCTACAGAACTGAACCATTTGTT 819  
 |||||

```
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
DB |||||||
DB 820 GAAATAAAGCAGCATTCAAGAACTGCTGGTTGGAGGTGCCCCACGCTCTG 879
QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
DB |||||||
DB 880 CTAGTGCTTGCTCTCTCTCTTTGGTGTGAGCTGGTCTTGATTTGCTATGTCAAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
DB |||||||
DB 940 AGGTATGTGAAGGCTCTCCCTTTTACAAACAAGAAATCAGCAGAAAGAAATGCAAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluLysSerLysLysThr 300
DB |||||||
DB 1000 AAAGTAGTAAGGAGAGAGAGCAATGATGCAACCTTAATGAGGAATCAAGAGAAACT 1059
QY 301 AspLysAsnProGluLysSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
DB |||||||
DB 1060 GNTAAAMACCCAGAGAGTCCAGAGTCCAGCAAACTACCGTGCATGCTGGAGCT 1119
QY 321 GluVal 322
DB |||||||
DB 1120 GAAGTT 1125
RESULT 25
ABX96181
ID ABX96181 standard; cDNA; 2372 BP.
AC ABX96181;
XX
XX
DT 13-MAY-2003 (first entry)
DE Human secreted/transmembrane protein cDNA, #38.
KW Human; gene; ss; PRO; secreted; transmembrane; pharmaceutical;
KW diagnostic; biosensor; bioreactor; therapeutic; hyperplasia;
KW endometriosis; cancer; tumour; ischaemia; coronary arterial disease;
KW polycystic kidney disease; renal failure; inflammatory response; asthma;
KW rheumatoid arthritis; psoriasis; multiple sclerosis; gene therapy;
KW cytostatic; gynecological; cardiac; nephrotropic; hepatotropic;
KW antiinflammatory.
OS Homo sapiens.
XX
XX
PN US2002160374-A1.
XX
XX
PD 31-OCT-2002.
XX
XX
PF 12-JUL-2001; 2001US-00905291.
XX
XX
PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
XX
XX
PA (GETH ) GENENTECH INC.
XX
PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Klijavin LJ;
PI Mather JP, Pan J, Faoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
XX
DR WPI; 2003-288105/28.
DR P-PSDB; ABU64534.
XX
XX
PT New secreted and transmembrane PRO polypeptides (e.g. PRO533 or PRO245)
PT and genes encoding them, useful for detecting or treating e.g.
PT hyperplasia, endometriosis, cancers, ischemia, coronary arterial disease
PT or inflammations.
XX
```

Claim 2; Fig 73; 477bp; English.

PS The invention discloses isolated PRO secreted/transmembrane polypeptides  
 XX and the nucleic acid encoding them. The polypeptides can be used to raise  
 CC antibodies that specifically bind to the PRO polypeptide, for linking a  
 CC bioactive molecule to a cell expressing a PRO protein and for modulating  
 CC at least one biological activity of a cell. The PRO polypeptides or  
 CC polynucleotides are also useful as pharmaceuticals, diagnostics or  
 CC biosensors or bioreactors, for detecting or treating e.g. hyperplasia,  
 CC endometriosis, cancers (e.g. those involving solid tumours), ischemia,  
 CC coronary arterial disease, polycystic kidney disease, chronic or acute  
 CC renal failure, or inflammatory responses (e.g. asthma, rheumatoid  
 CC arthritis, psoriasis or multiple sclerosis) in mammals. The PRO genes may  
 CC also be used in gene therapy, particularly for replacing a defective  
 CC gene. The sequences presented in ABX96017-ABX96378 are the genes  
 CC encoding the primers amplifying and the probes detecting the PRO  
 CC polynucleotides of the invention

SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.49e-304 Length: 2372  
 Score: 322.00 Matches: 322  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 7 Gaps: 0

US-10-079-111-1 (1-322) x ABX96181 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20  
 Db 160 ATGCCAGGTGCTTACGCTGGTGGTTCCTTCATCTCCATCGGACGAGGCTCTG 219  
 QY 21 ValGlnGlySerLeuArgAlaGluLeuLeuSerIleGlnValSerCysArgIleMetGly 40  
 Db 220 GTCCAAAGGCTCTTGGCTGCAGAAAGAGCTTCCATCGAGGTGTCATGCAGAAATTATGGG 279  
 QY 41 IleThrLeuValSerLysLysAlaAAsnGlnGlnLeuAAsnPheThrGluAlaLysGluAla 60  
 Db 280 ATCAACCTTGTGAGCAAAAGGCGCAACAGCAGCTGAATTTACAGAGCTAAGGAGGCC 339  
 QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
 Db 340 TGTAGGCTGCTGGAGCTAAGTTTGGCGCGCAAGCAAGTTGAAACAGCTTGAAGCT 399  
 QY 81 SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle 100  
 Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCTGGTCACTCTAGGATT 459  
 QY 101 SerProAsnProLysCysGlyLysAAsnGlyValGlyValLeuIleTrpLysValProVal 120  
 Db 460 AGCCCAAAACCCCAAGTGTGGGAAATGGGTGGTGTCTGATTTGGAGAGTTCCAGTG 519  
 QY 121 SerArgGlnPheAlaAlaTyrCysTyrAAsnSerSerAspThrTrpThrAAsnSerCysIle 140  
 Db 520 AGCCGACAGTTTGCAGCTTATGTTTACAACTCATCTGATCTTGGACTTAACCTCGTGCT 579  
 QY 141 ProGluIleIleThrLysAspProIlePheAAsnThrGlnThrAlaThrGlnThrThr 160  
 Db 580 CCAGAAATATATACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAA 639  
 QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
 Db 640 GAAATTTATGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699  
 QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgLysLysLeulle 200  
 Db 700 CTTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCACCGAGAAAAAATTGATT 759  
 QY 201 CysValThrGluValPheMetGluThrSerMetSerThrGluThrGluProPheVal 220  
 Db 760 TGTGTACAGAAAGTTTATGGAACTAGCACCATGTCTACAGAACTGAACATTGTTT 819

QY 221 GluAAsnLysAlaAlaPheLysAAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
 Db 820 GAAATAAAGCAGCATTTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCACGGCTCTG 879  
 QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
 Db 880 CTAGTGCTTCT 939  
 QY 261 ArgTyrValLysAlaPheProPheThrAAsnLysAAsnGlnGlnLysGluMetIleGluThr 280  
 Db 940 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAAATCAGAGAGGAAATGATCGAAACC 999  
 QY 281 LysValValLysGluGluLysAlaAAsnAspSerAAsnProAAsnGluGluSerLysLysThr 300  
 Db 1000 AAAGTAGTAAAGGAGGAGAGGAGGCAATGATAGCAACCTTAATGAGGAATCAAAAGAACT 1059  
 QY 301 AspLysAAsnProGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
 Db 1060 GATAAAACCCAGAGAGTCCAAAGATCCAGCAAAACTACCGTGCATCGCTGGAAAGCT 1119  
 QY 321 GluVal 322  
 Db 1120 GAAGTT 1125  
 RESULT 26  
 ACA05502  
 ID ACA05502 standard; cDNA; 2372 BP.  
 XX ACA05502;  
 AC ACA05502;  
 DT 29-MAY-2003 (first entry)  
 XX  
 DE cDNA encoding human secreted protein PRO263.  
 XX Human; gene therapy; mucosal lesion; ulcer; enterocolitis; skin disease;  
 KW psoriasis; cancer; lung cancer; colon cancer; nerve cell disease;  
 KW Alzheimer's disease; Parkinson's disease; Usher syndrome; angiodenesis;  
 KW atrophila areata; inflammatory disease; asthma; rheumatoid arthritis;  
 KW ischaemia; ss; gene.  
 XX Homo sapiens.  
 OS  
 XX  
 PN  
 XX  
 XX US2003023054-A1.  
 PD 30-JAN-2003.  
 XX  
 PF 16-JUL-2001; 2001US-00906742.  
 XX  
 PR 17-SEP-1997; 97US-0059113P.  
 PR 17-SEP-1997; 97US-0059113P.  
 PR 17-SEP-1997; 97US-0059117P.  
 PR 17-SEP-1997; 97US-0059119P.  
 PR 17-SEP-1997; 97US-0059121P.  
 PR 17-SEP-1997; 97US-0059122P.  
 PR 17-SEP-1997; 97US-0059184P.  
 PR 18-SEP-1997; 97US-0059263P.  
 PR 18-SEP-1997; 97US-0059266P.  
 PR 15-OCT-1997; 97US-0062125P.  
 PR 17-OCT-1997; 97US-0062285P.  
 PR 17-OCT-1997; 97US-0062287P.  
 PR 21-OCT-1997; 97US-0063486P.  
 PR 24-OCT-1997; 97US-0062814P.  
 PR 24-OCT-1997; 97US-0063045P.  
 PR 24-OCT-1997; 97US-0063120P.  
 PR 24-OCT-1997; 97US-0063121P.  
 PR 24-OCT-1997; 97US-0063127P.  
 PR 24-OCT-1997; 97US-0063128P.  
 PR 27-OCT-1997; 97US-0063327P.  
 PR 27-OCT-1997; 97US-0063329P.  
 PR 28-OCT-1997; 97US-0063541P.  
 PR 28-OCT-1997; 97US-0063542P.



QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
Db |||||  
640 GAATTTATTGTGTCAGTACAGTACCTACTCGGTGCATCCCTTACTTCAATACCTGCC 699  
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200  
Db |||||  
700 CCTACTACTACTCTCTCTCTCTCCAGCTTCCACTTCTATTCCACGGAGAAAAATTGATT 759  
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
Db |||||  
760 TGTGTACAGAAGTTTTTATGGAACCTAGCACCATGTCTACAGAACTGAACCATTTGTT 819  
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
Db |||||  
820 GAAATAAAGCAGCATTTCAAGATGAAGTGTCTGGTTTGGAGTGTCCCCACGGCTCTG 879  
QY 241 LeuValLeuAlaIleLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
Db |||||  
880 CTAGTGTCTCTCTCTCTCTCTCTTGTGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 939  
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
Db |||||  
940 AGTATGTGAGCGCTTCCCTTTTACAAACAGATCAGCAGAGGAATGATCGAAACC 999  
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
Db |||||  
1000 AAAGTAGTAAGCAGGAGAGGCAATGATAGCAACCTTAATGAGGAATCAAGAAACT 1059  
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
Db |||||  
1060 GATAAAACCCAGAGAGTCCAGAGTCCAGAGTCCAGCAAAACTACCGTGGGATCGCTGGAAGCT 1119  
QY 321 GluVal 322  
Db |||||  
1120 GAAGTT 1125  
RESULT 27  
ACA93699  
ID ACA93699 standard; cdna; 2372 BP.  
XX  
AC ACA93699;  
XX  
DT 17-JUL-2003 (first entry)  
XX  
DE Human cdna encoding secreted/transmembrane protein PRO263.  
XX  
KW Human; ss; gene; PRO; secreted protein; transmembrane protein;  
KW cystostatic; vulnary; osteopathic; antiarthritis; antirheumatic;  
KW lung tumour; colon tumour; breast tumour; prostate tumour; rectal  
KW liver tumour; tumour necrosis factor; pericyte cell proliferation;  
KW TNF-alpha; proteoglycans release; cartilage; cancer; wound healing;  
KW cartilage defect; osteoarthritis; rheumatoid arthritis.  
XX  
OS Homo sapiens.  
XX  
XX  
PN US2003045684-A1.  
PD  
PD  
XX 06-MAR-2003.  
XX  
XX 02-MAY-2002; 2002US-00063553.  
XX  
PR 30-DEC-1998; 98KR-00062142.  
PR 08-MAR-1999; 99WO-US005028.  
PR 14-MAY-1999; 99US-00311832.  
PR 14-MAY-1999; 99WO-US010733.  
PR 25-AUG-1999; 99US-00380137.  
PR 25-AUG-1999; 99US-00380138.  
PR 25-AUG-1999; 99US-00380139.  
PR 25-AUG-1999; 99US-00380142.  
PR 15-SEP-1999; 99US-00397342.  
PR 18-OCT-1999; 99US-00403297.  
PR 12-NOV-1999; 99US-00423844.  
PR 30-DEC-1999; 99WO-US031274.

PR 18-FEB-2000; 2000WO-US004341.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 21-MAR-2000; 2000WO-US007532.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 22-AUG-2000; 2000US-00644848.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 18-SEP-2000; 2000US-00664610.  
PR 18-SEP-2000; 2000US-00665350.  
PR 08-NOV-2000; 2000US-00709238.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 22-MAR-2001; 2001US-00816744.  
PR 10-MAY-2001; 2001US-00854208.  
PR 30-MAY-2001; 2001US-00854280.  
PR 01-JUN-2001; 2001US-00878574.  
PR 03-JUN-2001; 2001WO-US017800.  
PR 29-JUN-2001; 2001US-00874503.  
PR 18-JUL-2001; 2001US-00869599.  
PR 06-DEC-2001; 2001US-00908827.  
XX  
XX (GETH ) GENENTECH INC.  
PA  
XX  
XX  
PI Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;  
XX  
DR WPI: 2003-392892/37.  
DR P-PSDB; AB092478.  
XX  
PT New PRO994 polypeptide, useful for detecting tumors, or for stimulating  
PT Tumor Necrosis Factor alpha, or pericyte proliferation, especially for  
PT treating cancer, cartilage defects, osteoarthritis and rheumatoid  
PT arthritis in a mammal.  
XX  
PS Disclosure; Fig 5; 235pp; English.

CC The invention relates to a new isolated PRO994 polypeptide comprises an  
CC amino acid sequence appearing as AB092499, PRO994 lacking its associated  
CC signal peptide, the extracellular domain of PRO994, the extracellular  
CC domain of PRO994 (lacking it associated signal peptide) or the protein  
CC encoded by the full-length coding sequence of the cDNA ATCC 203018. Also  
CC included is a chimaeric molecule comprising the PRO994 polypeptide fused  
CC to a heterologous amino acid sequence. The PRO polypeptide is useful in  
CC pharmaceuticals, diagnostics, biosensors or bioreactors. It is  
CC particularly useful for detecting tumours (e.g. lung tumour, colon  
CC tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)  
CC in a mammal, for stimulating the release of tumour necrosis factor (TNF)-  
CC alpha from human blood, for stimulating the proliferation of pericyte  
CC cells, or stimulating the release of proteoglycans from cartilage. The  
CC polypeptide may be employed for a variety of therapeutic purposes, e.g.  
CC for treating cancer, wound healing, cartilage defects, osteoarthritis,  
CC rheumatoid arthritis. Also disclosed are the cDNA encoding PRO994, 83  
CC other PRO polypeptides and their encoding cDNAs. The present sequence  
CC encodes a PRO polypeptide of the invention  
XX

SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1.49e-304 Length: 2372  
Score: 322.00 Matches: 322  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 7 Gaps: 0

US-10-079-111-1 (1-322) x ACA93699 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTyrThrThrArgLeuLeu 20

Db 160 ATGGCCAGGTGGTTCAGCTGGTGGTTCCTTCATCTCCATCTGACACGAGGCTCCCTG 219  
 Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
 Db 220 GTCCAGGCTCTTGGCTGCAGAGAGCTTTCATCCAGGTGTCATGCAGAAATATGGGG 279  
 Qy 41 IleThrLeuValSerIlyslalasnGlnGlnLeuAsnPheThrGluAlalysGluAla 60  
 Db 280 ATCACCCCTTGTGAGCAAAAGCGAACAGCAGCTGAATTCACAGAAAGCTAAGGAGGCC 339  
 Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
 Db 340 TGTAGGCTCTGGACTAAGTTTGGCCGAGGACCAAGTTGAAACAGCCTTGAAGCT 399  
 Qy 81 SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle 100  
 Db 400 AGCTTTGAAACTTGCAGCTATGCTGGTGGAGATGGATTCGTGTCATCTCAGGATT 459  
 Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
 Db 460 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCGATTTGGAAAGGTTCCAGTG 519  
 Qy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
 Db 520 AGCCGACAGTTGACGCCATTGTTAACTATCTGATCTTGGACTAACTCGTGCATT 579  
 Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
 Db 580 CCAGAAATATCACCAACCAAGATCCATATTCACACTCAAACTGCAACACAAACA 639  
 Qy 161 GluPheIleValSerAspSerThrThrSerValAlaSerProTyrSerThrIleProAla 180  
 Db 640 GAATTTATTTGTACGACAGTACCTACTCGTGGCATCCCTTACTCTCAAAATACCTGCC 699  
 Qy 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200  
 Db 700 CCTACTACTACT 759  
 Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
 Db 760 TGTGTACAGAGAGTTTATGGAACCTAGCACCATGTCTACAGAACTGAACCATTTGTT 819  
 Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240  
 Db 820 GAAATAAAGACAGCATTTCAAGATGAAGCTGTGGGTGGGTGGGTGGGTGGGTGGGTGGT 879  
 Qy 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
 Db 880 CTAGTGTCTGCT 939  
 Qy 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
 Db 940 AGGTATGTGAAGGCTCTCCCTTTTACAAACAGAAATCAGCAGAGGAAATGATCGAAAC 999  
 Qy 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
 Db 1000 AAAGTAGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1059  
 Qy 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
 Db 1060 GATAAAACCCAGAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAG 1119  
 Qy 321 GluVal 322  
 Db 1120 GAAGTT 1125  
 RESULT 28  
 ACD20169  
 ID ACD20169 standard; cDNA; 2372 BP.  
 XX  
 AC ACD20169;  
 XX

DT 25-AUG-2003 (first entry)  
 XX Human secreted / transmembrane polypeptide PRO263 cDNA.  
 DE  
 XX Human; ss; gene; gene therapy; tumour; tissue typing; obesity; diabetes;  
 KW hypoinsulinaemia; hyperinsulinaemia; vascular permeability;  
 KW cardiac insufficiency disorder; immune response; regeneration; cartilage;  
 KW auditory hair cell; hearing loss; bone disorder; sports injury;  
 KW arthritis.  
 XX  
 OS Homo sapiens.  
 PN US2003036060-A1.  
 XX 20-FEB-2003.  
 PD  
 PF 12-JUL-2001; 2001US-00904859.  
 PF 17-SEP-1997; 97US-0059113P.  
 PR 17-SEP-1997; 97US-0059115P.  
 PR 17-SEP-1997; 97US-0059117P.  
 PR 17-SEP-1997; 97US-0059119P.  
 PR 17-SEP-1997; 97US-0059121P.  
 PR 17-SEP-1997; 97US-0059122P.  
 PR 17-SEP-1997; 97US-0059184P.  
 PR 18-SEP-1997; 97US-0059263P.  
 PR 18-SEP-1997; 97US-0059266P.  
 PR 15-OCT-1997; 97US-0062125P.  
 PR 17-OCT-1997; 97US-0062285P.  
 PR 17-OCT-1997; 97US-0062287P.  
 PR 21-OCT-1997; 97US-0063486P.  
 PR 24-OCT-1997; 97US-0062814P.  
 PR 24-OCT-1997; 97US-0062816P.  
 PR 24-OCT-1997; 97US-0063045P.  
 PR 24-OCT-1997; 97US-0063120P.  
 PR 24-OCT-1997; 97US-0063121P.  
 PR 24-OCT-1997; 97US-0063127P.  
 PR 24-OCT-1997; 97US-0063128P.  
 PR 27-OCT-1997; 97US-0063327P.  
 PR 27-OCT-1997; 97US-0063329P.  
 PR 28-OCT-1997; 97US-0063541P.  
 PR 28-OCT-1997; 97US-0063542P.  
 PR 28-OCT-1997; 97US-0063544P.  
 PR 28-OCT-1997; 97US-0063549P.  
 PR 28-OCT-1997; 97US-0063550P.  
 PR 28-OCT-1997; 97US-0063564P.  
 PR 29-OCT-1997; 97US-0063435P.  
 PR 29-OCT-1997; 97US-0063704P.  
 PR 29-OCT-1997; 97US-0063732P.  
 PR 29-OCT-1997; 97US-0063734P.  
 PR 29-OCT-1997; 97US-0063735P.  
 PR 29-OCT-1997; 97US-0063738P.  
 PR 29-OCT-1997; 97US-0064215P.  
 PR 31-OCT-1997; 97US-0063870P.  
 PR 31-OCT-1997; 97US-0064103P.  
 PR 03-NOV-1997; 97US-0064248P.  
 PR 07-NOV-1997; 97US-0064809P.  
 PR 12-NOV-1997; 97US-0065186P.  
 PR 17-NOV-1997; 97US-0065846P.  
 PR 18-NOV-1997; 97US-0065693P.  
 PR 21-NOV-1997; 97US-0066120P.  
 PR 21-NOV-1997; 97US-0066364P.  
 PR 24-NOV-1997; 97US-0066453P.  
 PR 24-NOV-1997; 97US-0066466P.  
 PR 24-NOV-1997; 97US-0066511P.  
 PR 24-NOV-1997; 97US-0066770P.  
 PR 24-NOV-1997; 97US-0066772P.  
 PR 25-NOV-1997; 97US-0066840P.  
 PR 12-DEC-1997; 97US-0069425P.  
 PR 04-JUN-1998; 98US-0088026P.  
 PR 10-SEP-1998; 98US-0099803P.  
 PR 10-SEP-1998; 98WO-US018824.  
 PR 14-SEP-1998; 98US-0100262P.  
 PR

PR 14-SEP-1998; 98WO-US019177.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98US-0100858P.  
PR 17-SEP-1998; 98WO-US019437.  
PR 13-OCT-1998; 98US-0104080P.  
PR 20-NOV-1998; 98US-0109304P.  
PR 01-DEC-1998; 98WO-US025108.  
PR 22-DEC-1998; 98US-0113296P.  
PR 07-JUL-1999; 99US-0143048P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 28-JUL-1999; 99US-0146222P.  
PR 08-SEP-1999; 99WO-US020594.  
PR 13-SEP-1999; 99WO-US020944.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 05-OCT-1999; 99WO-US023089.  
PR 29-NOV-1999; 99WO-US028214.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 02-DEC-1999; 99WO-US028564.  
PR 02-DEC-1999; 99WO-US028565.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 20-DEC-1999; 99WO-US030999.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 20-MAR-2000; 2000WO-US005841.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 18-SEP-2000; 2000US-00665350.  
XX

(GETH ) GENENTECH INC.

PA Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;  
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;  
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ,  
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;  
PI Williams PM, Wood WI;  
XX

DR WPI: 2003-417923/39.  
DR P-PSDB; ABO14900.  
XX

PT Novel secreted and transmembrane polypeptide for modulating biological  
PT activity of cell expressing the polypeptide, identifying agonists or  
PT antagonists of polypeptide, and as molecular weight markers.  
XX

PS Claim 2; Fig 73; 469pp; English.  
XX

CC The invention relates to an isolated, secreted and transmembrane  
CC polypeptide, termed PRO polypeptide. The polypeptide is useful for  
CC identifying agonists or antagonists of the polypeptide, for preparing  
CC variants of the polypeptide, as molecular weight markers for protein  
CC electrophoresis purpose and the nucleic acid is useful for recombinantly  
CC expressing those markers. The polypeptide is also useful as therapeutic  
CC agent. PRO is useful in assays to identify other proteins or molecules  
CC involved in binding interaction. The nucleic acid is useful as  
CC hybridisation probes, in chromosome and gene mapping, in generation of  
CC antisense RNA and DNA, in the preparation of PRO polypeptide, for  
CC generating transgenic animals or knockout animals which in turn are  
CC useful in the development and screening of therapeutically useful  
CC reagents, to construct hybridisation probes for mapping the gene which  
CC encodes the PRO and for the genetic analysis of individuals with genetic  
CC disorders, in gene therapy, for chromosome identification, as chromosome  
CC marker, and for generating probes for polymerase chain reaction (PCR),  
CC Northern analysis, Southern analysis and Western analysis. PRO antibody  
CC is useful in diagnostic assays for PRO, e.g. detecting its expression in  
CC specific cells, tissues or serum and for affinity purification of PRO

CC from recombinant cell culture or natural sources. The polypeptide or its  
CC antibody is useful for the preparation of medicament for treating  
CC conditions which is responsive to the PRO polypeptide or anti-PRO  
CC antibody e.g. tumour. The polypeptide and the nucleic acid is useful for  
CC tissue typing. The polypeptide is useful for treating obesity, diabetes  
CC or hypo- or hyper-insulinaemia and cardiac insufficiency disorders, for  
CC inhibiting tumour growth, enhances vascular permeability and immune  
CC response, for inducing regeneration of auditory hair cells and for  
CC treating hearing loss in mammals and for treating bone and/or cartilage  
CC disorders such as sports injuries and arthritis. The present sequence  
CC represents cDNA encoding a human secreted and transmembrane PRO  
CC polypeptide  
XX

SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1-49e-304	Length:	2372
Score:	322.00	Matches:	322
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	7	Gaps:	0

US-10-079-111-1 (1-322) x ACD20169 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20

Db 160 ATGCCAGGTCCTTACAGCTGGTGTTCCTTCTCATTCCATCTGGACCACGAGGCTCTG 219

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40

Db 220 GTCCAAAGCTCTTTGGTGTGCAGAAAGAGCTTTCATCCAGGTGTCTGCAGAAATATGGGG 279

QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPhethrGluAlaLysGluAla 60

Db 280 ATCAACCTTGTGAGCAAAAGGCGAACAGCAGCTGAATTTTCAGAGAGTAAAGAGGCC 339

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80

Db 340 TGTAGGCTGTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCTTTGAAAGCT 399

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100

Db 400 AGCTTTGAAACCTTGCAGCTATGGCTGGTGGAGATGGATTCGTGTCTCTAGGATT 459

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120

Db 460 AGCCCAAAACCCCAAGTGTGGAAAAATGGGTGGGTGTCTCGATTTGGAAAGTTCCAGTG 519

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140

Db 520 AGCCGACAGTTTGCAGCTTATTTGTACAACTCATCTGATCTGAGTAACTACTCGTCATT 579

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160

Db 580 CCAGAAATTTATCACCAACCAAGATCCATATTCAACACTCAAACTCAACACAAACAACA 639

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180

Db 640 GAAATTTATTGTTCAGTGACAGTACCTACTCGTGGCATCCCTTACTTCTACTCAATACCTGCC 699

QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200

Db 700 CCTACTACTACTCTCTCTCCAGCTTCCACTTCTTATTCACGAGGAAAAAATTTGATT 759

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220

Db 760 TGTGTTCACAGAGTTTATGGAAACTAGCACCATGTCTACAGAAACTGAAACATTTGTT 819

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240

Db 820 GAAATAAAGCAGCATTTCAAGATGAAGCTGTGGTGTGGAGGTGTCCCCACGGCTCTG 879





Db 640 GAATTTATTGTCAGTGACAGTACTACTCGTGGCATCCCTTACTCTACAAATACCTGCC 699  
 QY 181 ProThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeu 200  
 Db 700 CCTACTACTACTCTCTCTCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759  
 QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
 Db 760 TGTGTACAGAGTTTTATGGAACTAGCACCATGCTACAGAACTGAACCATTTGTT 819  
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 Db 820 GAAATTAAGCAGCAATCAAGATGAAGCTGCTGGTGGAGTGTCCCAACGGCTCTG 879  
 QY 241 LeuValLeuAlaLeuLeuPheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
 Db 880 CTAGTCTCTGCT 939  
 QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
 Db 940 AGGTATGTGAAGCCTTCCCTTTTACAAACAGAAATCAGCAGGAAGAAATGATCGAAACC 999  
 QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
 Db 1000 AAAGTAGTAAAGCAGAGAGGCAATGATAGCAACCTTAATGAGGAATCAAGAAAACT 1059  
 QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
 Db 1060 GATAAAACCCAGAGAGTCCAGAGTCCAAAGCAAAACTACCGTGGCATCTGGAAGCT 1119  
 QY 321 GluVal 322  
 Db 1120 GAAGTT 1125  
 RESULT 30  
 ACH66246  
 ID ACH66246 standard; cDNA; 2372 BP.  
 AC ACH66246;  
 XX  
 DT 14-OCT-2003 (first entry)  
 XX  
 DE Novel human secreted and transmembrane protein PRO263 cDNA.  
 XX Human; secreted and transmembrane protein; PRO; gene; ss.  
 XX Homo sapiens.  
 OS  
 XX US2003027986-A1.  
 XX  
 XX 06-FEB-2003.  
 XX  
 XX 02-MAY-2002; 2002US-00063549.  
 XX  
 XX 30-DEC-1998; 98KR-00062142.  
 XX 08-MAR-1999; 99WO-US005028.  
 XX 14-MAY-1999; 99US-00311832.  
 XX 14-MAY-1999; 99WO-US010733.  
 XX 25-AUG-1999; 99US-00380137.  
 XX 25-AUG-1999; 99US-00380138.  
 XX 25-AUG-1999; 99US-00380139.  
 XX 25-AUG-1999; 99US-00380142.  
 XX 15-SEP-1999; 99US-00397342.  
 XX 18-OCT-1999; 99US-00403297.  
 XX 12-NOV-1999; 99US-00423848.  
 XX 30-DEC-1999; 99WO-US031274.  
 XX 18-FEB-2000; 2000WO-US004341.  
 XX 01-MAR-2000; 2000WO-US005601.  
 XX 02-MAR-2000; 2000WO-US005841.  
 XX 21-MAR-2000; 2000WO-US007532.  
 XX 22-MAY-2000; 2000WO-US014042.  
 XX 02-JUN-2000; 2000WO-US015264.

PR 22-AUG-2000; 2000US-00644848.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 18-SEP-2000; 2000US-00664610.  
 PR 18-SEP-2000; 2000US-00665350.  
 PR 08-NOV-2000; 2000US-00709238.  
 PR 10-NOV-2000; 2000WO-US030873.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 20-DEC-2000; 2000US-00747259.  
 PR 20-DEC-2000; 2000WO-US034956.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 22-MAR-2001; 2001US-00816744.  
 PR 10-MAY-2001; 2001US-00854208.  
 PR 10-MAY-2001; 2001US-00854280.  
 PR 30-MAY-2001; 2001US-00870574.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 05-JUN-2001; 2001US-00874503.  
 PR 29-JUN-2001; 2001US-00869599.  
 PR 18-JUL-2001; 2001US-00908827.  
 PR 06-DEC-2001; 2001US-00006867.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baton DL, Filvaroff E, Gerritson ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;  
 XX  
 XX WPI; 2003-456358/43.  
 DR P-PSDB; ABO53263.  
 XX  
 PT PRO polypeptide, useful for preparing a medicament for treating a  
 condition associated with PRO polypeptide.  
 XX  
 PS Disclosure; Fig 5; 222pp; English.  
 XX  
 CC The invention describes an isolated polypeptide having at least 80, 85,  
 CC 90, 95 or 99% identity with: (a) a sequence having 46-335 amino acids, or  
 CC its extracellular domain; (b) a sequence having 46-335 amino acids,  
 CC lacking its associated signal peptide; or (c) an amino acid sequence  
 CC encoded by the full-length coding sequence of the cDNA (ATCC accession  
 CC number 209956). The PRO (secreted and transmembrane) polypeptide is  
 CC useful for preparing a medicament for treating a condition associated  
 CC with PRO polypeptide. This sequence encodes a novel human secreted and  
 CC transmembrane PRO polypeptide  
 XX  
 SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.49e-304 Length: 2372  
 Score: 322.00 Matches: 322  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 7 Gaps: 0  
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 Db 160 ATGGCCAGGTGCTTCAGCTGGTGTGTCTTCTCACTTCTCATCTGACCACGAGGCTCTGT 219  
 QY 21 ValGlnGlySerLeuArgAlaGluGlnLeuSerIleGlnValSerCysArgIleMetGly 40  
 Db 220 GTCCAAAGGCTCTTTCGTGTCAGAGAGCTTTCATCCAGGTGTCAAGCAAAATTATGGGG 279  
 QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
 Db 280 ATCACCTTGTGAGCAAAAGCGCAACCCAGCAGCTGAATTTTCACAGAAAGTAAAGAGGCC 339  
 QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
 Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTGAACAGCCCTTGAAGCT 399  
 QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100

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Db      400  ASCTTTGAACCTTGACGCTATGCTGGGTTGGAGATGGATTGCTGTCATCTCTAGGATT 459
QY      101  SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db      460  AGCCCAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCTGATTGGGAAGGTTCACAGTG 519
QY      121  SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db      520  AGCCGACAGTGTGGACGCTATTGTTTCAACTCATCTGATCTTGGACTTAACTCGTGCATT 579
QY      141  ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db      580  CAGAAATTATCACCAACCAAGATCCCATATTCACACTCAACTGCACACACAAACA 639
QY      161  GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db      640  GAATTATTGTGAGTACAGTACACTACTCGTGGCATCCCTTACTCTCAATACCTGCG 699
QY      181  ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLeuIle 200
Db      700  CCTACTACTACTCTCTCTCTCCAGCTTCCACTTCTATCCACGGAGAAAAAATTGATT 759
QY      201  CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db      760  TGTGTACACAGAGTATTTATGGAACTAGCACCATCTCTACAGAACTGAACCATTTGTT 819
QY      221  GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db      820  GAAATATAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 879
QY      241  LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db      880  CTAGTCTTGTCTCTCTCTCTCTTTGTTGCTGTCAGCTGGTCTTGATTTTGTATGCAAA 939
QY      261  ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db      940  AGGTATGTGAAGCCTTCTCTTTTACAAACAGAAATCAGCAGAGGAATGATCGAACC 999
QY      281  LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db      1000  AAAGTAGTAAAGGAGGAGGAGGCAATGATAGCAACCTTAATGAGGAATCAAGAAAAACT 1059
QY      301  AspLysAsnProGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db      1060  GATAAAACCCAGAGAGTCCAAAGAGTCCAAAGCAAAACTACCGTGGATGCTCTGGAAGCT 1119
QY      321  GluVal 322
Db      1120  GAAGTT 1125

RESULT 31
ACD02300
ID      ACD02300 standard; cDNA; 2372 BP.
XX
AC      ACD02300;
XX
DT      30-JUL-2003 (first entry)
XX
DE      Novel human secreted and transmembrane protein PRO263 cDNA.
XX
KW      Human; secreted and transmembrane protein; PRO; cytotstatic; gene therapy;
KW      cancer; chromosome mapping; gene mapping; diagnostic; biosensor;
KW      bioreactor; gene; ss.
XX
OS      Homo sapiens.
XX
PN      US2002183493-A1.
XX
PD      05-DEC-2002.
XX
PF      02-MAY-2002; 2002US-00063530.
XX
PR      30-DEC-1998; 98XR-00062142.
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PR      08-MAR-1999; 99WO-US005028.
PR      14-MAY-1999; 99US-00311832.
PR      14-MAY-1999; 99WO-US010733.
PR      25-AUG-1999; 99US-00380137.
PR      25-AUG-1999; 99US-00380138.
PR      25-AUG-1999; 99US-00380139.
PR      25-AUG-1999; 99US-00380142.
PR      15-SEP-1999; 99US-00397342.
PR      18-OCT-1999; 99US-00403297.
PR      12-NOV-1999; 99US-00423844.
PR      30-DEC-1999; 99WO-US031274.
PR      18-FEB-2000; 2000WO-US004341.
PR      01-MAR-2000; 2000WO-US005601.
PR      02-MAR-2000; 2000WO-US005841.
PR      21-MAR-2000; 2000WO-US007532.
PR      22-MAY-2000; 2000WO-US014042.
PR      02-JUN-2000; 2000WO-US015264.
PR      22-AUG-2000; 2000US-00644848.
PR      24-AUG-2000; 2000WO-US023328.
PR      18-SEP-2000; 2000US-0064610.
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PR      08-NOV-2000; 2000US-00709238.
PR      10-NOV-2000; 2000WO-US030873.
PR      01-DEC-2000; 2000WO-US032678.
PR      20-DEC-2000; 2000US-00747259.
PR      20-DEC-2000; 2000WO-US034956.
PR      28-FEB-2001; 2001WO-US006520.
PR      22-MAR-2001; 2001US-00816744.
PR      10-MAY-2001; 2001US-00854208.
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PR      30-MAY-2001; 2001US-00870574.
PR      01-JUN-2001; 2001WO-US017800.
PR      05-JUN-2001; 2001US-00874503.
PR      29-JUN-2001; 2001US-00869599.
PR      18-JUL-2001; 2001US-00908827.
PR      06-DEC-2001; 2001US-00006867.
XX
XX      (GETH ) GENENTECH INC.
PA
XX      Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI      Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
XX      WPI: 2003-328636/31.
DR      P-PSDB; AB098265.
XX
PT      New antibody that specifically binds to a PRO polypeptide, useful in
PT      preparing a medicament for treating a condition, e.g. cancer, responsive
PT      to the antibody, and in diagnostic and purification assays for the PRO
PT      polypeptide.
XX
XX      Disclosure; Fig 5; 236pp; English.
XX
XX      The invention describes an antibody that binds to a polypeptide having a
CC      sequence of 277 amino acids fully defined in the specification. The
CC      antibody, PRO polypeptide, or the agonist or antagonist of the
CC      polypeptide, is useful in preparing a medicament for treating a condition
CC      responsive to the PRO polypeptide, agonist or antagonist, or the
CC      antibody, such as cancer. The antibody may also be used in diagnostic
CC      assays for PRO polypeptide in specific cells, tissue or serum, and in
CC      affinity purification of the polypeptide. The nucleic acid molecule is
CC      useful in molecular biology, as hybridisation probes, in chromosome and
CC      gene mapping, in generating antisense RNA and DNA, in preparing PRO
CC      polypeptides by recombinant techniques, and in gene therapy. The
CC      oligonucleotide probes are useful for isolating genomic and cDNA
CC      nucleotide sequences or as antisense probes. The secreted proteins are
CC      useful in industrial applications, including as pharmaceuticals,
CC      diagnostics, biosensors and bioreactors. The PRO polypeptides may also be
CC      employed as molecular weight markers for protein electrophoresis
CC      purposes. This sequence encodes a novel human secreted and transmembrane
CC      PRO polypeptide
XX
XX      Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;
```

Alignment Scores:

Pred. No.:	1.49e-304	Length:	2372
Score:	322.00	Matches:	322
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	7	Gaps:	0

US-10-079-111-1 (1-322) x ACD02300 (1-2372)

QY	1	MetaLaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu	20
Db	160	ATGCCCAAGTCTTCAGCCTGGTGTGCTTCACCTCCACTCGACACAGGCTCCTG	219
QY	21	ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	220	GTCCAGGCTCTTTCGCTGCAGAGAGCTTCCATCCAGGTGTCAATCAGAAATATATGGG	279
QY	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	280	ATCACCTTGTGAGCAAAAGCGCAACACAGCAGCTGAATTTACAGAAAGCTAAGAGGCC	339
QY	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	340	TGTAGGCTGTCTGGACTAAGTTTGGCCGGCAAGACCAAGTTGAACAGCCCTTGAAGCT	399
QY	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle	100
Db	400	AGCTTTGNAACTTCAGACTATGGCTGGGTGGAGATGGATTTCGTGGTCAATCTTAGGATT	459
QY	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
Db	460	AGCCCAAAACCCCAAGTGTGGGAAATGGGGTGGGTCTCGATTTCGAAAGTTCCAGTG	519
QY	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	520	AGCCGACAGTTTGCAGCCCTATTGTTTACAACCTCATCTGATCTTGGACTTAACCTGTCATT	579
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	580	CCAGAAATTTACACCAAGATCCCATATTCAACACTCAAACTGCAACCAACAACAACA	639
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	640	GAAATTTATGTGTCAGTGACAGTACCTACTCGTGGCATCCCCCTTACTCTACAACTACCTGCC	699
QY	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgLysLysLeuIle	200
Db	700	CCTACTACTCTCTCTCTCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATGATT	759
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	760	TGTTGTACAGAAAGTTTTATGGAACTAGCAACCATGCTCAGAAACTGAACCACTTTGTT	819
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	820	GAAAAATAAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG	879
QY	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	880	CTAGTGTCTTGCTCTCTCTCTTTGGTGCTGCAGCTGCTCTTGGATTTTTGTATGTCAAA	939
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280
Db	940	AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAAATCAGCAAGAGGAAATGATCGAAACC	999
QY	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
Db	1000	AAAGTAGTAAAGGAGGAGAGGCCCAATCATAGCAACCCCTAATGAGGAATCAAGAAAACT	1059
QY	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1060	GATAAAAACCCAGAAGAGTCCAGAGGTCCAAAGCAAACTACCGTGCATGCTCTGAAGCT	1119







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QY      81  SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle 100
Db      400 AGCTTTGAACCTTGCAGCTATGCTGGTTGGAGATGGATTCGTGGTCATCTCTAGGATT 459
QY      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTyrLysValProVal 120
Db      460 AGCCCAACCCCAAGTGTGGAAATGGGTGGTGTCTCTGATTTGGAAGGTTCAGTG 519
QY      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db      520 AGCCGACAGTTTCAGCTATTCTTACAACTCATCTGATACCTTGGACTAACTCGTGCAAT 579
QY      141 ProGluIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db      580 CCAGAAATTATACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA 639
QY      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db      640 GAATTTATTGTCAGTCAGACAGTACCTACTCGGTGGCATCCCTTACTCTACAAATACCTGCC 699
QY      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db      700 CCTACTACTACTCTCTCTCTCCAGCTTCCACTTCTATTCCACGAGAAAAAATTGATT 759
QY      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db      760 TGTCACAGAAGTTTTTATGGAACTAGCACCATGCTACAGAAACTGAACATTGTGT 819
QY      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db      820 GAAATTAAGCAGCACTTCAAGAAATGAAGCTGCTGGTGTGGAGGTGTCCTCCACGGCTCTG 879
QY      241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db      880 CTAGTCCTGCTCTCTCTCTCTTTGTGCTGTCAGCTGGTCTTGGATTTTGCTATGTCAA 939
QY      261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db      940 AGGTATGTGAAGCCTTCCCTTTTACAAACAGAAATCAGCAGAGGAATGATCGAAACC 999
QY      281 LysValValLysGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db      1000 AAAGTAGTAAGAGAGAGAGGCAATGATAGCAACCCCTAATGAGGAATCAAAAGAAACT 1059
QY      301 AsnLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db      1060 GATAAAACCCAGAGAGTCCAAAGAGTCCAAAGACAAAACTACCGTCGATCGCTGGAAGCT 1119
QY      321 GluVal 322
Db      1120 GAAGTT 1125
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RESULT 35  
ID ACA98450  
AC ACA98450 standard; cDNA; 2372 BP.  
XX  
AC ACA98450;

DT 25-JUL-2003 (first entry)  
XX  
DE Human PRO polynucleotide #3.

XX Human; PRO; gene; ss; affinity purification.

OS Homo sapiens.

XX US2003027993-A1.

XX 06-FEB-2003.

XX 02-MAY-2002; 2002US-00063537.

FF

XX

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PR      30-DEC-1998; 98KR-00062142.  
PR      08-MAR-1999; 99WO-US005028.  
PR      14-MAY-1999; 99US-00311832.  
PR      14-MAY-1999; 99WO-US010733.  
PR      25-AUG-1999; 99US-00380137.  
PR      25-AUG-1999; 99US-00380138.  
PR      25-AUG-1999; 99US-00380139.  
PR      25-AUG-1999; 99US-00380142.  
PR      15-SEP-1999; 99US-00397342.  
PR      18-OCT-1999; 99US-00403297.  
PR      12-NOV-1999; 99US-00423844.  
PR      30-DEC-1999; 99WO-US031274.  
PR      18-FEB-2000; 2000WO-US004341.  
PR      01-MAR-2000; 2000WO-US005601.  
PR      02-MAR-2000; 2000WO-US005841.  
PR      21-MAR-2000; 2000WO-US007532.  
PR      22-MAY-2000; 2000WO-US014042.  
PR      02-JUN-2000; 2000WO-US015264.  
PR      22-AUG-2000; 2000US-00644848.  
PR      24-AUG-2000; 2000WO-US023328.  
PR      18-SEP-2000; 2000US-00664610.  
PR      18-SEP-2000; 2000US-00665350.  
PR      08-NOV-2000; 2000US-00709238.  
PR      10-NOV-2000; 2000WO-US030873.  
PR      01-DEC-2000; 2000WO-US032678.  
PR      20-DEC-2000; 2000US-00747259.  
PR      20-DEC-2000; 2000WO-US034956.  
PR      28-FEB-2001; 2001WO-US008520.  
PR      22-MAR-2001; 2001US-00816744.  
PR      10-MAY-2001; 2001US-00854208.  
PR      30-MAY-2001; 2001US-00854280.  
PR      01-JUN-2001; 2001US-00870574.  
PR      05-JUN-2001; 2001WO-US017800.  
PR      29-JUN-2001; 2001US-00874503.  
PR      18-JUL-2001; 2001US-00869599.  
PR      06-DEC-2001; 2001US-00908827.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;  
XX WPI; 2003-417284/39.  
XX P-PSDB; ABU96441.
```

XX New anti-PRO antibody, useful in diagnostic assays for PRO polypeptide or  
PT for affinity purification of PRO from the recombinant cell culture or  
PT natural source.

XX Disclosure; Fig 5; 236pp; English.

XX The invention relates to an antibody which binds to a PRO polypeptide.  
CC The antibody is useful in diagnostic assays for the PRO polypeptide or  
CC for affinity purification of PRO from a recombinant cell culture or  
CC natural source. Sequences ACA98448-ACA98531 represent cDNA molecules  
CC encoding human PRO polypeptides of the invention

XX Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

XX Alignment Scores:

Pred. No.:	1-49e-304	Length:	2372
Score:	322.00	Matches:	322
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	7	Gaps:	0

US-10-079-111-1 (1-322) x ACA98450 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20

Db 160 ATGGCCAGGTGCTTACGCTGGTGTGCTTCTCACTTCATTCGACACGAGGCTCCTG 219



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QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAAGGCTCTTGGCTGCAGAAAGCTTCCATCCAGGTGTATGCAGAAATATGGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCTTGTGAGCAAAAGGGAACACAGCAGCTGATTTACAGAACTAAGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGTGGGACTAAGTTTGGCGGCAAGACCAAGTGAACAGCCTTGAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAACCTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGTCATCTCTAGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAAAACCCCAAGGTGGGAAAATGGGTGGGTGCTCTGATTTGGAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaIleTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATATTACCAACCAAGATCCCATATTCAACACTCAAACTCAACAAACAAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTGTGAGTACAGTACCTACTCGGTGGCATCCCTTACTCTACATACCTGCG 699
QY 181 ProThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCTCTCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTACAGAAAGTTTTTATGAAACTAGCACCATGTCTACAGAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db 820 GAAATATAAGCAGCATTCAGAAATGAAGCTGGGTGGGTGGAGGTGTCCTCCAGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGTGTGCTCTCTCTCTCTTTGGTGTGCAGCTGTGTGGATTTTGTCTATGTCAAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCTTCCCTTTTCAACAACAGAAATCAGCAAGAAATGTCGAACCC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAAGTAGTAAGAGGAGAGGCCAATGATGACCAACCTTAATGAGGAATCAAGAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAAACCCAGAGAGTCCAAGAGTCCAAGAAACTACCGTGGATGCTGGAGGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125

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RESULT 36

ID ACA63375

XX ACA63375 standard; cDNA; 2372 BP.

AC ACA63375;

XX ACA63375;

DT 13-JUN-2003 (first entry)

XX

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DE CDNA encoding human PRO polypeptide #3.
XX Human; PRO polypeptide; secreted and transmembrane protein;
KW Anti-PRO antibody; diagnostic assay; gene expression; gene; ss.
XX Homo sapiens.
XX US2003023042-A1.
XX 30-JAN-2003.
XX 01-MAY-2002; 2002US-00063502.
XX 06-DEC-2001; 2001US-00068867.
XX (GETH ) GENENTECH INC.
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX WPI; 2003-331484/31.
DR P-PSDB; ABU72111.
XX Novel monoclonal antibody that binds to secreted and transmembrane
PT polypeptide, useful for detecting and purifying the polypeptide and also
PT for treating conditions responsive to the antibody.
XX PS Disclosure; Fig 5; 408pp; English.
XX CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a medicament
CC useful in the treatment of a condition responsive to anti-PRO antibody.
CC Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting
CC its expression in specific cells, tissues or serum, and for affinity
CC purification of PRO from recombinant cell culture or natural sources.
CC ACA63373-ACA63456 represent cDNA sequences encoding the human PRO
CC polypeptides of the invention
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

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## Alignment Scores:

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Prod. No.: 1.49e-304 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

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US-10-079-111-1 (1-322) x ACA63375 (1-2372)

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QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACACAGGCTCTCG 219
QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTCGTGTCAGAGAGCTTTCCATCCAGGTGTGTCAGAAATATGGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCTTGTGAGCAAAAGGGAACACAGCAGCTGAATTTACAGAACTAAGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGTGGGACTAAGTTTGGCGGCAAGACCAAGTGAACAGCCTTGAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAACCTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGTCATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120

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Db	460	AGCCCAACCCAGTGTGGAAAAATGGGTGGGTCTCTGATTTGGAGGTTCCAGTG	519	XX	17-SEP-1997;	97US-0059113P.
				PR	17-SEP-1997;	97US-0059115P.
QY	121	SerArgGlnPheAlaIaIaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140	PR	17-SEP-1997;	97US-0059117P.
				PR	17-SEP-1997;	97US-0059119P.
Db	520	AGCCGACAGTTTGCACGCTATTGTTACAACTCATCTGATCTTGGACTAACTCGTGCATT	579	PR	17-SEP-1997;	97US-0059121P.
				PR	17-SEP-1997;	97US-0059122P.
QY	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160	PR	17-SEP-1997;	97US-0059184P.
				PR	18-SEP-1997;	97US-0059263P.
Db	580	CCAGAAATATTATCACCAACCAAGATCCCATATTCAACACTCAAACTCAACACACAAACA	639	PR	18-SEP-1997;	97US-0059266P.
				PR	15-OCT-1997;	97US-0062125P.
QY	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180	PR	17-OCT-1997;	97US-0062285P.
				PR	17-OCT-1997;	97US-0062287P.
Db	640	GAATTTATGTAGTCAGTACCTACTCTGGTGGCATCCCTTACTCTACAACTACTGCC	699	PR	21-OCT-1997;	97US-0063486P.
				PR	24-OCT-1997;	97US-0062814P.
QY	181	ProThrThrThrProProAlaSerThrSerIleProArgArgLysLysLeuIle	200	PR	24-OCT-1997;	97US-0062816P.
				PR	24-OCT-1997;	97US-0063045P.
Db	700	CCTACTACTACTCTCTCTCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	759	PR	24-OCT-1997;	97US-0063120P.
				PR	24-OCT-1997;	97US-0063121P.
QY	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220	PR	24-OCT-1997;	97US-0063127P.
				PR	24-OCT-1997;	97US-0063128P.
Db	760	TGTGTACAGAAATTTTATGGAACACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	819	PR	27-OCT-1997;	97US-0063327P.
				PR	27-OCT-1997;	97US-0063329P.
QY	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu	240	PR	28-OCT-1997;	97US-0063541P.
				PR	28-OCT-1997;	97US-0063542P.
Db	820	GAATAATAAGCAGCATTCAGAAATGAAGCTGTGGGTTTGGAGGTGTCCCCACGGCTCTG	879	PR	28-OCT-1997;	97US-0063544P.
				PR	28-OCT-1997;	97US-0063549P.
QY	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260	PR	28-OCT-1997;	97US-0063550P.
				PR	29-OCT-1997;	97US-0063564P.
Db	880	CTAGTCTTGCTCTCTCTCTCTCTTCTTGTGTGTGCTGTGCTGTGCTGTGCTGTGCTG	939	PR	29-OCT-1997;	97US-0063435P.
				PR	29-OCT-1997;	97US-0063704P.
QY	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280	PR	29-OCT-1997;	97US-0063732P.
				PR	29-OCT-1997;	97US-0063734P.
Db	940	AGTATGTGAAGCCCTTCCCTTTTACAAACAAGATCAGCAGAGGAATGATCGAAACC	999	PR	29-OCT-1997;	97US-0063735P.
				PR	29-OCT-1997;	97US-0063738P.
QY	281	LysValValLysGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300	PR	31-OCT-1997;	97US-0064215P.
				PR	31-OCT-1997;	97US-0063870P.
Db	1000	AAAGTAGTAAGAGAGAGAGGCAATGATAGCAACCTTAATGAGGAATCAAGAAAACT	1059	PR	31-OCT-1997;	97US-0064103P.
				PR	03-NOV-1997;	97US-0064248P.
QY	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320	PR	07-NOV-1997;	97US-0064809P.
				PR	12-NOV-1997;	97US-0065186P.
Db	1060	GATAAAACCCAGAGAGTCCAAGAGTCCAAGAGTCCAAGAGTCCAAGAGTCCAAGAGT	1119	PR	17-NOV-1997;	97US-0065846P.
				PR	18-NOV-1997;	97US-0065693P.
QY	321	GluVal 322		PR	21-NOV-1997;	97US-0066120P.
				PR	21-NOV-1997;	97US-0066364P.
Db	1120	GAAGTT 1125		PR	24-NOV-1997;	97US-0066453P.
				PR	24-NOV-1997;	97US-0066466P.
RESULT 37				PR	24-NOV-1997;	97US-0066511P.
ACD19807				PR	24-NOV-1997;	97US-0066770P.
ID	ACD19807 standard; cDNA; 2372 BP.			PR	24-NOV-1997;	97US-0066772P.
XX				PR	25-NOV-1997;	97US-0066840P.
AC	ACD19807;			PR	12-DEC-1997;	97US-0069425P.
XX				PR	04-JUN-1998;	98US-0088026P.
DT	22-AUG-2003 (first entry)			PR	10-SEP-1998;	98US-0099803P.
XX				PR	10-SEP-1998;	98WO-US018824.
DE	Human secreted / transmembrane polypeptide PRO263 cDNA.			PR	14-SEP-1998;	98US-0100262P.
XX				PR	14-SEP-1998;	98WO-US019177.
KW	Human; ss; gene; gene therapy; apoptosis; bleeding; tumour; ALS;			PR	16-SEP-1998;	98WO-US019330.
KW	gynaecological disease; hysterectomy; angiogenesis; skin disease; cancer;			PR	17-SEP-1998;	98US-0100858P.
KW	coronary ischaemic condition; gastrointestinal mucosa disorder; asthma;			PR	17-SEP-1998;	98WO-US019437.
KW	mucosal lesion repair; keratinocyte differentiation; psoriasis;			PR	13-OCT-1998;	98US-0104080P.
KW	Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;			PR	20-NOV-1998;	98US-0109310P.
KW	neuropathy; blood coagulation cascade disorder; thrombosis; haemorrhage;			PR	01-DEC-1998;	98WO-US025108.
KW	neurodegenerative disease; endometrial bleeding; wound healing;			PR	22-DEC-1998;	98US-0113296P.
KW	tissue repair; rheumatoid arthritis; multiple sclerosis; tissue typing.			PR	07-JUL-1999;	99US-0143048P.
XX				PR	26-JUL-1999;	99US-0145698P.
OS	Homo sapiens.			PR	28-JUL-1999;	99US-0146222P.
XX	US2003027143-A1.			PR	08-SEP-1999;	99WO-US020594.
PN				PR	13-SEP-1999;	99WO-US020944.
XX				PR	15-SEP-1999;	99WO-US021090.
PD	06-FEB-2003.			PR	15-SEP-1999;	99WO-US021547.
XX				PR	05-OCT-1999;	99WO-US023089.
PF	16-JUL-2001; 2001US-00906838.			PR	29-NOV-1999;	99WO-US028214.



AC ADB29405;  
 XX DT 20-NOV-2003 (first entry)  
 XX DE DE  
 XX DE Human secreted/transmembrane protein cDNA, #40.  
 KW Human; gene; ss; PRO; secreted; transmembrane; gastrointestinal mucosa;  
 KW mucosal lesion; skin disease; keratinocyte differentiation; psoriasis;  
 KW Parkinson's disease; Alzheimer's diseases; amyotrophic lateral sclerosis;  
 KW ALS; neuropathy; cell growth; cancer; tumour; viral infection;  
 KW neurodegenerative disease; antithrombotic agent; haemorrhage;  
 KW endometrial bleeding angiogenesis; kidney tissue; apoptosis; therapeutic;  
 KW tissue typing; immunohistochemical staining; gene therapy; nootropic;  
 KW neuroprotective; cytostatic; virucide; anticoagulant.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2003092002-A1.  
 XX  
 XX 15-MAY-2003.  
 XX  
 XX 10-JUL-2001; 2001US-00902615.  
 XX  
 PR 17-SEP-1997; 97US-0059113P.  
 PR 17-SEP-1997; 97US-0059115P.  
 PR 17-SEP-1997; 97US-0059117P.  
 PR 17-SEP-1997; 97US-0059119P.  
 PR 17-SEP-1997; 97US-0059121P.  
 PR 17-SEP-1997; 97US-0059122P.  
 PR 17-SEP-1997; 97US-0059124P.  
 PR 18-SEP-1997; 97US-0059263P.  
 PR 18-SEP-1997; 97US-0059266P.  
 PR 15-OCT-1997; 97US-0062125P.  
 PR 17-OCT-1997; 97US-0062285P.  
 PR 17-OCT-1997; 97US-0062287P.  
 PR 21-OCT-1997; 97US-0063486P.  
 PR 21-OCT-1997; 97US-0062814P.  
 PR 24-OCT-1997; 97US-0062816P.  
 PR 24-OCT-1997; 97US-0063045P.  
 PR 24-OCT-1997; 97US-0063120P.  
 PR 24-OCT-1997; 97US-0063121P.  
 PR 24-OCT-1997; 97US-0063127P.  
 PR 24-OCT-1997; 97US-0063128P.  
 PR 27-OCT-1997; 97US-0063327P.  
 PR 28-OCT-1997; 97US-0063329P.  
 PR 28-OCT-1997; 97US-0063541P.  
 PR 28-OCT-1997; 97US-0063542P.  
 PR 28-OCT-1997; 97US-0063544P.  
 PR 28-OCT-1997; 97US-0063549P.  
 PR 28-OCT-1997; 97US-0063550P.  
 PR 28-OCT-1997; 97US-0063564P.  
 PR 29-OCT-1997; 97US-0063435P.  
 PR 29-OCT-1997; 97US-0063704P.  
 PR 29-OCT-1997; 97US-0063732P.  
 PR 29-OCT-1997; 97US-0063734P.  
 PR 29-OCT-1997; 97US-0063735P.  
 PR 29-OCT-1997; 97US-0063738P.  
 PR 29-OCT-1997; 97US-0064215P.  
 PR 31-OCT-1997; 97US-0063870P.  
 PR 31-OCT-1997; 97US-0064103P.  
 PR 03-NOV-1997; 97US-0064248P.  
 PR 07-NOV-1997; 97US-0064809P.  
 PR 12-NOV-1997; 97US-0065186P.  
 PR 17-NOV-1997; 97US-0065846P.  
 PR 18-NOV-1997; 97US-0065693P.  
 PR 21-NOV-1997; 97US-0066120P.  
 PR 21-NOV-1997; 97US-0066364P.  
 PR 24-NOV-1997; 97US-0066453P.  
 PR 24-NOV-1997; 97US-0066466P.  
 PR 24-NOV-1997; 97US-0066511P.  
 PR 24-NOV-1997; 97US-0066770P.  
 PR 24-NOV-1997; 97US-0066772P.  
 PR 25-NOV-1997; 97US-0066840P.

PR 12-DEC-1997; 97US-0069425P.  
 PR 04-JUN-1998; 98US-0088026P.  
 PR 10-SEP-1998; 98US-0099803P.  
 PR 10-SEP-1998; 98WO-US018824.  
 PR 14-SEP-1998; 98US-0100262P.  
 PR 14-SEP-1998; 98WO-US019177.  
 PR 16-SEP-1998; 98WO-US019330.  
 PR 17-SEP-1998; 98US-0100858P.  
 PR 17-SEP-1998; 98WO-US019437.  
 PR 13-OCT-1998; 98US-0104080P.  
 PR 20-NOV-1998; 98US-0109304P.  
 PR 01-DEC-1998; 98WO-US025108.  
 PR 22-DEC-1998; 98US-0113296P.  
 PR 07-JUL-1999; 99US-0143048P.  
 PR 26-JUL-1999; 99US-0145698P.  
 PR 28-JUL-1999; 99US-0146222P.  
 PR 08-SEP-1999; 99WO-US020594.  
 PR 13-SEP-1999; 99WO-US020944.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 15-SEP-1999; 99WO-US021547.  
 PR 05-OCT-1999; 99WO-US023089.  
 PR 29-NOV-1999; 99WO-US028214.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 02-DEC-1999; 99WO-US028564.  
 PR 02-DEC-1999; 99WO-US028565.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 20-DEC-1999; 99WO-US030911.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 11-FEB-2000; 2000WO-US003565.  
 PR 22-FEB-2000; 2000WO-US004414.  
 PR 24-FEB-2000; 2000WO-US005044.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 30-MAR-2000; 2000WO-US007377.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 18-SEP-2000; 2000US-00665350.  
 XX  
 (GETH ) GENENTECH INC.  
 XX  
 XX Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;  
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;  
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin LJ;  
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;  
 PI Williams PM, Wood WI;  
 DR WPI; 2003-765473/72.  
 DR P-PSDB; ADB29406.  
 XX  
 PT Novel isolated native PRO polypeptide useful for treating Parkinson's  
 PT disease, enterocolitis, Zollinger-Ellison syndrome gastrointestinal  
 PT ulceration, Alzheimer's disease, amyotrophic lateral sclerosis, Usher  
 PT syndrome.  
 XX  
 PS Claim 2; Fig 73; 469pp; English.  
 XX  
 CC The invention discloses isolated PRO secreted/transmembrane polypeptides  
 CC and the nucleic acid encoding them. The polypeptides can be used to raise  
 CC antibodies that specifically bind to the PRO polypeptide, for linking a  
 CC bioactive molecule to a cell expressing a PRO protein and for modulating  
 CC at least one biological activity of a cell. PRO polypeptides are useful  
 CC for detecting other PRO polypeptides in a sample and for linking a  
 CC bioactive molecule to a cell expressing a PRO polypeptide. The PRO  
 CC polypeptide antibodies are useful for modulating the biological activity  
 CC of a cell expressing PRO polypeptides. PRO polypeptides are also useful  
 CC for treating disorders associated with the preservation and maintenance  
 CC of gastrointestinal mucosa and the repair of acute and chronic mucosal  
 CC lesions, skin diseases associated with abnormal keratinocyte  
 CC differentiation (e.g. psoriasis), Parkinson's disease, Alzheimer's

CC diseases, amyotrophic lateral sclerosis (ALS), neuropathies and  
 CC additionally, disease related to uncontrolled cell growth, e.g. cancer.  
 CC PRO polypeptides also serves as tumour specific antigens which may be  
 CC exploited as therapeutic targets for anti-tumour drugs, and are also  
 CC employed therapeutically in vivo for lessening the effects of viral  
 CC infection. The PRO polypeptides can be also used in assays to determine  
 CC if it has a role in neurodegenerative diseases or their reversal, as an  
 CC antithrombotic agent with reduced risk for haemorrhage as compared with  
 CC heparin, in treating other PRO-associated disorders, in modulating  
 CC endometrial bleeding angiogenesis, and may also have an effect on kidney  
 CC tissue. PRO polypeptides and their portions affect the expression of  
 CC genes which have a role in apoptosis. The polynucleotides are useful in  
 CC molecular biology including uses as hybridisation probes for cDNA library  
 CC to isolate the full-length PRO cDNA or to isolate other cDNAs, in  
 CC chromosome and gene mapping, in the generation of antisense RNA and DNA,  
 CC for preparing PRO polypeptides, for generating transgenic animals or  
 CC knockout animals which are useful in the development and screening of  
 CC therapeutically useful reagents, as probes and for the genetic analysis  
 CC of individuals with genetic disorders as well as for recombinantly  
 CC expressing the protein and for chromosome identification. The proteins  
 CC are useful as molecular marker for protein electrophoresis purposes, as  
 CC therapeutic agents, for screening compounds to identify those that mimic  
 CC the PRO polypeptide (agonists) or prevent the effect of the PRO  
 CC polypeptide (antagonists). The polynucleotides and proteins are useful  
 CC for tissue typing. PRO antibodies are useful for immunohistochemical  
 CC staining and/or assay of sample fluids. Anti-PRO antibodies are useful in  
 CC diagnostic assays for PRO e.g. detecting its expression in specific  
 CC cells, tissues or serum and for affinity purification of PRO from  
 CC recombinant cell culture or natural sources. The PRO genes may also be  
 CC used in gene therapy, particularly for replacing a defective gene. The  
 CC sequence presented is a gene encoding a PRO polynucleotide of the  
 CC invention.

XX  
 SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1,49e-304 Length: 2372  
 Score: 322.00 Matches: 322  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 8 Gaps: 0

US-10-079-111-1 (1-322) x ADB29405 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu 20  
 DB 160 ATGGCCAGGTCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCCAGAGGCTCTG 219  
 QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
 DB 220 GTCCCAAGGCTCTTGGCTGCAGNAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGGG 279  
 QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
 DB 280 ATCACCCCTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTCACAGAAGCTAAGGAGGCC 339  
 QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
 DB 340 TGTAGGCTCTGGGACTAAGTTTGGCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 399  
 QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100  
 DB 400 AGCTTTGAAACTTCAGACTATGGCTGGGTGGAGATGGAAATCGTGGTCATCTCTAGAAAT 459  
 QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
 DB 460 AGCCCAAAACCCCAAGTGTGGAAAAATAGGGTGGGTGCTCTGATTTGGAGGTTCCAGTG 519  
 QY 121 SerArgGlnPheAlaIleTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
 DB 520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTGACTTAACCTCGTGCATT 579

QY 141 ProGluIleIleThrThrIysaspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
 DB 580 CCAGAAATTTATCACCAACCAAGATCCATATTCACAACTCAAACTCAACACCAACAACA 639  
 QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
 DB 640 GAATTTATTTGTAGTGACAGTACTTACTCGTGGCATCCCTTACTTCTACATACCTGCC 699  
 QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200  
 DB 700 CCTACTACTACTCTCTCTCCAGCTTCCACTTCTTATTCACGGAGAAAAAATTTGATT 759  
 QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
 DB 760 TGTGTCACAGAAAGTTTTTATGGAACCTAGCACCATGCTCTACAGAAACTGAACCATTTGTT 819  
 QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
 DB 820 GAAATTAAGCAGCATTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 879  
 QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
 DB 880 CTAGTCTTGTCT 939  
 QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
 DB 940 AGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAATCAGCAGAGGAAATGATCGAAACC 999  
 QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
 DB 1000 AAAGTAGTAAAGGAGGAGAGGAGGCCAATGATGACCACTTAATGAGGAATCAAGAAACT 1059  
 QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
 DB 1060 GATAAAACCCAGAGAGTCCAAGAGTCCAAGAAACTACCGTGCATCGCTGGAAGCT 1119  
 QY 321 GluVal 322  
 DB 1120 GAAGTT 1125  
 RESULT 39  
 ADB17062  
 ID ADB17062 standard; cDNA; 2372 BP.  
 AC ADB17062;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Human cDNA clone (SeqID 5) encoding the transmembrane PRO protein.  
 XX  
 KW ss; gene; PRO; transmembrane; immunoconjugate; cytotoxic; gene therapy;  
 KW cytostatic; cancer; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003050462-A1.  
 XX  
 PD 13-MAR-2003.  
 XX  
 PF 03-MAY-2002; 2002US-00063598.  
 XX  
 PR 30-DEC-1998; 98KR-00062142.  
 PR 08-MAR-1999; 99WO-US005028.  
 PR 14-MAY-1999; 99US-00311832.  
 PR 14-MAY-1999; 99WO-US010733.  
 PR 25-AUG-1999; 99US-00380137.  
 PR 25-AUG-1999; 99US-00380138.  
 PR 25-AUG-1999; 99US-00380139.  
 PR 25-AUG-1999; 99US-00380142.  
 PR 15-SEP-1999; 99US-00397342.  
 PR 18-OCT-1999; 99US-00403297.  
 PR 12-NOV-1999; 99US-00423844.  
 PR 30-DEC-1999; 99WO-US031274.



XX Homo sapiens.  
 OS US2003018172-AL.  
 FN  
 XX  
 XX 23-JAN-2003.  
 PD  
 XX  
 XX 01-MAY-2002; 2002US-00063513.  
 PF  
 XX  
 XX 06-DEC-2001; 2001US-00006867.  
 PR  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;  
 XX  
 XX WPI; 2003-479475/45.  
 DR P-PSDB; ABO44241.  
 DR  
 XX  
 XX Isolated antibody specifically binding a PRO polypeptide, useful for the  
 PT diagnosis and treatment of disorders with the aberrant expression or  
 PT activity of the PRO polypeptide, such as tumor conditions and cancer.  
 XX  
 XX Disclosure; Fig 5; 409pp; English.  
 PS  
 XX The invention relates to an antibody that binds to a fully defined PRO  
 CC polypeptide. The antibody is useful for the diagnosis, prevention and/or  
 CC treatment of disorders associated with the aberrant expression and/or  
 CC activity of the PRO polypeptide, such as tumour conditions and cancer.  
 CC They can also be used to generate transgenic or knockout animals useful  
 CC in the development and screening of therapeutically useful reagents. The  
 CC PRO polypeptides and encoding nucleic acids can be used as molecular  
 CC weight markers for protein electrophoresis, chromosome identification and  
 CC tissue typing. The antibodies may be used in various diagnostic,  
 CC competitive binding and/or immunoprecipitation assays. The present  
 CC sequence represents cDNA encoding a human secreted and transmembrane PRO  
 CC polypeptide  
 SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: Length: 2372  
 Score: 322.00 Matches: 322  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 8 Gaps: 0  
 US-10-079-111-1 (1-322) x ACH03578 (1-2372)  
 QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20  
 DB 160 ATGGCCAGGTCTTCAGCCTGGTGTGCTTCACCTTCATCTCCATCTGGACCCAGGCTCTCG 219  
 QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
 DB 220 GTCCAGGCTCTTCGGTGCAGAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGG 279  
 QY 41 IleThrLeuValSerLysLysAlaSerGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
 DB 280 ATCACCCCTGTGAGCAAAAGGCGAACACAGCAGCTGAATTTCCACAGAACTTAAGGAGGCC 339  
 QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
 DB 340 TGTAGGCTCTGGGACTTAAGTTTGGCCGACAGGACCAAGTTGAAACAGCCCTTGAAGCT 399  
 QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100  
 DB 400 AGCTTTGAACCTTGACGCTATGGCTGGGTGGAGATGGATTCTGGTCTCTTAGATT 459  
 QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
 DB 460 AGCCCAAAACCCCAAGTGGGAAAAAATGGGTGGGTGCTCTGATTGGGAAGGTTCAGTG 519

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
 DB 520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACCTTGGACTAACTCGTCATT 579  
 QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
 DB 580 CCAGAAATTTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA 639  
 QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
 DB 640 GAATTTATTGTCAGTGACAGTACTCTCGGTGGCATCCCTTACTCTACAATACCTGCC 699  
 QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200  
 DB 700 CCTACTACTACTCTCTCTCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759  
 QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
 DB 760 TGTGTACAGAAAGTTTTTATGGAACTAGCACCATGTCTACAGAACTGAACCATTTGTT 819  
 QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240  
 DB 820 GAAATATAAGCAGCATTTCAAGATGAAGCTGCTGGGTTTGAGGTGTCCTCCACGGCTCTG 879  
 QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
 DB 880 CTAGTGTCTGCTCTCTCTCTCTGCTGCTGAGCTGCTGTTGGATTTTGTATGTCAAA 939  
 QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
 DB 940 AGTATGTGAAGCCCTTCCCTTTTCAAAACAAGATTCACAGAAAGAAATGTCGAAACC 999  
 QY 281 LysValValLysGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
 DB 1000 AAAGTAGTAAAGGAGGAGAGGCAATGATGCAACCTTAATGAGGAATCAAGAAACT 1059  
 QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
 DB 1060 GATAAAACCCAGAGAGTCCAAGAGTCCAAGAAAACTACCGTGGATGCTGGGAAGCT 1119  
 QY 321 GluVal 322  
 DB 1120 GAAGTT 1125  
 RESULT 41  
 ADA18261  
 ID ADA18261 standard; cDNA; 2372 BP.  
 XX  
 AC ADA18261;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Human secreted/transmembrane protein cDNA, #40.  
 XX  
 KW Human; gene; ss; PRO; secreted; transmembrane; gastrointestinal mucosa;  
 KW mucosal lesion; skin disease; keratinocyte differentiation; psoriasis;  
 KW Parkinson's disease; Alzheimer's diseases; amyotrophic lateral sclerosis;  
 KW ALS; neuropathy; cell growth; cancer; tumour; viral infection;  
 KW neurodegenerative disease; antithrombotic agent; haemorrhage;  
 KW endometrial bleeding angiogenesis; kidney tissue; apoptosis; therapeutic;  
 KW tissue typing; immunohistochemical staining; gene therapy; neurotropic;  
 KW neuroprotective; cytostatic; virucide; anticoagulant.  
 OS Homo sapiens.  
 XX  
 XX US2003039971-AL.  
 PN  
 XX 27-FEB-2003.  
 PD  
 XX  
 XX 16-JUL-2001; 2001US-00906646.  
 PF  
 XX  
 XX 17-SEP-1997; 97US-0059113P.  
 PR

PR 17-SEP-1997; 97US-0059115P.  
PR 17-SEP-1997; 97US-0059117P.  
PR 17-SEP-1997; 97US-0059119P.  
PR 17-SEP-1997; 97US-0059121P.  
PR 17-SEP-1997; 97US-0059122P.  
PR 17-SEP-1997; 97US-0059184P.  
PR 18-SEP-1997; 97US-0059263P.  
PR 18-SEP-1997; 97US-0059266P.  
PR 15-OCT-1997; 97US-0062125P.  
PR 17-OCT-1997; 97US-0062285P.  
PR 17-OCT-1997; 97US-0062287P.  
PR 21-OCT-1997; 97US-0063486P.  
PR 24-OCT-1997; 97US-0062814P.  
PR 24-OCT-1997; 97US-0062816P.  
PR 24-OCT-1997; 97US-0063045P.  
PR 24-OCT-1997; 97US-0063120P.  
PR 24-OCT-1997; 97US-0063121P.  
PR 24-OCT-1997; 97US-0063127P.  
PR 24-OCT-1997; 97US-0063128P.  
PR 27-OCT-1997; 97US-0063327P.  
PR 27-OCT-1997; 97US-0063329P.  
PR 28-OCT-1997; 97US-0063541P.  
PR 28-OCT-1997; 97US-0063542P.  
PR 28-OCT-1997; 97US-0063544P.  
PR 28-OCT-1997; 97US-0063549P.  
PR 28-OCT-1997; 97US-0063550P.  
PR 28-OCT-1997; 97US-0063564P.  
PR 29-OCT-1997; 97US-0063435P.  
PR 29-OCT-1997; 97US-0063704P.  
PR 29-OCT-1997; 97US-0063732P.  
PR 29-OCT-1997; 97US-0063734P.  
PR 29-OCT-1997; 97US-0063735P.  
PR 29-OCT-1997; 97US-0063738P.  
PR 31-OCT-1997; 97US-0064215P.  
PR 31-OCT-1997; 97US-0063870P.  
PR 03-NOV-1997; 97US-0064103P.  
PR 07-NOV-1997; 97US-0064248P.  
PR 12-NOV-1997; 97US-0064809P.  
PR 17-NOV-1997; 97US-0065186P.  
PR 18-NOV-1997; 97US-0065693P.  
PR 21-NOV-1997; 97US-0066120P.  
PR 21-NOV-1997; 97US-0066364P.  
PR 24-NOV-1997; 97US-0066453P.  
PR 24-NOV-1997; 97US-0066466P.  
PR 24-NOV-1997; 97US-0066511P.  
PR 24-NOV-1997; 97US-0066770P.  
PR 25-NOV-1997; 97US-0066772P.  
PR 12-DEC-1997; 97US-0066840P.  
PR 04-JUN-1998; 97US-0069425P.  
PR 10-SEP-1998; 98US-0088026P.  
PR 10-SEP-1998; 98US-0099803P.  
PR 14-SEP-1998; 98US-0099804P.  
PR 14-SEP-1998; 98US-0100262P.  
PR 16-SEP-1998; 98US-0101917P.  
PR 16-SEP-1998; 98US-0101930P.  
PR 17-SEP-1998; 98US-0100858P.  
PR 17-SEP-1998; 98US-0101943P.  
PR 13-OCT-1998; 98US-0104080P.  
PR 20-NOV-1998; 98US-0109304P.  
PR 01-DEC-1998; 98US-0109304P.  
PR 22-DEC-1998; 98US-0113296P.  
PR 07-JUL-1999; 99US-0143048P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 28-JUL-1999; 99US-0146222P.  
PR 08-SEP-1999; 99US-0146222P.  
PR 13-SEP-1999; 99US-0146222P.  
PR 15-SEP-1999; 99US-0146222P.  
PR 15-SEP-1999; 99US-0146222P.  
PR 15-SEP-1999; 99US-0146222P.  
PR 05-OCT-1999; 99US-0146222P.  
PR 29-NOV-1999; 99US-0146222P.  
PR 30-NOV-1999; 99US-0146222P.  
PR 01-DEC-1999; 99US-0146222P.

PR 02-DEC-1999; 99US-0028564.  
PR 02-DEC-1999; 99US-0028565.  
PR 16-DEC-1999; 99US-0030095.  
PR 20-DEC-1999; 99US-0030911.  
PR 20-DEC-1999; 99US-0030999.  
PR 05-JAN-2000; 2000US-0000219.  
PR 11-FEB-2000; 2000US-0003565.  
PR 22-FEB-2000; 2000US-0004414.  
PR 24-FEB-2000; 2000US-0005004.  
PR 02-MAR-2000; 2000US-0005841.  
PR 20-MAR-2000; 2000US-0007377.  
PR 30-MAR-2000; 2000US-0008439.  
PR 22-MAY-2000; 2000US-0014042.  
PR 02-JUN-2000; 2000US-0015264.  
PR 28-JUL-2000; 2000US-0020710.  
PR 24-AUG-2000; 2000US-0023328.  
PR 18-SEP-2000; 2000US-00665350.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX  
PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;  
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;  
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin LJ;  
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;  
PI Williams PM, Wood WI;  
XX  
XX WPI; 2003-503392/47.  
DR P-PSDB; ADA18262.  
XX  
XX  
PT New secreted and transmembrane polypeptides useful for treating skin,  
PT neurodegenerative diseases, asthma, rheumatoid arthritis, psoriasis and  
PT multiple sclerosis.  
XX  
PS Claim 2; SEQ ID NO 200; 47pp; English.  
XX  
CC The invention discloses isolated PRO secreted/transmembrane polypeptides  
CC and the nucleic acid encoding them. The polypeptides can be used to raise  
CC antibodies that specifically bind to the PRO polypeptide, for linking a  
CC bioactive molecule to a cell expressing a PRO protein and for modulating  
CC at least one biological activity of a cell. PRO polypeptides are useful  
CC for detecting other PRO polypeptides in a sample and for linking a  
CC bioactive molecule to a cell expressing a PRO polypeptide. The PRO  
CC polypeptide antibodies are useful for modulating the biological activity  
CC of a cell expressing PRO polypeptides. PRO polypeptides are also useful  
CC for treating disorders associated with the preservation and maintenance  
CC of gastrointestinal mucosa and the repair of acute and chronic mucosal  
CC lesions, skin diseases associated with abnormal keratinocyte  
CC differentiation (e.g. psoriasis), Parkinson's disease, Alzheimer's  
CC diseases, amyotrophic lateral sclerosis (ALS), neuropathies and  
CC PRO polypeptides also serves as tumour specific antigens which may be  
CC exploited as therapeutic targets for anti-tumour drugs, and are also  
CC employed therapeutically in vivo for lessening the effects of viral  
CC infection. The PRO polypeptides can be also used in assays to determine  
CC if it has a role in neurodegenerative diseases or their reversal, as an  
CC antithrombotic agent with reduced risk for haemorrhage as compared with  
CC heparin, in treating other PRO-associated disorders, in modulating  
CC endometrial bleeding angiogenesis, and may also have an effect on kidney  
CC tissue. PRO polypeptides and their portions affect the expression of  
CC genes which have a role in apoptosis. The polynucleotides are useful in  
CC molecular biology including uses as hybridisation probes for cDNA library  
CC to isolate the full-length PRO cDNA or to isolate other cDNAs, in  
CC chromosome and gene mapping, in the generation of antisense RNA and DNA,  
CC for preparing PRO polypeptides, for generating transgenic animals or  
CC knockout animals which are useful in the development and screening of  
CC therapeutically useful reagents, as probes and for the genetic analysis  
CC of individuals with genetic disorders as well as for recombinantly  
CC expressing the protein and for chromosome identification. The proteins  
CC are useful as molecular marker for protein electrophoresis purposes, as  
CC therapeutic agents, for screening compounds to identify those that mimic  
CC the PRO polypeptide (agonists) or prevent the effect of the PRO  
CC polypeptide (antagonists). The polynucleotides and proteins are useful  
CC for tissue typing. PRO antibodies are useful for immunohistochemical  
CC





PR 29-OCT-1997; 97US-0063738P.  
 PR 29-OCT-1997; 97US-0064215P.  
 PR 31-OCT-1997; 97US-0063870P.  
 PR 31-OCT-1997; 97US-0064103P.  
 PR 03-NOV-1997; 97US-0064248P.  
 PR 07-NOV-1997; 97US-0064809P.  
 PR 12-NOV-1997; 97US-0065186P.  
 PR 17-NOV-1997; 97US-0065846P.  
 PR 18-NOV-1997; 97US-0065893P.  
 PR 21-NOV-1997; 97US-0066120P.  
 PR 21-NOV-1997; 97US-0066364P.  
 PR 24-NOV-1997; 97US-0066453P.  
 PR 24-NOV-1997; 97US-0066466P.  
 PR 24-NOV-1997; 97US-0066511P.  
 PR 24-NOV-1997; 97US-0066770P.  
 PR 24-NOV-1997; 97US-0066772P.  
 PR 25-NOV-1997; 97US-0066840P.  
 PR 12-DEC-1997; 97US-0069425P.  
 PR 04-JUN-1998; 98US-0088026P.  
 PR 10-SEP-1998; 98US-0099803P.  
 PR 10-SEP-1998; 98WO-US018824.  
 PR 14-SEP-1998; 98US-0100262P.  
 PR 14-SEP-1998; 98WO-US019177.  
 PR 16-SEP-1998; 98WO-US019330.  
 PR 17-SEP-1998; 98US-0100858P.  
 PR 17-SEP-1998; 98WO-US019437.  
 PR 13-OCT-1998; 98US-0104080P.  
 PR 20-NOV-1998; 98US-0109304P.  
 PR 01-DEC-1998; 98WO-US025108.  
 PR 22-DEC-1998; 98US-0113296P.  
 PR 07-JUL-1999; 99US-0143048P.  
 PR 26-JUL-1999; 99US-0145698P.  
 PR 28-JUL-1999; 99US-0146222P.  
 PR 08-SEP-1999; 99WO-US020594.  
 PR 13-SEP-1999; 99WO-US020944.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 15-SEP-1999; 99WO-US021547.  
 PR 05-OCT-1999; 99WO-US023089.  
 PR 29-NOV-1999; 99WO-US028214.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 02-DEC-1999; 99WO-US028564.  
 PR 16-DEC-1999; 99WO-US028565.  
 PR 20-DEC-1999; 99WO-US030095.  
 PR 20-DEC-1999; 99WO-US030911.  
 PR 20-DEC-1999; 99WO-US030999.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 11-FEB-2000; 2000WO-US003565.  
 PR 22-FEB-2000; 2000WO-US004414.  
 PR 24-FEB-2000; 2000WO-US005004.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 20-MAR-2000; 2000WO-US007377.  
 PR 20-MAR-2000; 2000WO-US008439.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 08-JUN-2000; 2000WO-US015264.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 18-SEP-2000; 2000US-00665350.  
 XX (GETH ) GENENTECH INC.  
 PA Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;  
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;  
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kijavini LJ;  
 PI Mathew JP, Pan J, Paoni NF, Roy MA, Stewart TA, Thomas D;  
 PI Williams FM, Wood WI;  
 XX WPI; 2003-512316/48.  
 DR P-PSDB; ABO32791.  
 XX  
 DR  
 XX  
 PT New genes and secreted and transmembrane polypeptides (e.g. PRO245 or  
 PT PRO1868), useful for treating or diagnosing e.g. cancers,  
 PT atherosclerosis, infertility, stroke, AIDS or multiple sclerosis in

PT mammals.  
 XX  
 PS  
 XX Claim 2; Fig 73; 476pp; English.  
 CC The invention relates to an isolated nucleic acid molecule comprising a  
 CC sequence with at least 80% identity to: (a) a nucleotide encoding any of  
 CC 61 PRO (secreted and transmembrane protein) polypeptides appearing as  
 CC ABO32756-ABO32816; or (b) any of 61 nucleotide sequences having 50-4053bp  
 CC fully defined in the specification; or the full length coding sequence of  
 CC any these 61 nucleotide sequences. Also included are the isolated PRO  
 CC polypeptide (lacking its associated signal peptide or an extracellular  
 CC domain of the PRO polypeptide, with or lacking its associated signal  
 CC peptide), a vector comprising the nucleic acid molecule, a host cell  
 CC comprising the vector (used to produce the PRO polypeptide), a chimeraic  
 CC molecule comprising the PRO polypeptide fused to a heterologous amino  
 CC acid sequence, an anti-PRO antibody, detecting PRO245 or PRO1868  
 CC or PRO1868 polypeptide and modulating at least one of these PRO  
 CC polypeptides, linking a bioactive molecule to a cell expressing a PRO245  
 CC or PRO1868 polypeptide and modulating at least one biological activity of  
 CC a cell expressing the PRO245 or PRO1868 polypeptide. The PRO polypeptides  
 CC or polynucleotides are useful as pharmaceuticals, diagnostics, biosensors  
 CC or bioreactors. These are particularly useful for diagnosing or treating  
 CC e.g. inflammations, rheumatoid arthritis, psoriasis, multiple sclerosis,  
 CC atherosclerosis, infertility, birth defects, premature aging, malignancy  
 CC (e.g. cancers), strokes, heart attacks, hypertension, gastrointestinal  
 CC ulcerations, Parkinson's diseases, Alzheimer's disease, or AIDS in  
 CC mammals. These are also useful for modulating cholesterol uptake in the  
 CC body, and in wound healing or tissue repair. The PRO polypeptides are  
 CC useful in drug screening. The PRO polypeptides are also useful as  
 CC molecular weight markers, or for chromosome identification. The PRO genes  
 CC are useful as hybridisation probes, or for screening libraries of human  
 CC cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene  
 CC therapy, particularly for replacing a defective gene. The present  
 CC sequence is a cDNA encoding a PRO polypeptide  
 XX  
 SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1,49e-304 Length: 2372  
 Score: 322.00 Matches: 322  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 8 Gaps: 0  
 US-10-079-111-1 (1-322) x ACD66954 (1-2372)  
 QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20  
 Db 160 ATGGCCAGGTGCTTCAGCGCTGGTGTGTTCTCTCACTTCATCGACACGAGGCTCCTG 219  
 QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40  
 Db 220 GTCCAAGGCTCTTTGCGTGCAGAGAGCTTTCCATCCAGGTGTCATGAGAAATATGGGG 279  
 QY 41 IleThrLeuValSerIleValAlaAsnGlnGlnLeuAsnPheThrGluAlaValGluAla 60  
 Db 280 ATCACCTTGTGAGCAAAAGCGCAACAGCAGCTGGAATTTCCACAGAGCTAAGGAGGCC 339  
 QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyIleValSerGlnValGluThrAlaLeuLysAla 80  
 Db 340 TGTAGCTGCTGGGACTAAGTTTGGCCGCAAGACCAAGTTGAACAGCCTTGAAGCT 399  
 QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100  
 Db 400 AGCTTTGAAACTTGCAGCTATGCGTGGGTTCGAGATGAGATTCTGCTCATCTCTAGGATT 459  
 QY 101 SerProAsnProLysCysGlyIleValGlyValGlyValLeuIleTrpIleValProVal 120  
 Db 460 AGCCCAACCCCAAGTGTGGGAAAATGCGGTGGGTGCTCTGATTGGAAGGTTCCAGTG 519  
 QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140

Db 520 AGCCGACAGCTTGGAGCCTATTGTTTACAACTCATCTGATACCTTGGACTAACTCGTGCAAT 579  
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
Db 580 CCAGAAATATCACCACCAAGATCCATATTCAACACTCAAACTGCAACACAAACA 639  
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
Db 640 GAATTTATGTGAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTCAATACCTGCG 699  
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgLysLysLeuIle 200  
Db 700 CCTACTACTACT 759  
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
Db 760 TGTGTGCACAGAAGTTTTTATGGAAGTACAGCATGTCTTACAGAACTGAACCATTTGTT 819  
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
Db 820 GAAATTAAGCAGCATTCAGATGAGCTGTGGTTTGGAGGTGTCCTCCACGGCTCTG 879  
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
Db 880 CTAGTGCTTGCT 939  
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
Db 940 AGGTATGTGAAGGCT 999  
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
Db 1000 AAAGTAGTAAAGAGGAGAGAGGCCAATGATGCAACCTTANTAGAGNATCAAGAAACT 1059  
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
Db 1060 GATAAAACCCAGAGAGTCCAAGAGTCCAAGAGTCCAAGCAAACTACCGTGCATGCTGGAAGCT 1119  
QY 321 GluVal 322  
Db 1120 GAAGTT 1125

RESULT 43  
ADA19867  
ID ADA19867 standard; cDNA; 2372 BP.

AC ADA19867;  
DT 20-NOV-2003 (first entry)  
XX Novel human secreted and transmembrane protein PRO263 cDNA.

DE human; PRO; membrane bound protein; membrane bound receptor;  
KW cell proliferation; cell migration; cell differentiation;  
KW mitogenic factor; survival factor; cytotoxic factor;  
KW differentiation factor; neuropeptide; hormone; cell receptor;  
KW receptor-ligand interaction; cytostatic; chondrocyte; tumour; ss; gene.

OS Homo sapiens.  
XX US2003069394-A1.  
PN 10-APR-2003.  
XX

XX 02-MAY-2002; 2002US-00063567.

PR 30-DEC-1998; 98XK-00062142.  
PR 08-MAR-1999; 99WO-US005028.  
PR 14-MAY-1999; 99US-00311832.  
PR 14-MAY-1999; 99WO-US010733.  
PR 25-AUG-1999; 99US-00380137.  
PR 25-AUG-1999; 99US-00380138.  
PR 25-AUG-1999; 99US-00380139.

PR 25-AUG-1999; 99US-00380142.  
PR 15-SEP-1999; 99US-00397342.  
PR 18-OCT-1999; 99US-00403297.  
PR 12-NOV-1999; 99US-00423844.  
PR 30-DEC-1999; 99WO-US031274.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 21-MAR-2000; 2000WO-US005841.  
PR 02-MAY-2000; 2000WO-US014042.  
PR 22-JUN-2000; 2000WO-US015264.  
PR 22-AUG-2000; 2000US-00644848.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 18-SEP-2000; 2000US-00664610.  
PR 18-SEP-2000; 2000US-00665350.  
PR 08-NOV-2000; 2000US-00709238.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 28-DEC-2000; 2000WO-US034956.  
PR 22-MAR-2001; 2001US-00816744.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 30-MAY-2001; 2001US-00870574.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 05-JUN-2001; 2001US-00874503.  
PR 29-JUN-2001; 2001US-00869599.  
PR 18-JUL-2001; 2001US-00908827.  
PR 06-DEC-2001; 2001US-00006867.

(GETH ) GENENTECH INC.

Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;  
WPI; 2003-669950/63.  
P-PSDB; ADA19868.

New isolated PRO polypeptide, useful in the preparation of a medicament  
for treating a condition responsive to PRO polypeptide, as therapeutic  
agent e.g. vaccine, and as molecular weight marker.

Disclosure; Fig 5; 239pp; English.

This invention relates to novel nucleic acids encoding human PRO secreted  
and transmembrane proteins. Extracellular proteins play important roles  
in the formation, differentiation and maintenance of multicellular  
organisms. The fate of many individual cells (for example proliferation,  
migration or differentiation) is typically governed by information  
received from other cells and the immediate environment. The information  
is often transmitted by secreted polypeptides (for example mitogenic  
factors, survival factors, cytotoxic factors, differentiation factors,  
neuropeptides and hormones) which are received and interpreted by diverse  
cell receptors or membrane bound proteins. These membrane bound proteins  
and receptors may be of use as pharmaceutical and diagnostic agents, such  
as in the blocking of receptor-ligand interactions. The current invention  
provides the amino acid sequences of novel human membrane bound receptors  
and proteins, along with the cDNA sequences encoding them. The novel  
proteins of the invention may have cytostatic activities through the  
stimulation of chondrocytes. The nucleic acids of the invention may be  
useful for the manufacture of a medicament for diagnosing or treating a  
tumour in a mammal. In addition, they may be useful for measuring or  
detecting the expression of a tumour associated gene. The present  
sequence is a cDNA sequence which encodes a human PRO protein of the  
invention.

SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.49e-304 Length: 2372  
Score: 322.00 Matches: 322  
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	8	Gaps:	0
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Qy	1	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrrPThrThrArgLeuLeu	20
Db	160	ATGGCCAGGTGCTTCAGCCTGGTGTGTCTTCATCTCCATCTGCACACGAGGCTCCTG	219
Qy	21	ValGIndgYSerLeuAtrqAlacluLeuSerIleGlnValSerCysArgIleMetGly	40
Db	220	GTCCAAAGGCTCTTTCGGTGCAGAGAGCTTTCCATCCAGGTGTCAATGCAGAAATATGGGG	279
Qy	41	IleThrIeuValSerLysLysAlaAsnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	280	ATCACCTTGTGAGCAAAAGCGAAACCCAGCAGCTGAATTTACAGAAAGCTAAGAGGACC	339
Qy	61	CysArgLeuLeuGlyIleuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	340	TGTAGCTGCTGGGACTTAAGTTTGGCCGGCAGAGACCAAGTTGAAACAGCCTTGAAGACT	399
Qy	81	SerPheGluThrCysSerTyrGlyTrrPValGlyAspGlyPheValValIleSerArgIle	100
Db	400	AGCTTTGAAACTTCGAGCTATGGCTGGGTTCGAGATGGATTTCGTGGTCACTCTTAGGATT	459
Qy	101	SerProAnProLysCysGlyIysAsnGlyValGlyValLeuIleTrrPlysValProVal	120
Db	460	AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCTGATTGGAAAGTTCCAGTG	519
Qy	121	SerArgGlnPheAlaIaTyCysTyrAsnSerSerAspThrTrrPThrAsnSerCysIle	140
Db	520	AGCCGACAGTTTGCAGCCTATTGTTACAACTCACTGATACCTTGGACTTAATCGTGCAAT	579
Qy	141	ProGluIleIleThrThrLysAspProllePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	580	CCAGAAATTTATCACCAACAAAGATCCCATATTCAACACTCAAACTGCACCAACCAACA	639
Qy	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	640	GAATTTATTTGTCAGTGACAGTACTACTCGGTGGCATCCCTTACTCTACAAATACCTGCC	699
Qy	181	ProThrThrThrProAlaProAlaSerThrSerIleProArgLysLysLeuIle	200
Db	700	CCTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGAGAGAAAAATTGATT	759
Qy	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	760	TGTGTACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCAATTTGTT	819
Qy	221	GluAsnLysAlaIaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Db	820	GAAAAATAAAGCAGCATTTCAAGATGAAGTGTCTGGTGTGGAGGTGTCCTCCACGCGCTCG	879
Qy	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	880	CTAGTGTCTGCTCTCTCTCTTTTGGTGTCTGAGTGTGTTGATGTTTGTATGTCAAA	939
Qy	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr	280
Db	940	AGGTATGTGAAGGCTTTCCCTTTTACAAACAAGAAATCAGCAGAGAGAAATGATCGAAACC	999
Qy	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
Db	1000	AAAGTAGTAAAGGAGGAGAGGCCCAATAGTACCAACCTTAATAGGAATCAAGAAAAACT	1059
Qy	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1060	GATAAAAACCCAGAAAGAGTCCAGAGTCCAAAGCAAAACTACCGTGCATGCTCGAAGCT	1119
Qy	321	GluVal	322
Db	1120	GAAGTT	1125

RESULT 44  
ADBI17250  
ID ADBI17250 standard; cDNA; 2372 BP.  
XX AC  
XX ADBI17250;  
XX  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Human cDNA clone (SeqID 5) encoding the transmembrane PRO protein.  
XX  
XX ss; gene; PRO; transmembrane; immunoconjugate; cytotoxic; gene therapy;  
KW cytostatic; cancer; human.  
XX  
XX  
OS Homo sapiens.  
XX  
XX  
PN US2003050465-A1.  
XX  
PD 13-MAR-2003.  
XX  
XX  
PF 26-AUG-2002; 2002US-00227693.  
XX  
PR 10-AUG-1998; 98US-0096012P.  
PR 02-JUN-1999; 99WO-US012252.  
PR 25-AUG-1999; 99US-00380137.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 06-DEC-2001; 2001US-00006867.  
XX  
XX  
PA (GETH ) GENENTECH INC.  
XX  
XX  
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;  
XX  
XX WPI; 2003-521821/49.  
XX P-PSDB; ADBI17251.  
XX  
XX New PRO nucleic acid, useful for manufacturing a medicament for  
PT diagnosing or treating tumor or for tissue typing.  
XX  
XX  
PS Claim 2; Fig 5; 406pp; English.  
XX  
XX  
CC This invention relates to a novel isolated and secreted PRO polypeptide.  
CC PRO is a transmembrane protein involved in the formation, differentiation  
CC and maintenance of multicellular organisms, and more particularly the  
CC proliferation, differentiation and migration of individual cells. The  
CC invention describes screening compounds to identify PRO polypeptide  
CC agonists and antagonists, anti-PRO antibodies, and immunoconjugates  
CC comprising an antibody conjugated to a cytotoxic agent. Specifically, the  
CC heterologous protein of the chimeric polypeptide is an epitope tag or an  
CC Fc region of an immunoglobulin. Through the use of gene therapy, the PRO  
CC polypeptide is useful for preparing cytostatic compositions for  
CC diagnosing or treating cancer. The polypeptide is also useful as a  
CC molecular weight marker for protein electrophoresis purposes. This  
CC polynucleotide sequence is a native cDNA clone that encodes human PRO  
XX polypeptide, found in the cDNA library of the invention.  
XX  
XX Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

```

Alignment Scores:
Pred. NO.:      1.49e-304      Length:      2372
Score:          322.00         Matches:      322
Percent Similarity: 100.00%      Conservative:  0
Best Local Similarity: 100.00%      Mismatches:   0
Query Match:      100.00%      Indels:       0
DB:               8            Gaps:         0

US-10-079-111-1 (1-322) x ADB17250 (1-2372)

Qy      1  MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db      160  ATGCCCAAGGTCCTCAGCCTGGTGCTTCTCACTTCATCTGGACCAACGAGGCTCCTG 219
Qy      21  ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40

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Db      220  GTCCAGGCTCTTGGTCGACAGAGCTTTTCATCCAGGTGCATGCAAGATTATGGGG 279
Qy      41  IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db      280  ATCACCCCTTGTGAGCAAAAAGGCGAACACGACGAGCTGAATTTACAGAAAGCTAAGGAGGCC 339
Qy      61  CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db      340  TGTAGGCTCTGGGACTAAGTTGGCCGCGACAGGACCAAGTTGAAACAGCCCTTGAAGCT 399
Qy      81  SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle 100
Db      400  AGCTTTGAACCTTGACGCTATGGCTGGGTGGAGATGGATTGGTGCATCTCTAGGATT 459
Qy     101  SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db      460  AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCCTGATTGGAAAGCTTCCAGTG 519
Qy     121  SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db      520  AGCCGACAGTTGACGCCATTGTTTACAACCTCATCTGATCTGGACTTAACCTCGTCATT 579
Qy     141  ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db      580  CCAGAAATTTATCACCAACCAAGATCCCATATTCACACTCAAACTGCAACACAAACA 639
Qy     161  GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db      640  GAAATTTATTTGTCAGTGACAGTACTACTCGGTGGCATGCCCTTACTCTACAATACCTGCC 699
Qy     181  ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db      700  CCTACTACTACTCCTCCTCCTCCAGCTTCCACTTCTATTCACGAGAAAAAATTTGATT 759
Qy     201  CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db      760  TGTGTGCACAGAGTTTATGGAACTAGCACCACTGCTCTACAGAACTGAACCATTTGTT 819
Qy     221  GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db      820  GAAATTAAGCAGCATTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 879
Qy     241  LeuValLeuAlaLeuLeuPheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db      880  CTAGTGCTTCCTCTCTCTCTTGTGCTGCTGAGCTGGTCTGGATTTTGCATATGCAAA 939
Qy     261  ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db      940  AGGTAATGTGAAGCCCTTCCCTTTTACAAACAGAAATCAGCAGAGAAATGATCGAAACC 999
Qy     281  LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db     1000  AAAGTAGTAAGAGGAGAGAGGCAATGATAGCAACCTTAATGAGGAATCAAGAAACT 1059
Qy     301  AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db     1060  GATAAAACCCGAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCGCTGGAAGCT 1119
Qy     321  GluVal 322
Db     1120  GAAGTT 1125
RESULT 45
ACD83115
ID   ACD83115 standard; cDNA; 2372 BP.
XX
AC   ACD83115;
XX
DT   22-SEP-2003 (first entry)
XX
DE   Human PRO polynucleotide #36.
XX
```

```
KW      Human; PRO; gene; ss; secreted polypeptide; transmembrane polypeptide;
KW      abnormal bleeding; gynaecological disease; hysterectomy; mucosal lesion;
KW      coronary ischaemic condition; gastrointestinal mucosa; skin disease; AUS;
KW      keratinocyte differentiation; psoriasis; Parkinson's disease; asthma;
KW      Alzheimer's disease; rheumatoid arthritis; multiple sclerosis; cancer;
KW      amyotrophic lateral sclerosis; neuropathy; uncontrolled cell growth.
XX
OS      Homo sapiens.
XX
PN      US2003044793-A1.
XX
XX      06-MAR-2003.
XX
PF      11-JUL-2001; 2001US-00903786.
XX
PR      17-SEP-1997; 97US-00591113P.
PR      17-SEP-1997; 97US-00591115P.
PR      17-SEP-1997; 97US-00591117P.
PR      17-SEP-1997; 97US-00591119P.
PR      17-SEP-1997; 97US-00591212P.
PR      17-SEP-1997; 97US-00591222P.
PR      17-SEP-1997; 97US-0059184P.
PR      18-SEP-1997; 97US-0059263P.
PR      18-SEP-1997; 97US-0059266P.
PR      15-OCT-1997; 97US-0062125P.
PR      17-OCT-1997; 97US-0062285P.
PR      17-OCT-1997; 97US-0062287P.
PR      21-OCT-1997; 97US-0063486P.
PR      24-OCT-1997; 97US-0062814P.
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PR      07-NOV-1997; 97US-0064809P.
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PR      12-DEC-1997; 97US-0069425P.
PR      04-JUN-1998; 98US-0088026P.
PR      10-SEP-1998; 98US-0099803P.
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PR      16-SEP-1998; 98US-0100262P.
PR      17-SEP-1998; 98US-0100858P.
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PR 17-SEP-1998; 98WO-US019437.  
 PR 13-OCT-1998; 98US-0104080P.  
 PR 20-NOV-1998; 98US-0109304P.  
 PR 01-DEC-1998; 98WO-US025108.  
 PR 22-DEC-1998; 98US-0113296P.  
 PR 07-JUL-1999; 99US-0143048P.  
 PR 26-JUL-1999; 99US-0145698P.  
 PR 28-JUL-1999; 99US-0146222P.  
 PR 08-SEP-1999; 99WO-US020594.  
 PR 13-SEP-1999; 99WO-US020944.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 15-SEP-1999; 99WO-US021547.  
 PR 05-OCT-1999; 99WO-US023089.  
 PR 29-NOV-1999; 99WO-US028214.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 02-DEC-1999; 99WO-US028564.  
 PR 02-DEC-1999; 99WO-US028565.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 20-DEC-1999; 99WO-US030911.  
 PR 05-JAN-2000; 99WO-US030999.  
 PR 11-FEB-2000; 2000WO-US000219.  
 PR 22-FEB-2000; 2000WO-US003565.  
 PR 24-FEB-2000; 2000WO-US004414.  
 PR 02-MAR-2000; 2000WO-US005004.  
 PR 20-MAR-2000; 2000WO-US005841.  
 PR 30-MAR-2000; 2000WO-US007377.  
 PR 22-MAY-2000; 2000WO-US008439.  
 PR 02-JUN-2000; 2000WO-US014042.  
 PR 28-JUL-2000; 2000WO-US015264.  
 PR 24-AUG-2000; 2000WO-US020710.  
 PR 18-SEP-2000; 2000US-00665350.  
 XX  
 PA (GETH ) GEMENTECH INC.  
 XX  
 PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;  
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;  
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;  
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;  
 PI Williams PM, Wood WI;  
 XX WPI; 2003-492256/46.  
 DR P-PSDB; ABO34851.  
 DR  
 XX  
 PT Novel secreted and transmembrane PRO polypeptides and polynucleotides  
 PT encoding them, useful for treating abnormal bleeding involved in  
 PT gynecological diseases, skin diseases and neurodegenerative diseases.  
 XX  
 PS Claim 2; Fig 73; 475pp; English.  
 PS  
 XX The invention relates to human PRO polypeptides (secreted and  
 CC transmembrane polypeptides) and the PRO polynucleotides encoding them.  
 CC The PRO polypeptides and polynucleotides can be used in diagnosing or  
 CC treating abnormal bleeding involved in gynaecological diseases e.g. to  
 CC avoid or lessen the need for hysterectomy. They can also be used in  
 CC treating coronary ischaemic conditions, disorders associated with the  
 CC preservation and maintenance of gastrointestinal mucosa and the repair of  
 CC acute and chronic mucosal lesions, skin diseases associated with abnormal  
 CC keratinocyte differentiation (e.g. psoriasis), Parkinson's disease,  
 CC Alzheimer's disease, asthma, rheumatoid arthritis, multiple sclerosis,  
 CC amyotrophic lateral sclerosis (ALS), neuropathies and diseases related to  
 CC uncontrolled cell growth, such as cancer. This sequence represents a  
 CC human PRO polynucleotide of the invention  
 XX  
 SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1.49e-304 Length: 2372  
 Score: 322.00 Matches: 322  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0

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 QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20  
 Db 160 ATGGCCAGGTGCTTCAGCCCTGGTGTCTTCTCATTCCATCTGGACACGAGGCTCTTG 219  
 QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
 Db 220 GTCCAAGGCTCTTGGCTGCAGAAAGCTTTCATCCAGGTGTCTATGCAAGATTATGGGG 279  
 QY 41 IleThrLeuValSerIleValAlaGlnGlnLeuAsnPheThrGluAlaValGluAla 60  
 Db 280 ATCACCCCTTGTGAGCAAAAGGCAACGAGCAGCTGAATTTTACAGAAGCTAAGGAGGCC 339  
 QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
 Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 399  
 QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100  
 Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGATTCGTGTCTATCTCTAGGATT 459  
 QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
 Db 460 AGCCCAACCCCAAGTGGGAAATGGGGTGGGTCTCTGATTTGGAAGGTTCCAGTG 519  
 QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
 Db 520 AGCCGACAGTTTGCAGCCTATTGTTTACAACCTCATCTGATACCTTGAACCTAAGTCTG 579  
 QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
 Db 580 CCAGAAATTTATCACCACCAAGATCCCATATTCAACACTCAAACTCAACACCAACAA 639  
 QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
 Db 640 GAAATTTATGTCAGTGACAGTACCTACTCGTGGGCATCCCTTACTTCTCAATACCTGCC 699  
 QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200  
 Db 700 CCTACTACTACT 759  
 QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
 Db 760 TGTGTACACAGAGTTTATGGAACCTAGCACCATGTCTACAGAACTGAAACCATTTGTT 819  
 QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
 Db 820 GAAATTAAGCAGCATTCAGAAATGAAGCTGTCTGGGTGTGGAGGTGTCCTCCACGGCTCTG 879  
 QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260  
 Db 880 CTAGTGTCTGCT 939  
 QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
 Db 940 AGGTATGTGAAGCCCTTCCCTTTTACAACAAGATTCAGCAGAGAAATGATCGAAACC 999  
 QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
 Db 1000 AAGTAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1059  
 QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
 Db 1060 GATAAAACCCAGAGAGTCCAAAGAGTCCAAAGAGTCCAAAGAGTCCAAAGAGTCCAAAG 1119  
 QY 321 GluVal 322  
 Db 1120 GAAGTT 1125  
 RESULT 46

ADA16236  
ID ADA16236 standard; cDNA; 2372 BP.  
XX  
AC ADA16236;  
XX  
DT 06-NOV-2003 (first entry)  
DE Human secreted/transmembrane protein cDNA, #40.  
XX  
KW Human; gene; ss; PRO; secreted; transmembrane; therapeutic;  
KW tissue typing; immunohistochemical staining; gene therapy;  
KW neonatal heart; vascular endothelial growth factor; VEGF; proliferation;  
KW endothelial cell; stimulated T-lymphocyte; retinal neuron;  
KW rod photoreceptor cell; c-fos; glucose; FFA; chondrocyte;  
KW cardiac insufficiency disorder; wound; cancer; tumour; retinal disorder;  
KW retinitis pigmentosa; obesity; diabete; hyperinsulinaemia;  
KW hypotinsulinaemia; bone disorder; cartilage disorder; sport injury;  
KW arthritis; cardiant; vulnerary; cytostatic; ophthalmological;  
KW osteopathic; antiarthritic; anorectic.  
XX  
OS Homo sapiens.  
XX  
PN US2003049621-A1.  
XX  
PD 13-MAR-2003.  
XX  
PF 11-JUL-2001; 2001US-00904119.  
XX  
PR 17-SEP-1997; 97US-0059113P.  
PR 17-SEP-1997; 97US-0059113P.  
PR 17-SEP-1997; 97US-0059117P.  
PR 17-SEP-1997; 97US-0059119P.  
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PR 15-OCT-1997; 97US-0062125P.  
PR 17-OCT-1997; 97US-0062285P.  
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PR 21-OCT-1997; 97US-0063486P.  
PR 24-OCT-1997; 97US-0062814P.  
PR 24-OCT-1997; 97US-0062816P.  
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PR 24-OCT-1997; 97US-0063121P.  
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PR 29-OCT-1997; 97US-0063734P.  
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PR 31-OCT-1997; 97US-0064103P.  
PR 03-NOV-1997; 97US-0064248P.  
PR 12-NOV-1997; 97US-0064809P.  
PR 17-NOV-1997; 97US-0065186P.  
PR 17-NOV-1997; 97US-0065846P.  
PR 18-NOV-1997; 97US-0065693P.  
PR 21-NOV-1997; 97US-0066120P.  
PR 21-NOV-1997; 97US-0066364P.  
PR 24-NOV-1997; 97US-0066453P.

PR 24-NOV-1997; 97US-0066466P.  
PR 24-NOV-1997; 97US-0066511P.  
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PR 24-NOV-1997; 97US-0066772P.  
PR 25-NOV-1997; 97US-0066840P.  
PR 12-DEC-1997; 97US-0069425P.  
PR 04-JUN-1998; 98US-0088026P.  
PR 10-SEP-1998; 98US-0099803P.  
PR 10-SEP-1998; 98WO-US018824.  
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PR 20-NOV-1998; 98US-0109304P.  
PR 01-DEC-1998; 98WO-US025108.  
PR 22-DEC-1998; 98US-0113296P.  
PR 07-JUL-1999; 99US-0143048P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 28-JUL-1999; 99US-0146222P.  
PR 08-SEP-1999; 99WO-US020594.  
PR 13-SEP-1999; 99WO-US020944.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 05-OCT-1999; 99WO-US023089.  
PR 29-NOV-1999; 99WO-US028214.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 02-DEC-1999; 99WO-US028564.  
PR 02-DEC-1999; 99WO-US028565.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 20-DEC-1999; 99WO-US030999.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 22-MAR-2000; 2000WO-US008439.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 18-SEP-2000; 2000US-00665350.

(GETH ) GENENTECH INC.

Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;  
Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;  
Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kijavini IJ;  
Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;  
Williams PM, Wood WI;

WPI; 2003-521801/49.  
P-PSDB; ADA16237.

New genes encoding for secreted and transmembrane PRO polypeptides,  
useful for treating e.g. cardiac insufficiency disorders, wounds,  
cancers, obesity, diabetes, hyperinsulinemia, hypotinsulinemia, or  
arthritis.

Claim 2; SEQ ID NO 200; 476pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides  
and the nucleic acid encoding them. The polypeptides can be used to raise  
antibodies that specifically bind to the PRO polypeptide, for linking a  
bioactive molecule to a cell expressing a PRO protein and for modulating  
at least one biological activity of a cell. PRO polypeptides are useful  
for detecting other PRO polypeptides in a sample and for linking a  
bioactive molecule to a cell expressing a PRO polypeptide. The PRO  
polypeptide antibodies are useful for modulating the biological activity







Db 1120 GAAGTT 1125

RESULT 48

ACD82092

ID ACD82092 standard; cDNA; 2372 BP.

XX AC ACD82092;

XX DT 19-SEP-2003 (first entry)

XX DE Human secreted/transmembrane polypeptide PRO 263 cDNA.

XX KW Human; ss; gene therapy; cancer; tissue typing; gene.

XX OS Homo sapiens.

XX US2003060601-A1.

XX 27-MAR-2003.

XX 02-MAY-2002; 2002US-00063541.

XX 30-DEC-1998; 98KR-00062142.

XX 08-MAR-1999; 99WO-US005028.

XX 14-MAY-1999; 99US-00311832.

XX 14-MAY-1999; 99WO-US010733.

XX 25-AUG-1999; 99US-00380137.

XX 25-AUG-1999; 99US-00380138.

XX 25-AUG-1999; 99US-00380139.

XX 25-AUG-1999; 99US-00380142.

XX 15-SEP-1999; 99US-00397342.

XX 18-OCT-1999; 99US-00403297.

XX 12-NOV-1999; 99US-00423844.

XX 30-DEC-1999; 99WO-US031274.

XX 18-FEB-2000; 2000WO-US004341.

XX 01-MAR-2000; 2000WO-US005601.

XX 02-MAR-2000; 2000WO-US005841.

XX 21-MAR-2000; 2000WO-US007532.

XX 22-MAY-2000; 2000WO-US014042.

XX 02-JUN-2000; 2000WO-US015264.

XX 22-AUG-2000; 2000WO-US064488.

XX 24-AUG-2000; 2000WO-US023328.

XX 18-SEP-2000; 2000US-00664610.

XX 18-SEP-2000; 2000US-00665350.

XX 08-NOV-2000; 2000US-00709238.

XX 10-NOV-2000; 2000WO-US030873.

XX 01-DEC-2000; 2000WO-US032678.

XX 20-DEC-2000; 2000US-00747259.

XX 20-DEC-2000; 2000WO-US034956.

XX 28-FEB-2001; 2001WO-US006520.

XX 22-MAR-2001; 2001US-00816744.

XX 10-MAY-2001; 2001US-00854208.

XX 10-MAY-2001; 2001US-00854280.

XX 30-MAY-2001; 2001US-00870574.

XX 01-JUN-2001; 2001WO-US017800.

XX 05-JUN-2001; 2001US-00874503.

XX 29-JUN-2001; 2001US-00869599.

XX 18-JUL-2001; 2001US-00908827.

XX 06-DEC-2001; 2001US-00068667.

XX (GETH ) GENENTECH INC.

XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;

XX Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

XX WPI; 2003-521927/49.

XX P-PSDB; ABO34169.

XX New PRO polypeptide, useful for preparing a composition for diagnosing or

XX treating cancer or for tissue typing.

XX Disclosure; Fig 5; 236pp; English.

XX

CC The invention relates to an isolated PRO polypeptide. The polypeptide is

CC useful for preparing a composition for diagnosing or treating cancer or

CC for tissue typing. The present sequence represents cDNA encoding a human

CC secreted/transmembrane PRO polypeptide

XX

SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.49e-304 Length: 2372

Score: 322.00 Matches: 322

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 8 Gaps: 0

US-10-079-111-1 (1-322) x ACD82092 (1-2372)

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DB 160 ATGGCCAGGTGCTTACGCTGGTGTCTTCTCATTCCATTCGACCGAGGCTCCTG 219

QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40

DB 220 GTCCAAAGGCTCTTGGTGCAGAGAGCTTCCATCCAGGTGTCAATGAGATTATGGGG 279

QY 41 IleThrLeuValSerIlysalahenGlnGlnLeuAsnPhetheThrGluAlaLysGluAla 60

DB 280 ATCACCCTTGTGAGCAAAAGCGAACACAGAGCTGAATTTCCAGAGCTAAGGAGGCC 339

QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGlnThrAlaLeuLysAla 80

DB 340 TGTAGCTGTGGACTAAGTTTGGCCGCAAGCAAGTTGAAACAGCCITGAAGCT 399

QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100

DB 400 AGCTTTGAAACTTGCAGCTATGCTGGTGGAGATGGATTGCTGCTCATCTAGGATT 459

QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120

DB 460 AGCCCAAAACCCCAAGTGTGGGAAATGGGGTGGGTGCTCTGATTGGAGGTTCAGTG 519

QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140

DB 520 AGCCGACAGTTTGCAGCTTATTTGTACAACTCATCTGATCTTGGACTTGAATCTGCAIT 579

QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160

DB 580 CCAGAAATTTATCACCACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACA 639

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180

DB 640 GAATTTATTGTGAGTGACAGTACCTACTCGGGTGGCATCCCTTACTCTACATACCTGCC 699

QY 181 ProThrThrProProAlaProAlaSerThrSerIleProArgLysLysLeuIle 200

DB 700 CCTACTACT 759

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220

DB 760 TGTGTACAGAAAGTTTTTATGGAACACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819

QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240

DB 820 GAAATAAAGCAGCAATCAAGATGAAGCTGTGGGTGGAGGTGCTCCCAAGGCTCTG 879

QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260

DB 880 CTAGTGTCT 939

QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280

DB 940 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGATCAGAGAGAAATGATCGAAACC 999





```
KW diabetic complication.
XX
OS Homo sapiens.
XX
PN US2003064367-A1.
XX
XX 03-APR-2003.
XX
PF 13-JUL-2001; 2001US-00904485.
XX
XX 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
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PR 18-SEP-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
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PR 24-OCT-1997; 97US-0063120P.
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PR 24-OCT-1997; 97US-0063127P.
PR 27-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
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PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
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PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
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PR 04-JUN-1998; 98US-0088026P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98US-0100262P.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.

PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 22-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX
XX (GETH ) GENENTECH INC.
PA
XX
XX Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PU, Grimaldi JC, Gurney AL, Hillan KJ, Kijavini IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
XX WPI: 2003-567176/53.
DR P-PSDB; ABO17529.
XX
XX Novel isolated PRO polypeptides e.g. PRO245 and PRO1869, useful for
PT treating e.g. Parkinson's disease, Alzheimer's disease, amyotrophic
PT lateral sclerosis, cancer, neuropathies, diabetes and psoriasis.
XX
XX Claim 2; Fig 73; 477pp; English.
XX
XX The invention relates to human PRO polypeptides and the polynucleotides
CC encoding them. The polypeptides and polynucleotides are used for treating
CC diseases related to growth or survival of nerve cells such as Parkinson's
CC disease, Alzheimer's disease, amyotrophic lateral sclerosis (ALS) and
CC neuropathies, diseases related to uncontrolled cell growth such as
CC cancer, viral infections, Usher's syndrome, haemorrhage, enterocolitis,
CC Zollinger-Ellison syndrome, gastrointestinal ulceration, congenital
CC microvillus atrophy, skin diseases such as psoriasis and epithelial
CC cancers, endometrial bleeding, angiogenesis, ischaemic conditions,
CC asthma, rheumatoid arthritis, multiple sclerosis, inflammatory diseases,
CC atherosclerosis, cardiac injury, infertility, birth defects, premature
CC aging, AIDS, stroke and diabetic complications. The polynucleotides are
CC also useful in chromosome and gene mapping. This sequence represents a
CC human PRO polynucleotide of the invention
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1,49e-304 Length: 2372
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Best Local Similarity: 100.00% Mismatches: 0
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US-10-079-111-1 (1-322) x ACD23293 (1-2372)
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QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db |||||
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QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
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QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
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460 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCTGATTTGGAAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrThrTrpThrAsnSerCysIle 140
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QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db |||||
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QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db |||||
640 GAATTTATTGTGAGTACAGTACCTACTCGGTGGCATCCCTTACTCTCAATACCTGCC 699
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1120 GAAGTT 1125
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 15, 2004, 21:23:25 ; Search time 2278 Seconds  
(without alignments)  
713.467 Million cell updates/sec

Title: US-10-079-111-1

Perfect score: 322

Sequence: 1 MARCFSLVLLTSIWTREL.....NPEESKSPSKTIVRCLEAEV 322

Scoring table: OLIGO

Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3327077 seqs, 2523723180 residues

Word size: 12

Total number of hits satisfying chosen parameters: 337

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Command line parameters: -MODEL=frame, p2n.model -DEV=xlh

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Database : Published Applications NA:

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- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq.\*
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- 14: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*
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- 17: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 18: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	322	100.0	2372	9	US-09-909-088B-200	Sequence 200, App
4	322	100.0	2372	9	US-09-905-291A-200	Sequence 200, App
5	322	100.0	2372	9	US-09-902-853-200	Sequence 200, App
6	322	100.0	2372	9	US-09-907-824-200	Sequence 200, App
7	322	100.0	2372	9	US-09-907-841-200	Sequence 200, App
8	322	100.0	2372	10	US-09-904-011-200	Sequence 200, App
9	322	100.0	2372	10	US-09-906-742-200	Sequence 200, App
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# ALIGNMENTS

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RESULT 1
US-10-079-111-2
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; Publication No. US20030124543A1
; GENERAL INFORMATION:
; APPLICANT: Stuart, Susan G.
; APPLICANT: Streeter, David G.
; TITLE OF INVENTION: BREAST CANCER MARKER
; FILE REFERENCE: PC-0053 CIP
; CURRENT APPLICATION NUMBER: US/10/079,111
; CURRENT FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 09/232,160
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 2029
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030124543A1 3044710CB1
US-10-079-111-2

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Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

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US-10-079-111-1 (1-322) x US-10-079-111-2 (1-2029)

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QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 903 CTAGTGTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 962
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 963 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAAATCAGCAGAAAGAAATGATCGAAACC 1022
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1023 AAGTATAGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1082
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1083 GATAAAAACCCAGAGAGTCCAGAGTCCCAAGCAAAACTACCGTGGATGCGCTGGAAGCT 1142
QY 321 GluVal 322
Db 1143 GAAGTT 1148

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## RESULT 2

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US-09-909-320-200
; Sequence 200, Application US/09909320
; Patent No. US20020132240A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen

```



APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, A.  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, Christopher J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Hillan, Kenneth, J.  
 APPLICANT: Kljavin, Ivar J.  
 APPLICANT: Mather, Jennie P.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas P.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William, I.  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 TITLE OF INVENTION: Acids Encoding the Same  
 FILE REFERENCE: 10466-14  
 CURRENT APPLICATION NUMBER: US/09/909,320  
 CURRENT FILING DATE: 2002-01-04  
 PRIOR APPLICATION NUMBER: PCT/US00/04414  
 PRIOR FILING DATE: 2000-02-22  
 PRIOR APPLICATION NUMBER: US 60/143,048  
 PRIOR FILING DATE: 1999-07-07  
 PRIOR APPLICATION NUMBER: US 60/145,698  
 PRIOR FILING DATE: 1999-07-26  
 PRIOR APPLICATION NUMBER: US 60/146,222  
 PRIOR FILING DATE: 1999-07-28  
 PRIOR APPLICATION NUMBER: PCT/US99/20594  
 PRIOR FILING DATE: 1999-09-08  
 PRIOR APPLICATION NUMBER: PCT/US99/20944  
 PRIOR FILING DATE: 1999-09-13  
 PRIOR APPLICATION NUMBER: PCT/US99/21090  
 PRIOR FILING DATE: 1999-09-15  
 PRIOR APPLICATION NUMBER: PCT/US99/21547  
 PRIOR FILING DATE: 1999-09-15  
 PRIOR APPLICATION NUMBER: PCT/US99/23089  
 PRIOR FILING DATE: 1999-10-05  
 PRIOR APPLICATION NUMBER: PCT/US99/28214  
 PRIOR FILING DATE: 1999-11-29  
 PRIOR APPLICATION NUMBER: PCT/US99/28313  
 PRIOR FILING DATE: 1999-11-30  
 PRIOR APPLICATION NUMBER: PCT/US99/28564  
 PRIOR FILING DATE: 1999-12-02  
 PRIOR APPLICATION NUMBER: PCT/US99/28565  
 PRIOR FILING DATE: 1999-12-02  
 PRIOR APPLICATION NUMBER: PCT/US99/30095  
 PRIOR FILING DATE: 1999-12-16  
 PRIOR APPLICATION NUMBER: PCT/US99/30911  
 PRIOR FILING DATE: 1999-12-20  
 PRIOR APPLICATION NUMBER: PCT/US99/30999  
 PRIOR FILING DATE: 1999-12-20  
 PRIOR APPLICATION NUMBER: PCT/US00/00219  
 PRIOR FILING DATE: 2000-01-05  
 NUMBER OF SEQ ID NOS: 423  
 SEQ ID NO 200  
 LENGTH: 2372  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-909-320-200

Alignment Scores:  
 Pred. No.: 0  
 Score: 322.00  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 100.00%  
 DB: 9  
 Length: 2372  
 Matches: 322  
 Mismatches: 0  
 Indels: 0  
 Gaps: 0

US-10-079-111-1 (1-322) x US-09-909-320-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20  
 DB 160 ATGGCCAGGTGCTTTCAGCTGGTGTCTTCTCACTTCCATCGGACCGAGGCTCTG 219  
 QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
 DB 220 GTCCAGGCTCTTTCGGTGCAGAGAGCTTTCATCCAGGTGTATGCAGAAATATATGGG 279  
 QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
 DB 280 ATCACCTTTGTGAGCAAAAGCGAACACAGAGCTGAATTTCCAGAGCTAAGGAGGCC 339  
 QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
 DB 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 399  
 QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100  
 DB 400 AGCTTTGAACCTTGAGCTATGCTGGGTGGAGATGGATCTGTGTCATCTTAGATT 459  
 QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
 DB 460 AGCCCAAAACCCCAAGTGGGAAAATGGGTGGGTCTCTCATTTGGAAGGTTCCAGTG 519  
 QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
 DB 520 AGCCGACAGTTTTCAGCCTTATTTTACAACTCATCTGACTTGGACTTAACCTGTCANT 579  
 QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
 DB 580 CCAGAAATATCACCACCAAGATCCATATTTCAACACTCAAACTGCAACACAAACA 639  
 QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
 DB 640 GAATTTATTTGTCAGTGACAGTACTACTCGTGGCATCCCTTACTCTACAATACCTGCC 699  
 QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200  
 DB 700 CCTACTACTACTCTCTCTCTCCAGCTTCCACTTCTATTTCCACGGAGAAAAATGATT 759  
 QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
 DB 760 TGTGTACACAGAGTTTATGGAACCTAGCACCATGTCTACAGAACTGAACCATTTGTT 819  
 QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
 DB 820 GAAATAAAGCAGCATTCAGGAATCAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 879  
 QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
 DB 880 CTAGTGTCTGCTCTCTCTCTCTCTGCTGCTGAGCTGGTCTTGGATTTTGTATGTCAA 939  
 QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
 DB 940 AGGTATGTGAAGGCTTCCCTTTTACAAACAGAAATCAGCAGAGGAAATGATCGAACC 999  
 QY 281 LysValValLysGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
 DB 1000 AAAGTAGTAAAGGAGGAGGAGGCAATGATAGCAACCTTAATGAGGAATCAAGAAACT 1059  
 QY 301 AspLysAsnProGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
 DB 1060 GATAAAACCCAGAGAGTCCAAGAGTCCAAGAAAACTACCGTCGATGCTCGAAGCT 1119  
 QY 321 GluVal 322  
 DB 1120 GAAGTT 1125

RESULT 3

US-09-909-088B-200

; Sequence 200, Application US/09909088B

; Patent No. US20020146709A1

```

; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,088B
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-909-088B-200
Alignment Scores:

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QY      321 GluVal 322
Db      1120 GAAGTT 1125

; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-905-291A-200

Alignment Scores:
Pred. No.:      0      Length:      2372
Score:          322.00      Matches:      322
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:              9      Gaps:      0

US-10-079-111-1 (1-322) x US-09-905-291A-200 (1-2372)

QY      1 MetAlaAArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db      160 ATGGCCAGGTGCTTTCAGCCTGGTGTGCTTCTCATTCCATCTGGACCCAGAGGCTCCG 219
QY      21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db      220 GTCCAAAGGCTCTTTGCGTCAGAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGG 279
QY      41 IleThrLeuValSerIlyslsAlaGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db      280 ATCACCTTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTTTCACAGAACTAAGGAGGCC 339
QY      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db      340 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACACGCCCTTGAAGCT 399
QY      81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db      400 AGCTTTGAAACTTGCAGCTATGCTGGTGGTGGAGATGGATTCGTGCTCATCTCTAGGATT 459
QY      101 SerProAsnProIlyslsCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db      460 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGCTCTGATTTGGAAAGGTTCCAGTG 519
QY      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db      520 AGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATCTGGACTAACTCGTGCAATT 579
QY      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db      580 CCAGAAATTTATCACCAACCAAGATCCCATATTTCAACACTCAAACTGCAACCAACAACA 639
QY      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db      640 GAATTTATTGTGAGTGACAGTACCTACTCGGGGGCATCCCTTACTCTACAATACCTGCC 699
QY      181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db      700 CCTACTACTACTCTCTCTCTCCCTCCAGCTTCCACTTTCTATTCACGAGAGAAAAATTGATT 759
QY      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db      760 TGTGTACAGAAAGTTTATGGAACCTAGCACCATGTCTACAGAAACTGAACCACTTTGTT 819
QY      221 GluAsnLysAlaAlaPheIlyslsAsnGluAlaGlyPheGlyGlyValProThrAlaLeu 240
Db      820 GAAATAAAGCAGCAGCATTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGCTCTG 879
QY      241 LeuValLeuAlaLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db      880 CTAGTGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 939
QY      261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db      940 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAANTCAGACAGAGAAATGATCGAAACC 999
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## RESULT 4

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US-09-905-291A-200
; Sequence 200, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,291A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
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Db 700 CCTACTACTCTCTCTCTCAGCTTCCAGCTTCTATTCCACGGAGAAAAATTGATT 759
Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTACAGAAAGTTTTATGGAACCTAGCACCATGCTACAGAAACCTGAACCAATTGTT 819
Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db 820 GAAATTAAGACGACCAATCAAGATGAAGCTGCTGGGTTTGGAGGTTCCTCCACGGCTCTG 879
Qy 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTCTTGCTCTCTCTCTCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 939
Qy 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetLleGluThr 280
Db 940 AGGTATGTGAAGCCCTCCCTTTTACAAACAAGATCAGCAGAGAAATGATCGAAACC 999
Qy 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAGAGAGAGAGGCCAATGATAGCAACCTTAATGAGGAATCAAGAAACT 1059
Qy 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGATGCTGGGAAGCT 1119
Qy 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 7
US-09-907-841-200
; Sequence 200, Application US/09907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
; APPLICANT: Gentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,841
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
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; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-841-200

Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-079-111-1 (1-322) x US-09-907-841-200 (1-2372)

Qy 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrrpThrThrArgLeuLeu 20
Db 160 AITGGCCAGTGTCTTCCAGCTGTGTGTTCTTCTACCTTCCATCTGGACACAGAGCTCTCG 219
Qy 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTGCGTGCAGAGAGCTTTCCATCCAGGTGTCTATGAGAAATTATGGG 279
Qy 41 IleThrLeuValSerLysLysAlaGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCCTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTTCCACAGAACTAAGGAGGCC 339
Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGCTGTGGACTAAGTTTGGCCGCGCAGGACCAAGTTGAAACACAGCTTGAAGCT 399
Qy 81 SerPheGluThrCysSerTyrGlyTrrpValGlyAspGlyPheValLysSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCTGTGTCTCTAGGATT 459
Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrrpLysValProVal 120
Db 460 AGCCCCAAACCCCAAGTGTGGGAAAATGGGGTGGTCTCTGATTGGGAAGTTCAGTG 519
Qy 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrrpThrAsnSerCysIle 140
Db 520 AGCCCGACAGTTTGGACCTATTGTTACAACTCATCTGATCTGGACTTAACCTCGTGCT 579
Qy 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATATATCACCACCAAGATCCCATATTTCAACACTCAAACTGCAACACAAACA 639
Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATGTCAGTGACAGTACCTACTCGGGGGATCCCTTACTTCAATACTACTGCC 699
Qy 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeu 200
Db 700 CCTACTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 759
Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTACAGAAAGTTTTATGGAACCTAGCACCATGCTACAGAAACCTGAACCAATTGTT 819
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QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db 820 GAAATAAAGCAGCATTCAGAAATGAAGCTGTGGGTTTGGAGGTGCCCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGCTCTCTCTCTTTGGTGTGAGCTGGTCTGGATTTGGCTATGTCAAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCTCTCCCTTTTCAAAACAAGAAATCAGCAGAAGGAAATGATCGAAAC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGAGAGAGAGGCAATGATGACCAACCTTAATGAGGAATCAAGAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATNAACCCAGAGAGTCCAGAGAGTCCAGCAAAACTACCGTGGATGCTTGGAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 8
US-09-904-011-200
; Sequence 200, Application US/09904011
; Publication No. US20030003530A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,011
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
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; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-904-011-200

Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-904-011-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTyrThrThrArgLeuLeu 20
Db 160 ATGGCCAGGTGTTTCAGCTGGTGTGTCTTCTTCATCTCCATCTGGACCAAGGCTCTCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTCGTGCAGAGAGCTTTCATCCAGGTGTCATCCAGAGATTTATGGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCCCTGTGAGCAAAAGCGAAACCGACGACGTGAATTTTCACAGAACTAAGGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGTGGGACTAAGTTTGGCCGCAAGGACCAAGTTTGAACACGCCCTTGAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGTCATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAAAACCCCAAGTGGGAAAAAATGGGGTGGGTGTCCTGATTGTGAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTyrThrAsnSerCysIle 140
Db 520 AGCCGACGATTTGCAGCCTATTGTACAACTCATCTGATCTTGGACTAACCTCGCAT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACCAACAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
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640	GAATTTATTGTCTAGTGCAGTACCTACTCGTGGCATCCCTTACTCTCAAACTACCTGCC	699
181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
700	CCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT	759
201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
760	TGTGTCCACGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT	819
221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
820	GAAATTAAGCAGCATTTCAAGATGAAGCTGTGGGTTTGAGGTGTCCCCACGGCTCTG	879
241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
880	CTAGTGTCTCTCTCTCTTTGGTGTCTGCAGCTGCTCTTGGATTTTCTGTATGTCAA	939
261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr	280
940	AGGTATGTGAAGGCTTCCCTTTTACAAAACAAGAAATCAGCAGAGGAAATGATCGAAACC	999
281	LysValLysLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
1000	AAAGTAGTAAGGAGGAGAGGCGCAATGATAGCAACCTTAATAGGAAATCAAAAGAAACT	1059
301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
1060	GATAAAAACCCAGNAGAGTCCAGAGTCCAAAGTCCAAAGCDAAACTACCGTGCATGCTTGGAGCT	1119
321	GluVal	322
1120	GAAGTT	1125

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RESULT 9
US-09-906-742-200
; Sequence 200, Application US/09906742
; Publication No. US20030023054A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, David
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,742
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414

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QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 ACCGACAGATTGGAGCCTATTGTTACAACTCATCTGATCTTGAGCTAACTCGTGCATT 579
QY 141 ProGluIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATATACACCAAGATCCCATATTCAACACTCAACTGCAACACAAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTGTGAGTACAGTACTACTCGTGGCATCCCTTACTCTACAATACTGCTGC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CTTACTACTACTCCCTGCTGCTCCAGCTTCCATCTTATTCACGGAGAAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTACAGAGATTGTTTATGGAACCTAGCACCATGCTTACAGAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAAAATAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGGAGGTGTCGCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGCCTTCCCTTTTACAAACAGATCAGCAGAGAAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaLysAspSerAsnProAsnGluGluSerLysThr 300
Db 1000 AAAGTAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 10
US-09-906-838-200
; Sequence 200, Application US/09906838
; Publication No. US20030027143A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel

```

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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,838
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-906-838-200

Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-906-838-200 (1-2372)
QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrArgLeuLeu 20
Db 160 ATGGCCAGGTCTTCAGCCTGTGTTCCTTCATCTTCATCTGCACACAGGCTCCGT 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAGGCTCTTTGGCTGTCAGAGAGCTTTCATCCAGGTGTATGCAGATTAATGGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCTTGTGAGCAAAAGCGAAACCCAGCAGCTGAATTTACAGAGCTTAAGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80

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Db 340 TGTAGGCTGCTGGACTAGTTTGGCGCGCAGAGCAAGTTGAAACAGCCCTTGAAAGCT 399  
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgile 100  
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTGCTGTCATCTCTAGGATT 459  
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
Db 460 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGTCTCATTTGGGAAGGTTCAGTGG 519  
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
Db 520 ACCGACAGCTTTCAGCCCTATTGTTACAACTCATCTGATCTTGACCTACCTCGTCATT 579  
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
Db 580 CCAGAAATATATCACCACCAAGATGCCATATTCACACCTCAAACTGCAACACAAACA 639  
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
Db 640 GAATTTATGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTTCAATACATCTGCC 699  
QY 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200  
Db 700 CCTACTACTCTCTCTCTCCAGCTTCCACTTCTATTCCACGGAGAAAAATTGATT 759  
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
Db 760 TGTGTACAGAAAGTGTATGTAAGAACTAGCACCAATGCTTACAGAACTGAACCAATTTGT 819  
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240  
Db 820 GAAATATAAGCAGCATTCAAGATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879  
QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLysGlyPheCysTyrValLys 260  
Db 880 CTAGTGTCTGCTCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 939  
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
Db 940 AGGTATGTGAAGCCCTTCCCTTTTACAAACAAGAAATCAGCAGAAGAAATGATCGAAACC 999  
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
Db 1000 AAAGTAGTAAAGAGAGAGAGGCCAATGATGACCAACCCCTAATGAGGAATCAAGAAACT 1059  
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
Db 1060 GATAAAACCCAGAGAGTCCAGAGTCCAGCAAAACCTACCGTGCATGCCTGGAAGCT 1119  
QY 321 GluVal 322  
Db 1120 GAAGTT 1125

RESULT 11  
US-09-907-613-200  
; Sequence 200, Application US/09907613  
; Publication NO. US20030027145A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/907,613  
; CURRENT FILING DATE: 2001-07-17  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 200  
; LENGTH: 2372  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-907-613-200

Alignment Scores:  
Pred. No.: 0 Length: 2372  
Score: 322.00 Matches: 322  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-907-613-200 (1-2372)  
QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20  
Db 160 ATGGCCAGGTGCTTCAGCTGGTGTGCTTCATCTCCATTCACACACAGAGCTCCCG 219  
QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40

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Db      220  GTCCAGGCTCTTTGGTGCAGAGAGCTTTCCATCCAGTGTGTCAGAAATNTGGGG 279
QY      41  IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db      280  ATCACCCCTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGCC 339
QY      61  CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db      340  TGTAGGCTGCTGGGACTAAGTTTGGCCGCGCAAGACCAAGTTGAAACAGCCCTTGAAGCT 399
QY      81  SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle 100
Db      400  AGCTTTGAAACTTGCAGCTATGCTGGTGGAGATGGATTCGTGTCATCTCAGGATT 459
QY      101  SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db      460  AGCCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGTGCCTGATTTGGAAGGTTCCAGTG 519
QY      121  SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db      520  AGCGGACAGTTTGCACGCTATGTTTAACTCACTCACTGATCTTGGACTAACTCGTGCAAT 579
QY      141  ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db      580  CCAGAAATTTATCACCAAGATCCATATTTCAACACTCAAACTGCAACACAAACAACA 639
QY      161  GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db      640  GAATTTATTTGTGAGTGACAGTACTACTCGGTGGCATCCCTTACTCTCAATACCTGCC 699
QY      181  ProThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db      700  CCTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 759
QY      201  CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db      760  TGTGTACAGAAAGTTTTTATGGAACCTAGCACCATGTCTACAGAACTGAACCATTTGT 819
QY      221  GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db      820  GAAATAAAGCAGCATTTCAAGATGAAGCTGTGGTGTGGAGGTGTCGCCACGGCTCTG 879
QY      241  LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db      880  CTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 939
QY      261  ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db      940  AGGTATGTGAAGGCCTTCCCTTTTACAAACAAGATCACAGAGGAAATGATCGAAACC 999
QY      281  LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db      1000  AAAGTAGTAAAGAGAGAGAGGAGGCAATGATGACCAACCCCTTAATGAGGAATCAAGAA 1059
QY      301  AspLysAsnProGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db      1060  GATAAAACCCAGAGAGCTCCAGAGTCCAGCAAAACTACCTGGTGGTGGCTGGAAAGCT 1119
QY      321  GluVal 322
Db      1120  GAAGTT 1125
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## RESULT 12

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US-09-907-942-200
; Sequence 200, Application US/09907942
; Publication No. US20030027146A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
```

## Alignment Scores:

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Pred. No.: 0
Score: 322.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 10
Length: 2372
Matches: 322
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0
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; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jemie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,942
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-942-200
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i ORGANISM: Homo Sapien
US-09-904-859-200

Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-904-859-200 (1-2372)

QY 1 MetAlaAtqCysPheSerLeuValLeuLeuLeuThrSerIleTrrpThrThrArgLeuLeu 20
Db 160 ATGCCAGGTGCTTCAGCCTGGTGTGCTTCACCTTCATCCAGTGTGCAGAAATTAATGGG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAGGCTCTTGGGTGCAGAGAGCTTTCATCCAGTGTGCATGCAGAAATTAATGGG 279
QY 41 IleThrLeuValSerLysLysAlaGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCCCTTGTGAGCAAAAGGCGAACACAGCAGCTGAATTCACAGAACTTAAGGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGCTCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAACAGCCCTTGAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrrpValGlyAspGlyPheValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGCTGGGTGGATGGATGCTGTCATCTCTAGGAT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrrpLysValProVal 120
Db 460 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTGCTGATTTGGAAGCTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTrrpAsnSerSerAspThrTrrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGGAGCTTATGTTACAACTCATCTGATCTGACCTAACTCGTGCAAT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATATCACCAACCAAGATCCCATATTCACACTCAACTGCAACACAAACAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAAATTTATTTGTCAGTGCAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTACAGAAAGTTTATGGAACACTAGCACCATGCTACAGAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATAAAGCAGCATTCAGAAATGAAGCTGCTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 879
QY 241 LeuValLeuAlaLeuLeuPheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGCCCTTCCCTTTTACAAACAGAAATCAGCAGAGAAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1059
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QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCCAGAGAGTCCAGAGATCCAGCAAAACTACCGTGCATCGCTGGAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 14
US-09-909-204-200
: Sequence 200, Application US/09909204
: Publication No. US20030036061A1
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc.
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, A.
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth, J.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Mather, Jennie P.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William, I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: TITLE OF INVENTION: Acids Encoding the Same
: FILE REFERENCE: 10466-14
: CURRENT APPLICATION NUMBER: US/09/909,204
: CURRENT FILING DATE: 2001-07-18
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: 2000-02-22
: PRIOR APPLICATION NUMBER: US 60/143,048
: PRIOR FILING DATE: 1999-07-07
: PRIOR APPLICATION NUMBER: US 60/145,698
: PRIOR FILING DATE: 1999-07-26
: PRIOR APPLICATION NUMBER: US 60/146,222
: PRIOR FILING DATE: 1999-07-28
: PRIOR APPLICATION NUMBER: PCT/US99/20594
: PRIOR FILING DATE: 1999-09-08
: PRIOR APPLICATION NUMBER: PCT/US99/20944
: PRIOR FILING DATE: 1999-09-13
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/21547
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/23089
: PRIOR FILING DATE: 1999-10-05
: PRIOR APPLICATION NUMBER: PCT/US99/28214
: PRIOR FILING DATE: 1999-11-29
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: 1999-11-30
: PRIOR APPLICATION NUMBER: PCT/US99/28564
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/28565
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: PCT/US99/30911
: PRIOR FILING DATE: 1999-12-20
```



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; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-904-820-200

Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-904-820-200 (1-2372)
QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrrPThrThrArgLeuLeu 20
DB 160 ATGGCCAGGCTCTTGGCTGCAGAGAGCTTCCATCCAGGTGTCATGCAGATTTATGGG 219
QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
DB 220 GTCCAGGCTCTTGGCTGCAGAGAGCTTCCATCCAGGTGTCATGCAGATTTATGGG 279
QY 41 IleThrLeuValSerIleLysAlaGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
DB 280 ATCCACCTTGTGAGCAAAAGGCGAAGCAGCAGCTGAATTTCCACAGAGCTAAGGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAsnGlnValGluThrAlaLeuLysAla 80
DB 340 TGTAGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAACACAGCCTTGAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrrValGlyAspGlyPheValValIleSerArgile 100
DB 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTGCTGTCATCTTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrrLysValProVal 120
DB 460 AGCCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGTGTCTGATTGGGAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrrPThrAsnSerCysIle 140
DB 520 AGCCGACAGTTTGCAGCTATTTGTACAACTCATCTGATCTTGGACTAATCTGGCATT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
DB 580 CCAGAAATATACACCAACCAAGATCCCATATTCACACTCAAACTGCAACACCAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
DB 640 GAAATTTATTTGTCAGTCACAGTACTACTCGGTGGCATCCCTTACTTACAATACCTGCC 699
QY 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuLeu 200
DB 700 CCTACTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220

```

```

DB 760 TGTGTCACAGAGTTTTTTATGGAAACTAGCACCATTGCTACAGAAACTGAACCAATTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
DB 820 GAAATAAAGCAGCATTCAAGATCAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
DB 880 CTAGTGCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
DB 940 AGTATGTGAAGCCCTTCCCTTTTACAAACAGAAATCAGCAGAGAAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
DB 1000 AAAAGTAGTAAAGAGGAGAGGCCAATGATGCAACCTTAATGAGGAATCAAGAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
DB 1060 GATAAAAAACCCAGAGAGTCCAAAGAGTCCAAAGAACTTACCGTCGATGCGCTGGAAGCT 1119
QY 321 GluVal 322
DB 1120 GAAGTT 1125

RESULT 16
US-09-904-786-200
; Sequence 200, Application US/09904786
; Publication No. US2003003996A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,786
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-904-786-200

Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322

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; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-903-786-200

Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-903-786-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGGCCAGGTGCTCAGCCCTGGTGTCTCTCACTTCCATCTGGACACGAGGCTCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAGGCTCTTGGTGCAGAGAGCTTTCCATCCAGGTGTCATGCAAGATTATGGGG 279
QY 41 IleThrLeuValSerLysLysAlaGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCTTGTGAGCAAAAGCGAACACGACGCTGAATTCACAGAGCTAAGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399
QY 81 SerPheGluThrCysSerTyrglyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAACATTGACGCTATGGCTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAACCCCAAGTGTGGGAAAATGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrglyAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGCTTGGAGCCCTATTGTTACAACTCATCTGATCTGGACTAACTCGTGCAAT 579
QY 141 ProGluIleIleThrThrLysAppProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATATTACCAACCAAGATCCATATTCAACACTCAAACTGCAACCAACCAACCA 639
QY 161 GluPheIleValSerAspSerThrTyrglyValAlaSerProTyrglySerThrIleProAla 180
Db 640 GAATTTATTGTAGTGACGACGACCTACTCGTGGCATCCCTTACTCTACATACCTGCC 699
QY 181 ProThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCTCTCTCCAGCTTCCACTTCTTATTCACCGGAGAAAAAATTGATT 759

201 CysValThrGluValPheMetClnThrSerThrMetSerThrGluThrGluProPheVal 220
760 TGTGTACAGAAAGTTTATGGAACCTAGCACCATTGTCTACAGAAACTGAACCAATTGTT 819
221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
820 GAAANATAAGCAGCAGCATTCAGAAATCAAGCTGCTGGTTGGAGGTGTCCCCACGCTCTG 879
241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrglyLys 260
880 CTAGTGCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 939
261 ArgTyrglyValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
940 AGGTATGTGAAGGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 999
281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
1000 AAAGTAGTAAGGAGGAGAGGCGCAATGATACCACTTAATGAGGAATCAAGAAACT 1059
301 AspLysAsnProGluGluSerLysSerProSerLysThrValArgCysLeuGluAla 320
1060 GATAAAAAACCCAGAGAGTCCAAGAGTCCAAGAAAACTACCGTGCATGCGCTGGAAGCT 1119

321 GluVal 322
1120 GAAGTT 1125

RESULT 20
US-09-902-903-200
; Sequence 200, Application US/09902903
; Publication No. US20030044839A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,903
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
```

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; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-902-903-200

Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-902-903-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGGCCAGGTGCTTCAGCGTGGTGTCTCTCTCCTCCATCTGGACACAGAGGCTCCGT 219
QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCCAAGGCTCTTTGGTGCAGAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCTTGTGAGCAAAAGCGAACACGAGCTGAATTTACAGAACTAAGAGGGCC 339
QY 61 CysArgLeuLeuGlySerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTCTGGGACTAAGTTTGGCGGCAAGGACCAAGTTGAAACAGCCCTTGAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAACACTTGACGTATGGCTGGGTGGAGATGGATTCTGTGTCATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAACCCCAAGTGTGGGAAAATGGGGTGGGTGCTCTGATTTGGAAAGGTCCAGATG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGCTTGGACCCCTATTGTTACAACTCATCTGATCTTGGACTTAACCTCGTGCA 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTTATCCACCCCAAGATCCCATATTTCAACACTCAAACTGCAACACAAACAA 639

QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAAATTTATTGTGAGTGACAGTACCTACTCGGTGGCATCCCTTACTTCTCAATACCTGCC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
Db 760 TGTGTACACAGAAAGTTTATGTAAGAACTAGCACCATGTCTACAGAAACTGAACCATTTGT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db 820 GAAATATAAGCAGCATTTCAAGAAATGAAGCTGTCTGGGTTTGGAGGTGTCCTCCAGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAATCAGCAGAGGAAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGAGAGAGAGGCCCAATGATAGCAACCCCTAATGAGGAATCAAGAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCCAGAGAGTCCAAAGAGTCCCAAGCAAAACTACCGTGGATGCTGGAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 21
US-09-903-749A-200
; Sequence 200, Application US/09903749A
; Publication NO. US20030045693A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/903,749A
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
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APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kijavin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/904,956  
CURRENT FILING DATE: 2001-07-12  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 200  
LENGTH: 2372  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-904-956-200

Alignment Scores:  
Pred. No.: 0 Length: 2372  
Score: 322.00 Matches: 322  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-904-956-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrArgLeuLeu 20  
Db 160 ARGCCAGGTGCTTACGCTGGTGTCTTCACCTCCATCTGGACCAACGAGGCTCTG 219  
QY 21 ValGlnGlySerArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40

Db 220 GTCCAGAGGCTCTTTGGTGCAGAGAGCTTTCCATCCAGGTGTATGCAAGAAATTATGGGG 279  
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
Db 280 ATCACCCCTTGTGAGCAAAAGCGCAACAGCAGCAGCTGAATTTCCACAGAACTAAGGAGGCC 339  
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
Db 340 TGTAGGCTGTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACACAGCCCTTGAAGCT 399  
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyValGlyValGlyValValIleSerArgIle 100  
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGGTCACTCTAGGATT 459  
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
Db 460 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCTCATTTGGAAGGTTCCAGTG 519  
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
Db 520 AGCCGACAGATTGTCAGCCCTATTGTACAACTCATCTGATCTTGGACTTAACCTCGTCATT 579  
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
Db 580 CCAGAAATATACCAACCAAGATCCATATTCAACACTCAACTCAACACCAACAAACA 639  
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
Db 640 GAAATTTATTGTCAGTCAGTACTACTCGTGGTGGCATCCCTTACTCTACAATACCTGCC 699  
QY 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200  
Db 700 CCTACTACT 759  
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
Db 760 TGTGTACAGAGATTTTATGGAACACTAGCACCATGTCTACAGAAACTGAACCAATTGTT 819  
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
Db 820 GAAATATAAGCAGCATTCAGAAATCAAGCTGCTGGGTGGAGGTGTCCTCCACGGCTCTG 879  
QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
Db 880 CTAGTGTCT 939  
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
Db 940 AGGTATGTGAAGCCCTTCCCTTTTACAAACAAGAAATCAGCAGAGAAATGATCGAAACC 999  
QY 281 LysValValLysGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
Db 1000 AAAAGTAGTAAGGAGGAGAGGCCCAATGATGCAACCCCTTAATGAGGAATCAAGAAACT 1059  
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
Db 1060 GATAAAAACCCAGAGAGTCCAAAGAGTCCAGAAAACTACCGTCGATGCTCGTGAAGCT 1119  
QY 321 GluVal 322  
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; Sequence 200, Application US/09902736  
; Publication No. US20030049676A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/902,736  
CURRENT FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: 09/665,350  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 200  
LENGTH: 2372  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-09-902-736-200

Alignment Scores:  
Pred. No.: 0  
Score: 322.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Length: 2372  
Matches: 322  
Conservative: 0  
Mismatch: 0  
Indels: 0

DB: 10 Gaps: 0  
US-10-079-111-1 (1-322) x US-09-902-736-200 (1-2372)  
QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20  
Db 160 ATGCCAGGTGCTTACGCTGGTGGTCTTCTCACCTCCATCTGGACACAGGCTCTG 219  
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
Db 220 GTCCAGGCTCTTTGGTGCAGAGAGCTTCCATCCAGGTGTCTATGCAAAATATGGG 279  
QY 41 IleThrLeuValSerIleValAlaGlnGlnLeuAsnPheThrGluAlaValGluAla 60  
Db 280 ATCACCCCTTGTGAGCAAAAGGCAACAGAGCTGAATTTACAGAGCTAAGGAGGCC 339  
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
Db 340 TGTAGGCTCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 399  
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100  
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGGTCTATCTCTAG 459  
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
Db 460 AGCCCAAAACCCCAAGTGTGGGAAATGGGGTGGGTGCTCTGATTTGGAGAGGTTC 519  
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
Db 520 AGCCGACAGTTTGCAGCTATTGTTACAACTCATCTGATCTTGGACTAATCGTGCA 579  
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
Db 580 CCAGAAATTTATCACCAAGATCCCATATTTCAACACTCAAACTCAACACACAAACA 639  
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
Db 640 GAATTTATGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTCAATACCTGC 699  
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeu 200  
Db 700 CCTACTACTACT 759  
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
Db 760 TGTGTACAGAAAGTTTTTATGGAATCTAGCACCATGTCTACAGAAATCAACCATTT 819  
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
Db 820 GAAATTAAGCAGCATTCAGAAATGAAGCTGTGGGTGGAGGTGTCCTCCACGGCTCTG 879  
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260  
Db 880 CTAGTGTCT 939  
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
Db 940 AGGTATGGAAGGCTTCCCTTTTACAAACAGAAATCAGCAAGAAATGATCGAAAC 999  
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysThr 300  
Db 1000 AAAGTAGTAAGGAGGAGAGGCCAATGATAGCAACCTAATGAGGAATCAAGAAACT 1059  
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
Db 1060 GATAAAACCCAGAGAGTCCAGAGTCCAGAGTCCAGCAAAACTACCGTGGTGGAGCT 1119  
QY 321 GluVal 322  
Db 1120 GAAGTT 1125  
RESULT 25



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US-09-907-794-200
; Sequence 200, Application US/09907794
; Publication No. US20030049677A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
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; PRIOR APPLICATION NUMBER: PCT/US99/28214
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; PRIOR APPLICATION NUMBER: PCT/US99/28313
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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
```

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; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-907-794-200
Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-10-079-111-1 (1-322) x US-09-907-794-200 (1-2372)
QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGGCCAGGTGCTTCAGCGTGGTGTCTCTCACTCCATCGACACGAGGCTCTGTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCCAAGGCTCTTTGCGTGCAGAAAGCTTCCATCCAGGTGTCATGCAAGATTATGGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCCCTGTGAGCAAAAAGCGAACCAGCAGCTGAATTCACAGAAGCTTAAGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCCTTGAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACCTTGACAGCTATGGCTGGGTGGAGATGGATTCGTGTCATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAAAACCCCAAGCTGTGGGAAAATGGGGTGGGTGCTCTGATTGGGAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGCTTTCAGCCCTATTTGTTACAACTCATCTGATCTACTTGGACTAACTCGTGCAAT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTTATCACCACCAAGATCCCATATTTCAACACTCAAACTCAAACTGCAACAAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAAATTTATGTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACATATACCTGCC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTACAGAAAGTTTATGGAACACTAGCACCCTCTCTACAGAACTGAAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATATAAGCAGCAGCATTCAGAAATGAAAGCTGCTGGGTTTGGAGGTGTCCCCACGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 939
QY 261 ArgTyrValLysAlaPhePheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGGCCCTTCCCTTTTACAAACAAAGATCAGCAGAGGAATGATGCAAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGAGAGGCCCAATCATAGCAACCTTATGAGAACTCAAAGAAACT 1059
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QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTACACGAAGTTTTTATGGAACCTAGCACCATGTCTACAGAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db 820 GAAATTAAGACGACATTCAGAAATGAAGCTGTGGGTTCGAGCTGGTCTTGGATTTCTATGTCAAA 879
QY 241 LeuValLeuAlaLeuPhePheGlyValAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGTCTGCTCTCTCTCTTTTGGTGTGCTGAGCTGGTCTTGGATTTCTATGTCAAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGTATGTGAAGCCCTTCCCTTTTACAAACAAGATCAGCAGAGGAATGATCGAAACC 999
QY 281 LysValLysGluGluLysAlaAsnAspSerAsnProAsnGluLysLysLysThr 300
Db 1000 AAGTGTAGTAAGAGGAGGAGGCAATGATAGCAACCTTAATGAGGATCAAGAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCACAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGATCGCTGGAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 28
US-09-907-925-200
; Sequence 200, Application US/09907925
; Publication No. US20030054352A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tunas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,925
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
```

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; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-907-925-200

Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-907-925-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGCCAGGTGCTTCAGCCTGGTGTCTTCTCATTCCATCTGGACACAGAGCTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAAGCTCTTTGGTGCAGAGAGCTTCCATCCAGGTGTCAGCAATATATGGGG 279
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCTTTGTGAGCAAAAGGCGAACACAGCAGCTGAATTTTCACAGAACTAAGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGlnThrAlaLeuLysAla 80
Db 340 TGTAGAGCTGCTGGAGCTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCTTTGAAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTTGGAGATGGATTCGTGGTCACTCTAGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAACCCCAAGGTGGGAAAAATGGGGTGGTCTCTGATTTGGAAGGTTCAGATG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTTGGACTAACTCGTGATT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
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Db 580 CCAGAAATTTATCACCACCAAGAGTCCCATATTCACACACTCAAACTGCAACCAACAACA 639
Qy 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAAATTTATGTCAGTGACAGTACTACTCGGTGGCATCCCTTACTCTACATACCTGCC 699
Qy 181 ProThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysIleu 200
Db 700 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 759
Qy 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTACACAGAAGTTTTATGGAACACTAGCACCATGTCTACAGAACTGAACCATTTGTT 819
Qy 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATTAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 879
Qy 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGTCTGCTCTCTCTCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 939
Qy 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGTATGTGAAGCCCTTCCCTTTTACAAACAAGATCAGCAAGAAATGATCGAAACC 999
Qy 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGGAGGCAATGATAGCAACCTTAATGAGGAATCAAGAAACT 1059
Qy 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAACTACCGTGGATGCTGGGAAGCT 1119
Qy 321 GluVal 322
Db 1120 GAAGTT 1125
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## RESULT 29

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US-09-902-692-200
; Sequence 200, Application US/09902692
; Publication No. US20030054400A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertitsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,692
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; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/900219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-902-692-200
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## Alignment Scores:

Pred. No.:	0	Length:	2372
Score:	322.00	Matches:	322
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-079-111-1 (1-322) x US-09-902-692-200 (1-2372)

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Qy 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGGCCAGGTGCTTCAGCCTGGTGTCTTCTCACTCCATCGACCACGAGGCTCCTG 219
Qy 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAGGCTCTTTCGTGTCAGAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGG 279
Qy 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db 280 ATCACCTTGTGAGCAAAAGCGAACCCAGCAGCTGAAATTTCCAGAAAGCTAAGAGGCC 339
Qy 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGlnThrAlaLeuLysAla 80
Db 340 TGTAGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 399
Qy 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGACAGCTATGCTGGTGGATGGATGCTGCTGCTATCTCTAGGATT 459
Qy 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
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Db      460 AGCCCAACCCCAAGTGTGGAAAAATGGGTGGGTGCTCGATTTTGGAGGTTCCAGTG 519
QY      121 SerArgGlnPheAlaIaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db      520 AGCCGACAGTTTGCAGCTATTGTGTACAACTCATCTGATCTTGGACTTAACCTCGTGCAAT 579
QY      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db      580 CCAAGAAATTATCACCAACCAAGATCCCATATTCACACACTCAAACTCAACACACAAACA 639
QY      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db      640 GAATTTATTGTCACTGACAGTACTTCTCGGTGGCATCCCTTACTTCTCAATACCTGCC 699
QY      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db      700 CCTACTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 759
QY      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db      760 TGTGTACACAGAGTTTTTATGGAACTAGCACCATGTCTACAGAACTGAACCATTTGTT 819
QY      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db      820 GAAATAAAGCAGCATTCAGAAATGAAGCTGCTGGGTGGAGGTGTCCTCCACGGCTCTG 879
QY      241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db      880 CTAGTGTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 939
QY      261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db      940 AGGTATGTGAAGCCCTTCCCTTTTACAAACAAGATTCAGCAAGAGAAATGATCGAAACC 999
QY      281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db      1000 AAAGTAGTAAAGAGGAGAGGAGGCAATGATAGCAACCTTAATGAGGAATCAAGAAACT 1059
QY      301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db      1060 GATATAAAACCCAGAGAGTCCAGAGTCCCAAGCAAACTACCGTGGATGCCTGGGAAGCT 1119
QY      321 GluVal 322
Db      1120 GAAGTT 1125

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RESULT 30

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US-09-903-520-200
; Sequence 200, Application US/09903520
; Publication No. US20030054401A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/903,520
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-903-520-200

Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-1111-1 (1-322) x US-09-903-520-200 (1-2372)
QY      1 MetAlaArgCysPheSerIleuValIleuLeuThrSerIleTrrThrThrArgIleuLeu 20
Db      160 ATGGCCAGGTGCTTCAGCTGGTGTCTTCATCTTCATCTGCACACCGAGGCTCTGTG 219
QY      21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db      220 GTCCAAAGGCTCTTTCGCTGCAGAGAGGCTTCCATCCAGGTGTCATGCAGAAATTAAGGG 279
QY      41 IleThrLeuValSerLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db      280 ATCACCTTGTGAGCAAAAGCGCAACAGCAGCTGAATTTTCAAGAGCTAAGAGGCC 339

```

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QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAACATTGACAGCTATGGCTGGGTGGAGATGGATTGGTGCATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAACCCCAAGTGGGAAATGGGTGGGTGCTCTGATTTGGGAAGTTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTTACAACTCATCTGATCTTGGACTTAACCTGTCGATT 579
QY 141 ProGluIleIleThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTGTCAGTGACAGTACTACTCGGTGGCATCCCTTACTCTACAATACTCTGCC 699
QY 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db 700 CCTACTACTACTCCTCTCTCCAGCTTCCACTTCTTAATCCACGGAGAAAAAATTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTCACAGAGTTTATGGAACACTAGCACCATGCTACAGAAACTGAAACATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATAAAGCAGCATTCAAGATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGCTTGTCTCTCTCTTCTTGTGTGCTGAGCTGCTTGGATTTTGTATGTCAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGCCTTCTCTTTTCAAAACAGAAATCACAGAGAAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGGAGGCAATGATAGCAACCTTAATGAGGAATCAAAGAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCCCAAGAGTCCAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCCCTGGAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 31
US-09-905-056-200
; Sequence 200, Application US/09905056
; Publication No. US2003005441A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
```

```
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,056
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-905-056-200
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Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
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US-10-079-111-1 (1-322) x US-09-905-056-200 (1-2372)

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QY 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrArgLeuLeu 20
Db 160 ATGGCCAGGTGGTTCAGCTGGTGTGCTTCTCACTTCATCTGGACCACGAGGCTCTG 219
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QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
Db 220 GTCAGAGCTCTTTGGTGCAGAGAGCTTTCATCCAGGTGTCATGCAGAAATATGGGG 279  
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
Db 280 ATCAACCTTGAGCAAAAGGGCAACAGCAGCTGAATTTCAAGAGCTAAGAGGCC 339  
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
Db 340 TGTAGGCTGCTGGCACTAAGTTTGGCGGCAAGGACCAAGTTGAAACAGCTTGAAGCT 399  
QY 81 SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle 100  
Db 400 AGCTTTGAACCTTGCAGCTATGCTGGTGGAGATGGATTCGTGTCATCTCTAGGATT 459  
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
Db 460 AGCCCAACCCCAAGTGTGGAAATAATGGGTGGTGTCTGATTTGGAAGGTTCCAGTG 519  
QY 121 SerArgGlnPheAlaLysTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
Db 520 AGCCGACAGTTGACGCCATTGTTTACAACCTCATCTGATACCTTGGACTAACTCGTGCAIT 579  
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
Db 580 CCAGAAATATATACCAACCAAGATCCCATATTCACACTCAAACTCAACACACAAACA 639  
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
Db 640 GAAATTTATGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTCAATACCTGCC 699  
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200  
Db 700 CCTACTACTACTCCTCCTCCTCCAGCTTCCAGCTTCTATTCCACGGAGAAAAAATGAT 759  
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
Db 760 TGTGTACAGAGATGTTTTATGAAACTAGCACCATGCTACAGAAACTGAACATTTGTT 819  
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240  
Db 820 GAAATAAAGCAGCATTCAGAATGAAGCTGTGCTGGTGTGGAGGTGTCGCCCGCTCTG 879  
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
Db 880 CTAGTGCTTGCTCTCTCTCTTGTGCTGCTGCTGGTCTTGGATTTTGTCTATGTCAA 939  
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
Db 940 AGGTATGTGAAGGCTTCCCTTTTACAACACAGATTCACAGAGGAATGATCGAACC 999  
QY 281 LysValValLysGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
Db 1000 AAAGTAGTAAGAGGAGAGGAGGCAATGATAGCAACCTTAATGAGGAATCAAGAAACT 1059  
QY 301 AspLysAsnProGluLysSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
Db 1060 GATAAAACCCAGAGAGTCCAGAGTCCAGCAAAACTTACCGTGCATGCTGGAAGCT 1119  
QY 321 GluVal 322  
Db 1120 GAAATT 1125

RESULT 32

US-09-909-064-200  
; Sequence 200, Application US/09909064  
; Publication No. US20030059772A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David

Alignment Scores:  
Pred. No.: 0  
Score: 322.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Length: 2372  
Matches: 322  
Conservative: 0  
Mismatch: 0

; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/909,064  
; CURRENT FILING DATE: 2001-07-18  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 200  
; LENGTH: 2372  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-909-064-200



Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0
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Qy	1	MetAlaAcySpheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu	20
Db	160	ATGGCCAGGTGTTTCAGCCTGGTGTGCTTCCTCCTCCATCTGGACACACAGGCTCCGTG	219
Qy	21	ValGlnGlySerLeuArgAlaGluLeuLeuSerIleGlnValSerCysArgIleMetGly	40
Db	220	GTCCAGGCTCTTTCGCTGCAGAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGGG	279
Qy	41	IleThrLeuValSerIlyslsAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Db	280	ATCACCCCTTGTGAGCAAAAAGCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGGAGGC	339
Qy	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Db	340	TGTAGCTGCTGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAGCT	399
Qy	81	SerpheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
Db	400	AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGCTCATCTCTAGGATT	459
Qy	101	SerProAsnProIysCysGlyLysAsnGlyValGlyValIleTrpIlyslsValProVal	120
Db	460	AGCCCAAAACCCCAAGGTGGGAAAAATGGGGTGGGTCTCTGATTTGGGAAGGTTCCAGTG	519
Qy	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Db	520	AGCCGACAGTTTGCAGCCTATTGTACAACTCATCTGATACTTGGACTTAACCTCGTGCA	579
Qy	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Db	580	CCAGAAATATATCACCAACCAAGATCCATATTCAACACTCAAACTGCAACACAAACA	639
Qy	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Db	640	GAATTTATTGTGAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTCAATACCTGCC	699
Qy	181	ProThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Db	700	CCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAATTGATT	759
Qy	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Db	760	TGTGTACAGAAAGTTTATTGAAACTAGCACCATGCTTACAGAAACTGAACCATTTGTT	819
Qy	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu	240
Db	820	GAATAATAAGCAGCATTCAGAAATGAAGTGTGGGTGGGTGGGTGGGTGGGTGGGTGG	879
Qy	241	LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Db	880	CTAGTGCTTCT	939
Qy	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr	280
Db	940	AGGTATGTGAAGGCTTCCCTTTTCAAAACAAGAAATCAGCAGAGAAATGATCGAAACC	999
Qy	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluLysSerIlyslsThr	300
Db	1000	AAAGTAGTAAAGAGAGAGAGGCAATGATAGCAACCTTAATGAGAAATCAAGAAAACT	1059
Qy	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Db	1060	GATAAAAACCCAGAGAGTCCAGAGTCCAGCAAAACTACCGTGCATGCTCGGAAGCT	1119
Qy	321	GluVal	322
Db	1120	GAAGTT	1125

RESULT 33	
US-09-904-553-200	
/ Sequence 200, Application US/09904553	
/ Publication No. US20030059828A1	
/ GENERAL INFORMATION:	
/ APPLICANT: Genentech, Inc.	
/ APPLICANT: Ashkenazi, Avi	
/ APPLICANT: Botstein, David	
/ APPLICANT: Desnoyers, Luc	
/ APPLICANT: Eaton, Dan L.	
/ APPLICANT: Ferrara, Napoleone	
/ APPLICANT: Filvaroff, Ellen	
/ APPLICANT: Fong, Sherman	
/ APPLICANT: Gao, Wei-Qiang	
/ APPLICANT: Gerber, Hanspeter	
/ APPLICANT: Gerritsen, Mary E.	
/ APPLICANT: Goddard, A.	
/ APPLICANT: Godowski, Paul J.	
/ APPLICANT: Grimaldi, Christopher J.	
/ APPLICANT: Gurney, Austin L.	
/ APPLICANT: Hillan, Kenneth, J.	
/ APPLICANT: Kljavin, Ivar J.	
/ APPLICANT: Mather, Jennie P.	
/ APPLICANT: Pan, James	
/ APPLICANT: Paoni, Nicholas P.	
/ APPLICANT: Roy, Margaret Ann	
/ APPLICANT: Stewart, Timothy A.	
/ APPLICANT: Tumas, Daniel	
/ APPLICANT: Williams, P. Mickey	
/ APPLICANT: Wood, William, I.	
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic	
/ TITLE OF INVENTION: Acids Encoding the Same	
/ FILE REFERENCE: 10466-14	
/ CURRENT APPLICATION NUMBER: US/09/904,553	
/ CURRENT FILING DATE: 2002-01-22	
/ PRIOR APPLICATION NUMBER: PCT/US00/04414	
/ PRIOR FILING DATE: 2000-02-22	
/ PRIOR APPLICATION NUMBER: US 60/143,048	
/ PRIOR FILING DATE: 1999-07-07	
/ PRIOR APPLICATION NUMBER: US 60/145,698	
/ PRIOR FILING DATE: 1999-07-26	
/ PRIOR APPLICATION NUMBER: US 60/146,222	
/ PRIOR FILING DATE: 1999-07-28	
/ PRIOR APPLICATION NUMBER: PCT/US99/20594	
/ PRIOR FILING DATE: 1999-09-08	
/ PRIOR APPLICATION NUMBER: PCT/US99/20944	
/ PRIOR FILING DATE: 1999-09-13	
/ PRIOR APPLICATION NUMBER: PCT/US99/21090	
/ PRIOR FILING DATE: 1999-09-15	
/ PRIOR APPLICATION NUMBER: PCT/US99/21547	
/ PRIOR FILING DATE: 1999-09-15	
/ PRIOR APPLICATION NUMBER: PCT/US99/23089	
/ PRIOR FILING DATE: 1999-10-05	
/ PRIOR APPLICATION NUMBER: PCT/US99/28214	
/ PRIOR FILING DATE: 1999-11-29	
/ PRIOR APPLICATION NUMBER: PCT/US99/28313	
/ PRIOR FILING DATE: 1999-11-30	
/ PRIOR APPLICATION NUMBER: PCT/US99/28564	
/ PRIOR FILING DATE: 1999-12-02	
/ PRIOR APPLICATION NUMBER: PCT/US99/28565	
/ PRIOR FILING DATE: 1999-12-02	
/ PRIOR APPLICATION NUMBER: PCT/US99/30095	
/ PRIOR FILING DATE: 1999-12-16	
/ PRIOR APPLICATION NUMBER: PCT/US99/30911	
/ PRIOR FILING DATE: 1999-12-20	
/ PRIOR APPLICATION NUMBER: PCT/US99/30999	
/ PRIOR FILING DATE: 1999-12-20	
/ PRIOR APPLICATION NUMBER: PCT/US00/00219	
/ PRIOR FILING DATE: 2000-01-05	
/ NUMBER OF SEQ ID NOS: 423	
/ SEQ ID NO 200	
/ LENGTH: 2372	
/ TYPE: DNA	

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i      ORGANISM: Homo sapiens
US-09-904-553-200

Alignment Scores:
Pred. No.:      0      Length:      2372
Score:          322.00    Matches:      322
Percent Similarity: 100.00%  Conservative:  0
Best Local Similarity: 100.00%  Mismatches:  0
Query Match:      100.00%  Indels:      0
DB:              10      Gaps:        0

US-10-079-111-1 (1-322) x US-09-904-553-200 (1-2372)

QY      1  MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db      160  ATGCCAGGCTGCTTACGCTGGTGTCTCTCCTCCTCCTCCTCCTCCTCCTCCTG 219

QY      21  ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db      220  GTCCAAAGGCTCTTTGGTGCAGAAAGAGCTTCCATCCAGGTGTCATGCAGAAATTATGGG 279

QY      41  IleThrLeuValSerIlylsAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
Db      280  ATCACCTTTGTGAGCAAAAGCGAAACCCAGCAGCTGAATTTTCAGAAAGCTAAGGAGGCC 339

QY      61  CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db      340  TGTAGGCTGCTGGACTAGTTGGTGGCGGCAAGACCAAGTTGAAACAGCTTTGAAGCT 399

QY      81  SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle 100
Db      400  AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTCTGTGTCATCTCTAGGATT 459

QY      101  SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db      460  AGCCCAAAACCCCAAGTGTGGGAAATATGGGTGGTCTCTGATTTGGAAAGGTTCAGTG 519

QY      121  SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db      520  AGCCGACAGTTTGCAGCTATTGTTACAACTATCTGATCTATCTGGACTTACTCTGTCATT 579

QY      141  ProGluIleIleThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db      580  CCAGAAATTTATCACCAACCAAGATCCCATATTCAACACTCAAACTCAACACAAACA 639

QY      161  GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db      640  GAATTTATTTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAAATACCTGCC 699

QY      181  ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
Db      700  CCTACTACTACTCTCTCTCTCTCCAGCTTCCACTTCTATTTCCACGGGAAAAAATTTGATT 759

QY      201  CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db      760  TGTGTACAGAAAGTTTTATGAAATAGCAGCATGCTACAGAACTGAACCACTTTGTT 819

QY      221  GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db      820  GAAATAAAGCAGCATTTAAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879

QY      241  LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLysGlyPheCysTyrValLys 260
Db      880  CTAGTGTCTCTCTCTCTCTCTTCTTGGTGTGCTGAGCTGCTTGGATTGCTATGTCAAA 939

QY      261  ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db      940  AGGTATGTGAAGCCCTTCCCTTTTACAAACAAGAAATCAGCAAGGAAATGATCGAAACC 999

QY      281  LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db      1000  AAAGTAGTAAAGAGGAGGAGGCCAATGATAGCAACCCCTAATGAGGAATCAAGAAAACT 1059

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QY      301  AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
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QY      321  GluVal 322
Db      1120  GAAGTT 1125

RESULT 34
US-09-905-381-200
; Sequence 200, Application US/09905381
; Publication No. US20030059829A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,381
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
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; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16

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; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-905-381-200

Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-905-381-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleThrThrArgLeuLeu 20
DB 160 ATGCCAGGCTTCAGCCCTGGTGTCTCTCACTCCATCTGGACCCAGGCTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
DB 220 GTCCAGGCTCTTGGGTGCAGAGAGCTTTCCATCCAGGTGTCTCCAGAAATTATGGG 279
QY 41 IleThrLeuValSerIlyslsAlaAsnGlnGlnLeuAsnPheThrGluAla 60
DB 280 ATCACCCCTGTGAGCAAAAGGCGACACGACGCTGAATTTACAGAGCTAAGGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
DB 340 TGTAGCTCTGGACTAAGTTTGGCGGCGAGACCAAGTTGAACAGCCTTGAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle 100
DB 400 AGCTTTGAAACTTGACAGTATGCTGGTGGAGATGGATTCGTGCTCATCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleThrLysValProVal 120
DB 460 AGCCCAAAACCCCAAGTGTGGAAAAATGGGTGGGTGCTCTGATTTGGAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
DB 520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTTGGACTTAACCTGTCATT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
DB 580 CCAGAAATTTATCACCCCAAGATCCCATATTCACACTCAAACTCAACACACAAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
DB 640 GAATTTATTGTGAGTACAGTACCTACTCGTGGCATCCCTTACTCTACAAATACCTGCC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
DB 700 CCTACTACTCTCTCTCTCAGCTTCCACTTCTATTCACCGAGAGAAAAATTTGATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
DB 760 TGTGTACAGAAATTTTATGGAACCTAGCACCATGTCTACAGAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
DB 820 GAAAAATAAGCAGATTCAAGATGAAGCTGTGGGTTCGAGGTGTCCCGGCTCTG 879
QY 241 LeuValLeuAlaLeuPhePheGlyAlaAlaGlyLeuGlyPheCysTyrValLys 260

DB 880 CTAGTGCTTGCTCTCTCTCTTGGTGCTGCAGCTGGTCTTGGATTTCGTATGTCAAA 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
DB 940 AGGTATGTGAGGCTTCCCTTTTACAAACAAGAATCAGCAGAGGAAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
DB 1000 AAGTAGTAAAGAGGAGAGGCCAATGATGACACCCCTAATGAGGAATCAAGAAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
DB 1060 GATAAAACCCAGAGAGTCCAAGAGTCCAAGAAAACTACCGTGGATGCTCGGAAGCT 1119
QY 321 GluVal 322
DB 1120 GAAGTT 1125

RESULT 35
US-09-905-088-200
; Sequence 200, Application US/09905088
; Publication No. US20030073077A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,088
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05

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/ PRIOR APPLICATION NUMBER: PCT/US99/28214
/ PRIOR FILING DATE: 1999-11-29
/ PRIOR APPLICATION NUMBER: PCT/US99/28313
/ PRIOR FILING DATE: 1999-11-30
/ PRIOR APPLICATION NUMBER: PCT/US99/28564
/ PRIOR FILING DATE: 1999-12-02
/ PRIOR APPLICATION NUMBER: PCT/US99/28565
/ PRIOR FILING DATE: 1999-12-02
/ PRIOR APPLICATION NUMBER: PCT/US99/30095
/ PRIOR FILING DATE: 1999-12-16
/ PRIOR APPLICATION NUMBER: PCT/US99/30911
/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: PCT/US99/30999
/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: PCT/US00/00219
/ PRIOR FILING DATE: 2000-01-05
/ NUMBER OF SEQ ID NOS: 423
/ SEQ ID NO 200
/ LENGTH: 2372
/ TYPE: DNA
/ ORGANISM: Homo Sapien
/ US-09-905-088-200

Alignment Scores:
Pred. No.: 0          Length: 2372
Score: 322.00         Matches: 322
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%    Mismatches: 0
Query Match: 100.00%             Indels: 0
DB: 10                        Gaps: 0

US-10-079-111-1 (1-322) x US-09-905-088-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGGCCAGGTCTTTCAGCTGGTGTCTTCTCACCTTCCATCTCCAGCCACGAGGCTCCTG 219
QY 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAGAGCTCTTGGTGCAGNAGAGCTTTCATCCAGTGTTCATGCAGAAATATGGGG 279
QY 41 IleThrLeuValSerIleLysAlaGlnGlnLeuAsnGlnLeuAsnGlnLeuAla 60
Db 280 ATCACCTTGTGAGCAAAAGGCAACAGCAGCTCAATTTCCACAGAGCTAAGGAGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGlnThrAlaLeuLysAla 80
Db 340 TGTAGGCTCTGGGACTAAGTTTGGCCGCGCAAGCAAGTGAACACAGCCTTGAAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAACTTGCAGCTATGGCTGGTTGGAGATGGATTCTGTGTCATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
Db 460 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGTCTGATTTTGGAAAGGTTCCAGTG 519
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 ACCCGACAGTTTGCAGCCCTATTGTTACAACTCATCTGATCTGGACTTAACCTCGTCATT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATTTATCACCAACAAAGATCCATATTCAACACTCAACTGCAACACACAAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTGTGAGTGACAGTACTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgLysLysLeuIle 200
Db 700 CTTACTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 759

QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPropheVal 220
Db 760 TGTGTACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
Db 820 GAAATTAAGCAGCATTCAGATGAAGCTGTGGTGGTGGAGGTGTCCCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAAGCCCTTCCCTTTTACAAACAAGATCAGCAGAGGAAATGATCGAAACC 999
QY 281 LysValValLysGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
Db 1000 AAAGTAGTAAGGAGGAGAGGCCAATGATAGCAACCTAATAGGAGNATCAAGAAACT 1059
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCCAGAGAGTCCAGAGTCCAAAGCAAAACTACCGTGGCATGCTGGAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125

RESULT 36
US-09-907-575-200
/ Sequence 200, Application US/09907575
/ Publication No. US20030073079A1
/ GENERAL INFORMATION:
/ APPLICANT: Genentech, Inc.
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, A.
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, Christopher J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth, J.
/ APPLICANT: Kljavin, Ivar J.
/ APPLICANT: Mather, Jennie P.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William, I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ TITLE OF INVENTION: Acids Encoding the Same
/ FILE REFERENCE: 10466-14
/ CURRENT APPLICATION NUMBER: US/09/907,575
/ PRIOR FILING DATE: 2001-12-18
/ PRIOR APPLICATION NUMBER: PCT/US00/04414
/ PRIOR FILING DATE: 2000-02-22
/ PRIOR APPLICATION NUMBER: US 60/143,048
/ PRIOR FILING DATE: 1999-07-07
/ PRIOR APPLICATION NUMBER: US 60/145,698
/ PRIOR FILING DATE: 1999-07-26
/ PRIOR APPLICATION NUMBER: US 60/146,222
/ PRIOR FILING DATE: 1999-07-28
/ PRIOR APPLICATION NUMBER: PCT/US99/20594
/ PRIOR FILING DATE: 1999-09-08
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; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-979-200

Alignment Scores:
Pred. No.: 0 Length: 2372
Score: 322.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-907-979-200 (1-2372)

QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
Db 160 ATGGCCAGGTGCTTTCAGCTGGTGTCTTCACCTTCATTCGACCCACGAGGCTCCGTG 219
QY 21 ValGInGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
Db 220 GTCCAAAGGCTCTTTCGCTGCAGAGAGCTTCCATCCAGGTGTCTATGCAAGATTATGGGG 279
QY 41 IleThrLeuValSerIlyslsAlaGlnGlnLeuAenPheThrGluAlaLysGluAla 60
Db 280 ATCAACCTTGTGAGAAAAGCGCAACCCAGCAGCTGAATTTCCACAGAAGCTAAGAGGGCC 339
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
Db 340 TGTAGGCTGCTGGAGCTAGTTTGGCCGCAAGGACCAAGTTGAACAGCCCTTGAAGCT 399
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
Db 400 AGCTTTGAAACTTGCAGCTATGCTGGTGGAGATGGATTCGTGCTCATCTCTAGGATT 459
QY 101 SerProAsnProLysCysGlyLysAenGlyValGlyValLeuIleTrpIysValProVal 120
Db 460 AGCCCAAAACCCCAAGGTGGGAAAAATGGGGTGGGTGCTCTGATTGTGGAAGGTTCCAGTG 519

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QY 121 SerArgGlnPheAlaAlaTyrCysTyrAenSerSerAspThrTrpThrAsnSerCysIle 140
Db 520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACCTTGGACTTAACCTGTCATT 579
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
Db 580 CCAGAAATATATCACCACCAAGATCCCATATTCAACACTCAAACTCAACACACAAACA 639
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
Db 640 GAATTTATTGTGTCAGTCAGTACCTACTCGGTGGCATCCCTTACTTCAATACCTGCC 699
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgIlyslsLeuIle 200
Db 700 CCTACTACTACTCTCTCTCCAGCTTCCACTTCTATTCCACGAGAAAAAATTCATT 759
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
Db 760 TGTGTACAGAAAGTTTTATGGAACCTAGCACCATGTCTACAGAACTGAACCTTTGTT 819
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
Db 820 GAAATATAAGCAGCATTCAAGAAATGAAGCTGCTGGGTGTTGGAGGTGTCCCCACGGCTCTG 879
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
Db 880 CTAGTGTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 939
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
Db 940 AGGTATGTGAGGCTTCCCTTTTACAAACAAGATCACAGAAAGAAATGATCGAAACC 999
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysThr 300
Db 1000 AAAGTAGTAAAGGAGGAGAGCCCAATGATAGCAACCTTAATGAGGAATCAAGAAACT 1059
QY 301 AspLysAsnProGluLysSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
Db 1060 GATAAAACCCAGAAAGTCCAAAGAGTCCAAAGAACTACCGTGGATGCGCTGGAAGCT 1119
QY 321 GluVal 322
Db 1120 GAAGTT 1125
RESULT 42
US-09-902-615-200
; Sequence 200, Application US/09902615
; Publication No. US20030092002A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel

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	PRIOR APPLICATION NUMBER:	US /09/665,350	
	PRIOR FILING DATE:	2000-09-18	
	PRIOR APPLICATION NUMBER:	US 60/143,048	
	PRIOR FILING DATE:	1999-07-07	
	PRIOR APPLICATION NUMBER:	US 60/145,698	
	PRIOR FILING DATE:	1999-07-26	
	PRIOR APPLICATION NUMBER:	US 60/146,222	
	PRIOR FILING DATE:	1999-07-28	
	PRIOR APPLICATION NUMBER:	PCT/US99/20594	
	PRIOR FILING DATE:	1999-09-08	
	PRIOR APPLICATION NUMBER:	PCT/US99/20944	
	PRIOR FILING DATE:	1999-09-13	
	PRIOR APPLICATION NUMBER:	PCT/US99/21090	
	PRIOR FILING DATE:	1999-09-15	
	PRIOR APPLICATION NUMBER:	PCT/US99/21547	
	PRIOR FILING DATE:	1999-09-15	
	PRIOR APPLICATION NUMBER:	PCT/US99/23089	
	PRIOR FILING DATE:	1999-10-05	
	PRIOR APPLICATION NUMBER:	PCT/US99/28214	
	PRIOR FILING DATE:	1999-11-29	
	PRIOR APPLICATION NUMBER:	PCT/US99/28313	
	PRIOR FILING DATE:	1999-11-30	
	PRIOR APPLICATION NUMBER:	PCT/US99/28564	
	PRIOR FILING DATE:	1999-12-02	
	PRIOR APPLICATION NUMBER:	PCT/US99/28565	
	PRIOR FILING DATE:	1999-12-02	
	PRIOR APPLICATION NUMBER:	PCT/US99/30095	
	PRIOR FILING DATE:	1999-12-16	
	PRIOR APPLICATION NUMBER:	PCT/US99/30911	
	PRIOR FILING DATE:	1999-12-20	
	PRIOR APPLICATION NUMBER:	PCT/US99/30999	
	PRIOR FILING DATE:	1999-12-20	
	PRIOR APPLICATION NUMBER:	PCT/US00/00219	
	PRIOR FILING DATE:	2000-01-05	
	NUMBER OF SEQ ID NOS:	423	
	SEQ ID NO	200	
	LENGTH:	2372	
	TYPE:	DNA	
	ORGANISM:	Homo Sapien	
	US -09-903-823-200		
	Alignment Scores:		
	Pred. No.:	0	Length: 2372
	Score:	322.00	Matches: 322
	Percent Similarity:	100.00%	Conservative: 0
	Best Local Similarity:	100.00%	Mismatches: 0
	Query Match:	100.00%	Indels: 0
	DB:	10	Gaps: 0
	US -10-079-111-1 (1-322) x US -09-903-823-200 (1-2372)		
Qy	1 MetAlaArgCysPheSerLeuValLeuThrSeriIleTrrpThrTrpThrArgLeuLeu 20		
Db	160 ATGGCCAGGTGTCATTACCGTGTTGCATCTTCACTTCCATCTGCCACCACGAGGCTCCTG 219		
Qy	21 ValGlubGlySerLeuArgAlaGluLgLuSeuSeriIleGlnValSerCysArgileMetGly 40		
Db	220 GTCCAAGGCTCTTGGTGCGAAGAAGGCTTCCATCCAGGTGTATGCGAGAAATTATGGGG 279		
Qy	41 IleThrLeuValSerLylysylalaahengInGlnLeuanPhetrGluAlalyeGluLa 60		
Db	280 ATCACCTTGTGAGCAAAAAGCGAACACAGCATGTAATTTACAGAAAGCTTAAGGAGGCC 339		
Qy	61 CysArgLeuLeuGlySerLeukalagilyAspglnValGluThrAlaleuLyala 80		
Db	340 TGTAGGCTCTGGGAATAAGTTTGGCCGCAAGGACCAAGTTGAACAAGCCTTCAAAGCT 399		
Qy	81 SerPheGluThrCysSerTyrglYtTpValglyAspGlyPheValValIlleserArgile 100		
Db	400 AGCTTTGAAACTGACGATATGCTGGGTTGGAGATGATTCGTGGTCATCTTAGGATT 459		
Qy	101 SerProAnSProllysCysGlyLyasnglyValglYvalLeulleTrrpLysValproVal 120		









; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/005,125

; CURRENT FILING DATE: 2001-07-12

; PRIOR APPLICATION NUMBER: 09/665,350

; PRIOR FILING DATE: 2000-09-18

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26

; PRIOR APPLICATION NUMBER: US 60/146,222

; PRIOR FILING DATE: 1999-07-28

; PRIOR APPLICATION NUMBER: PCT/US99/20594

; PRIOR FILING DATE: 1999-09-08

; PRIOR APPLICATION NUMBER: PCT/US99/20944

; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: PCT/US99/21090

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/21547

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/23089

; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: PCT/US99/28214

; PRIOR FILING DATE: 1999-11-29

; PRIOR APPLICATION NUMBER: PCT/US99/28313

; PRIOR FILING DATE: 1999-11-30

; PRIOR APPLICATION NUMBER: PCT/US99/28564

; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: PCT/US99/28565

; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: PCT/US99/30095

; PRIOR FILING DATE: 1999-12-16

; PRIOR APPLICATION NUMBER: PCT/US99/30911

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US99/30999

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US00/00219

; PRIOR FILING DATE: 2000-01-05

; NUMBER OF SEQ ID NOS: 423

; SEQ ID NO 200

; LENGTH: 2372

; TYPE: DNA

; ORGANISM: Homo Sapien

US-09-905-125-200

Alignment Scores:

Pred. No.: 0 Length: 2372  
Score: 322.00 Matches: 322  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0

US-10-079-111-1 (1-322) x US-09-905-125-200 (1-2372)

QY 1 MetaAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrThrArgLeuLeu 20

Db 160 ATGGCCAGGTGCTTCCAGCTGGTGGTCTTCTCACTTCCATCTGACACAGAGGCTCCG 219  
QY 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40  
Db 220 GTCCAAGGCTCTTTCGGTGCAGAGAGCTTTCATCCAGGTCTCATGCAAGAAATATGGG 279  
QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
Db 280 ATCACCTTGTGAGCAAAAGCGAACCCAGCAGCTGAATTTTCACAGAGCTAAGGAGGCC 339  
QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
Db 340 TGTAGGCTGTGGGACTAAGTTTGGCCGCGCAAGGACCAAGTTGAACAGCCTTGAAAGCT 399  
QY 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100  
Db 400 AGCTTTGAAACTTGCAGCTATGGCTGGTGGAGATGGATTCTGGTCACTCTAGGATT 459  
QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
Db 460 AGCCCAAAACCCCAAGTGTGGGAAATGGGTGGGTGCTCTGATTGGGAAGGTTCCAGTG 519  
QY 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
Db 520 AGCCGACAGTTTGCAGCTATTTGTACACTCATCTGATCTTGGACTTAACCTCGTCATT 579  
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
Db 580 CCAGAAATTTATCACCAACAGATCCCATATTTCAACACTCAAACTGCAACACAAACA 639  
QY 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrTrpSerThrIleProAla 180  
Db 640 GAAATTTATGTGTCAGTCAGATCACTTCTGGTGGATCCCTTACTCTACAATACCTGCC 699  
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgLysLysLeuIle 200  
Db 700 CCTACTACTACTCTCTCTCTCTCCAGCTTCCATCTTATTCACGAGAGAAAAATTTGATT 759  
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
Db 760 TGTGTCAAGAAAGTTTTTATGAAACTAGCACCATGTCTACAGAAACTGAACCAATTTGTT 819  
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240  
Db 820 GAAATAAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 879  
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
Db 880 CTAGTGTCT 939  
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
Db 940 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAAATCAGCAGAGAAATGATCGAAACC 999  
QY 281 LysValValLysGluLysAlaAsnAspSerAsnProAsnGluLysSerLysLysThr 300  
Db 1000 AAAGTAGTAAAGGAGAGAGGCCCAATGATACCAACCTTAATGAGAAATCAAGAAACT 1059  
QY 301 AspLysAsnProGluLysSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
Db 1060 GATAAAACCCAGAGAGTCCAGAGATCCAGCAAACTACCGTGGATCGCTGGAGCT 1119  
QY 321 GluVal 322  
Db 1120 GAAGTT 1125

RESULT 50

US-09-906-815A-200

; Sequence 200, Application US/09906815A

; Publication No. US20030113838A1

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnovers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, A.  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, Christopher J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth, J.  
 ; APPLICANT: Kljavin, Ivar J.  
 ; APPLICANT: Mather, Jennie P.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William, I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: 10466-14  
 ; CURRENT APPLICATION NUMBER: US/09/906, 815A  
 ; PRIOR FILING DATE: 2001-07-16  
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414  
 ; PRIOR FILING DATE: 2000-02-22  
 ; PRIOR APPLICATION NUMBER: US 60/143, 048  
 ; PRIOR FILING DATE: 1999-07-07  
 ; PRIOR APPLICATION NUMBER: US 60/145, 698  
 ; PRIOR FILING DATE: 1999-07-26  
 ; PRIOR APPLICATION NUMBER: US 60/146, 222  
 ; PRIOR FILING DATE: 1999-07-28  
 ; PRIOR APPLICATION NUMBER: PCT/US99/20594  
 ; PRIOR FILING DATE: 1999-09-08  
 ; PRIOR APPLICATION NUMBER: PCT/US99/20944  
 ; PRIOR FILING DATE: 1999-09-13  
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090  
 ; PRIOR FILING DATE: 1999-09-15  
 ; PRIOR APPLICATION NUMBER: PCT/US99/21547  
 ; PRIOR FILING DATE: 1999-09-15  
 ; PRIOR APPLICATION NUMBER: PCT/US99/23089  
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 ; PRIOR FILING DATE: 1999-11-29  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313  
 ; PRIOR FILING DATE: 1999-11-30  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28564  
 ; PRIOR FILING DATE: 1999-12-02  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28565  
 ; PRIOR FILING DATE: 1999-12-02  
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095  
 ; PRIOR FILING DATE: 1999-12-16  
 ; PRIOR APPLICATION NUMBER: PCT/US99/30911  
 ; PRIOR FILING DATE: 1999-12-20  
 ; PRIOR APPLICATION NUMBER: PCT/US99/30999  
 ; PRIOR FILING DATE: 1999-12-20  
 ; PRIOR APPLICATION NUMBER: PCT/US00/00219  
 ; PRIOR FILING DATE: 2000-01-05  
 ; NUMBER OF SEQ ID NOS: 423  
 ; SEQ ID NO 200  
 ; LENGTH: 2372  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-906-815A-200

Alignment Scores:  
 Pred. No.: 0  
 Score: 322.00  
 Length: 2372  
 Matches: 322

Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 100.00%  
 DB: 10  
 Gaps: 0  
 US-10-079-111-1 (1-322) x US-09-906-815A-200 (1-2372)  
 QY 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerileTrpThrThrArgLeuLeu 20  
 DB 160 ATGCCAGGTGCTTCAGCCCTGGTGTCTTCTCATTCCATCTGGACCACAGGCTCTG 219  
 QY 21 ValGlnGlySerLeuArgAlaGluLeuSerileGlnValSerCysArgileMetGly 40  
 DB 220 GTCCAGGGCTCTTTGGCTGCAGAGAGCTTTCCATCCAGGTGTCATGCAGAAATATGGG 279  
 QY 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
 DB 280 ATCACCTTGTGAGCAAAAAGGCAACACGACCTGAATTCACAGAAAGCTAAGGAGGCC 339  
 QY 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
 DB 340 TGTAGGCTGCTGGGACTAAGTTTGGCCGCGCAAGGACCAAGTTCAACAGCCTTGAAGCT 399  
 QY 81 SerPheGluThrCysSerTyrglyTrpValGlyAspGlyPheValVallleSerArgile 100  
 DB 400 AGCTTTGAAACTTGCAGCTATGCTGGTGGAGATGGATTCGTGTCTCATCTCTAGATT 459  
 QY 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuLeuTrpLysValProVal 120  
 DB 460 AGCCCAAAACCCCAAGTGTGGGAAAATGGGTGGGTGCTCTGAATTTGGAGGTTCCAGTG 519  
 QY 121 SerArgGlnPheAlaAlaTyrcystyrAsnSerSerAspThrTrpThrAsnSerCysile 140  
 DB 520 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACCTTGAATTCATCTGCATT 579  
 QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
 DB 580 CCAGAAATATCACCAACCAAGATCCATATTTCAACACTCAAACTCAACACAAACAACA 639  
 QY 161 GluPheIleValSerAspSerThrTyrsValAlaSerProTyrsSerThrileProAla 180  
 DB 640 GAATTTATGTCAGTGACAGTACCTACTCGTGGGATCCCTTACTCTCAATACCTGCC 699  
 QY 181 ProThrThrThrProProAlaProAlaSerThrSerileProArgArgLysLysLeuile 200  
 DB 700 CCTACTACT 759  
 QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
 DB 760 TGTGTCACAGAAAGTTTTTATGGAAACTAGCACCATGTCTACAGAACTGAACCATTTGTT 819  
 QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240  
 DB 820 GAAATAAAGCAGCATTCAAGATGAAGTCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 879  
 QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaGlyLeuGlyPheCysfyrValllys 260  
 DB 880 CTAGTCTTGTCT 939  
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 QY 281 LysValValLysGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
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 QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
 DB 1060 GATAAAACCCAGAAAGAGTCCCAAGAGTCCCAAGCAAACTACCGTGGATGCTCGAGCT 1119  
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Search completed: September 16, 2004, 05:29:16  
Job time : 2347 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 15, 2004, 03:45:39 ; Search time 7898 Seconds  
(without alignments)  
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Title: US-10-079-111-2

Perfect score: 2029

Sequence: 1 cctgacaagtcagaagctt.....aaacatttaaaaaaaaaa 2029

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl :

- 1: gb.ba.\*
- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sv.\*
- 13: gb.un.\*
- 14: gb.vi.\*
- 15: em.ba.\*
- 16: em.fun.\*
- 17: em.hum.\*
- 18: em.in.\*
- 19: em.mu.\*
- 20: em.om.\*
- 21: em.or.\*
- 22: em.ov.\*
- 23: em.pat.\*
- 24: em.ph.\*
- 25: em.pl.\*
- 26: em.ro.\*
- 27: em.sts.\*
- 28: em.un.\*
- 29: em.vi.\*
- 30: em.htg\_hum.\*
- 31: em.htg\_inv.\*
- 32: em.htg\_other.\*
- 33: em.htg\_mus.\*
- 34: em.htg\_pln.\*
- 35: em.htg\_rod.\*
- 36: em.htg\_nam.\*
- 37: em.htg\_vrt.\*
- 38: em.sy.\*
- 39: em.htgo\_hum.\*
- 40: em.htgo\_mus.\*
- 41: em.htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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1	2029	100.0	2029	6	AR204700	Sequence
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4	1994	98.3	2372	6	AX092274	Sequence
5	1994	98.3	2372	6	AX454446	Sequence
6	1994	98.3	2372	6	AX490924	Sequence
7	1994	98.3	2372	6	AX697609	Sequence
8	1994	98.3	2372	6	BD075532	Secretory
9	1994	98.3	2372	6	BD172392	Secreted
10	1994	98.3	2372	6	BD172711	Secreted
11	1994	98.3	2372	6	BD173030	Secreted
12	1994	98.3	2372	6	BD173349	Secreted
13	1994	98.3	2372	6	BD175383	Secretory
14	1994	98.3	2372	9	AY358925	Homo sapi
15	1907.2	94.0	2313	9	AF118108	Homo sapi
16	1876.8	92.5	2282	9	BC026231	Homo sapi
17	1735.4	85.5	1755	6	AX136227	Sequence
18	1735.4	85.5	1755	6	BD123566	Secretory
19	1735.4	85.5	1755	9	AK075443	Homo sapi
20	1191.4	58.7	1285	9	AF127670	Homo sapi
21	1059.2	52.2	165698	9	AC009532	Homo sapi
22	927.2	45.7	1613	4	AY372937	Bos tauru
23	654.8	32.3	716	6	AX136529	Sequence
24	654.8	32.3	716	6	BD123769	Secretory
25	631	31.1	2027	10	BC038653	Mus muscu
26	631	31.1	2027	10	BC038892	Mus muscu
27	616.4	30.4	1516	10	MMU311501	Mus muscu
28	499.4	24.6	516	6	AX331191	Sequence
29	499.4	24.6	516	6	AX331600	Sequence
30	499.4	24.6	516	6	AX332298	Sequence
31	499.4	24.6	516	6	AX333352	Sequence
32	499.4	24.6	516	6	AX333777	Sequence
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34	458.8	22.6	591	6	AX136672	Sequence
35	458.8	22.6	591	6	BD123912	Secretory
36	450	22.2	451	6	BD076146	5' EST of
37	386.2	19.0	603	4	AY304537	Sus scrof
38	354.8	17.5	373	6	BD073800	5' EST of
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44	239	11.8	241	6	AR351281	Sequence
45	239	11.8	241	6	AX303004	Sequence

ALIGNMENTS

RESULT 1

LOCUS AR204700 2029 bp DNA linear PAT 20-JUN-2002

DEFINITION Sequence 13 from patent US 6368794.

ACCESSION AR204700

VERSION AR204700.1 GI:21502094

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2029)

AUTHORS Daniel S., Gilmore, J., Stuart, S.G. and Stuve, L.L.

TITLE Detection of altered expression of genes regulating cell proliferation

JOURNAL Patent: US 6368794-A 13 09-APR-2002;

FEATURES		Location/Qualifiers			
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		/mol_type="unassigned DNA"			
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Query Match		100.0%;	Score 2029;	DB 6;	Length 2029;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 2029;	Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;
QY	1	CTTTGACAAAGTCAGAAAGCTTGAAGCAGGGAATCCGGATGTCCTCGGTTATGAAGTCGAG	60		
Db	1	CTTTGACAAAGTCAGAAAGCTTGAAGCAGGGAATCCGGATGTCCTCGGTTATGAAGTCGAG	60		
QY	61	CAGTGAGTGTGAGCCTCAACATAGTTCAGAACTCTCCATCCGACTAGTTATTGAGCAT	120		
Db	61	CAGTGAGTGTGAGCCTCAACATAGTTCAGAACTCTCCATCCGACTAGTTATTGAGCAT	120		
QY	121	CTGCGCTCTCATATCACCAAGTGGCCATCTCAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCA	180		
Db	121	CTGCGCTCTCATATCACCAAGTGGCCATCTCAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCA	180		
QY	181	CGATGCCAGGTGCTTTCAGCCTGGTGTCTTCTCACTTCCATCTGGACCAACAGGCTCC	240		
Db	181	CGATGCCAGGTGCTTTCAGCCTGGTGTCTTCTCACTTCCATCTGGACCAACAGGCTCC	240		
QY	241	TGGTCCAAAGGCTCTTGGCGTCAGAGAGCTTTCATCCAGGTGTCAATGCAGAAATTATGG	300		
Db	241	TGGTCCAAAGGCTCTTGGCGTCAGAGAGCTTTCATCCAGGTGTCAATGCAGAAATTATGG	300		
QY	301	GGATCACCCCTTGTGAGCAAAAAGGCGAACACAGCAGCTGAATTTACAGAAAGCTTAAGGAGG	360		
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QY	361	CTGTGAGCTGTCTGGACTAAGTTTGGCGCGCAAGCAAGTGAAGTGAAGCTTGAAG	420		
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QY	661	CAGAAATTTATGTGAGTGCAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGTG	720		
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QY	781	TTTGTGTACAGAAAGTTTATGAAACTAGCACCATGCTACAGAAACTGAACCATTTTG	840		
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QY	901	TGCTAGTGTGCTCTCTCTCTTTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGCA	960		
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QY	1081	CTGTAAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAACTACCGTGCATGCTCGAAG	1140
Db	1081	CTGTAAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAACTACCGTGCATGCTCGAAG	1140
QY	1141	CTGAGTTTATAGTAGACAGAAATGAGGAGACACACTGAGGCTGGTTCCTTCATGCTC	1200
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QY	1261	CTTGGTTCCCTAACTGGAATCAGCTCAGGACTGCCATTTGACTATGAGTGCACCAAGAG	1320
Db	1261	CTTGGTTCCCTAACTGGAATCAGCTCAGGACTGCCATTTGACTATGAGTGCACCAAGAG	1320
QY	1321	AATGCCCTTCTCCTTATTGTAAACCTGTCTGGATCCTATCTCTACCTCCAAAGCTTCC	1380
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QY	1561	CGCAGCTCAGACCTTCTTCTCAGCTCTGAAAGAGAAACACGTATCCACCTGACATGTC	1620
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QY	1621	CTTCTGAGCCCGGTAAAGCAAAAGAAATGGCAGAAAAAGTTTAGCCCTGAAAGCCATGA	1680
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QY	1861	CTACCACTGCTGATATTTTCTCTAGGAAATATCTTTTACAGTAAACAAAAATAAAACT	1920
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QY	1921	CTTATAAATTTCTATTTTATCTGAGTTTACAGAAATGATTACTAAGGAGATTACTCAGT	1980
Db	1921	CTTATAAATTTCTATTTTATCTGAGTTTACAGAAATGATTACTAAGGAGATTACTCAGT	1980
QY	1981	AATTTGTTTAAAAAGTAATAAATTTCAACAAACATTTAAAAAATAAAAAA 2029	
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ACCESSION	BD222718.1	GI:33032488					
VERSION	JP 2002519030-A/64.						
KEYWORDS	Homo sapiens (human).						
SOURCE	Homo sapiens						
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.						
REFERENCE	1 (bases 1 to 2029)						
AUTHORS	Lal, P., Tang, Y.T., Gorgone, G.A., Corley, N.C., Guegler, K.J., Baughn, M.R., Akerblom, I.E., Young, J.A., Yue, H., Patterson, C., Reddy, R., Hillman, J.L. and Bandman, O.						
TITLE	Human signal peptide-containing protein						
JOURNAL	Patent: JP 2002519030-A 64 02-JUL-2002;						
COMMENT	INCYTE PHARMACEUTICALS INC						
	OS Homo sapiens (human)						
	PN JP 2002519030-A/64						
	PD 02-JUL-2002						
	PF 25-JUN-1999 JP 2000557363						
	PR 26-JUN-1998 US 60/090762, 31-JUL-1998 US 60/094983 PR						
	01-OCT-1998 US 60/102686, 11-DEC-1998 US 60/112129 PI PREETI						
	LAL, Y TOM TANG, GINA A GORGONE, NEIL C CORLEY, KARL J PI GUEGLER,						
	PI MARIATH R BAUGHN, INGRID E AKERBLOM, JANICE AU YOUNG, HENRY YUE,						
	PI CHANDRA PATTERSON, ROOPA REDDY, JENNIFER L HILLMAN, OLGA BANDMAN						
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	PC A61P29/00, A61P35/00, A61P43/00, C07K14/47, C07K16/18, C12N1/15, PC						
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	PC C12N1/21, C12N5/10, C12P21/02, C12Q1/68, G01N33/68//C12P21/08, PC						
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Qy	301	GGATATCCCTTGTAGCAAAAGCGAACACAGAGCTGAAATTTTCAAGAAAGCTTAAGGAGG 360					
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DEFINITION Sequence 200 from patent US 6635468.
ACCESSION AR410761
VERSION AR410761.1 GI:40162261
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 2372)
Ashkenazi, A., Botstein, D., Desnovers, L., Eaton, D. L., Ferrara, N.,
Filvaroff, E., Fong, S., Gao, W.-Q., Gerber, H., Gertschen, M. E.,
Goddard, A., Godowski, P. J., Grimaldi, J. C., Gurney, A. L., Hillan, K. J.,
Klavin, I. J., Mather, J. P., Pan, J., Paoni, N. F., Roy, M. A.,
Stewart, T. A., Tamas, D., Williams, P. M. and Wood, W. I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: US 6635468-A 200 21-OCT-2003;
FEATURES Location/Qualifiers
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 61 GTTCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGC 120
QY 144 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGCCAGGTGCTTCCAGCTG 203
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QY 204 GTTGTGCTTCTCACTTCCATCTGACACAGAGGCTCTGGTCCAAAGGCTTTTGGGTGCA 263
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ACCESSION	AX092274		
VERSION	AX092274.1	GI:13444451	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1		

AUTHORS	Baton, D.L., Filvaroff, B., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, C.J., Gurney, A.L., Watanabe, C.K. and Wood, W.I.			
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same			
JOURNAL	Patent: WO 0116318-A 5 08-MAR-2001; Genentech, Inc. (US)			
FEATURES	Location/Qualifiers			
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QY	264	GAAGACTTTCCATCCAGGTGTCTGCAAGATTTATGGGATCACCTTGTGAGCAAAAAG	323	
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ACCESSION	AX454446			
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KEYWORDS				
SOURCE				
ORGANISM				
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REFERENCE				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
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	Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J., Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I. and Ye,W.			
TITLE	Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis			
JOURNAL	Patent: WO 0208284-A 31 31-JAN-2002; Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone (US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard, Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ; Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US) ; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ; Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William I. (US)			
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Best Local Similarity	99.8%	Pred. No. 0;		
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			Indels	0;
Gaps				
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Goddard, A., Godowski, P.J., Grimaldi, C.J., Gurney, A.L., Hillan, K.J.,  
Kljavin, I.J., Mather, J.P., Pan, J., Paoni, N.F., Roy, M.A.,  
Stewart, T.A., Tunes, D., Williams, P.M. and Wood, W.I.  
Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0104311-A 200 18-JAN-2001;  
Genentech Inc. (US)

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ORIGIN

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Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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DB 121 CATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGGCACGATGCCAGGCTGCTTCAGCCTG 180  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 2372)  
REFERENCE  
AUTHORS  
Wood,W.I., Gurney,A.L., Goddard,A., Penica,D., Chen,J. and Yuan,J.  
TITLE  
Secretory and transmembrane polypeptide and nucleic acid encoding  
the same  
JOURNAL  
Patent: JP 2001516580-A 165 02-OCT-2001;  
GENENTECH INC

COMMENT  
OS Homo sapiens (human)  
PN JP 2001516580-A/165  
PD 02-OCT-2001  
PF 16-SEP-1998 JP 2000511867  
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PI WILLIAM I WOOD,AUSTIN L GURNEY,AUDLEY GODDARD,DIANE PENICA, PI  
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PI JEAN YUAN  
PC C12N15/00,C07K14/47,C07K14/705,C07K16/18,C07K16/28,C07K19/00,  
PC C12N1/19,  
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LOCUS BD172392 2372 bp DNA linear PAT 18-FEB-2003

DEFINITION Secreted and transmembrane polypeptides and nucleic acids encoding the same.

ACCESSION BD172392

VERSION BD172392.1 GI:28413692

KEYWORDS JP 2002223786-A/165

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2372)

AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: JP 2002223786-A 165 13-AUG-2002;

COMMENT GENENTECH INC

OS Homo sapiens (human)

PN JP 2002223786-A/165

PD 13-AUG-2002

PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR

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WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI

JIAN ZHENG,

PI JEAN YUAN

PC C12N15/09,C07K16/18,C07K19/00,C12N1/19,C12N1/21, PC

C12N5/10,

PC C12P21/02,C12P21/08,(C12P21/02,C12R1:19),(C12P21/02,C12R1:91), PC

(C12P21/02,C12R1:645),C12N15/00,C12N5/00

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QY 144 CATCTGAGGTGTTTCCCTGGCTCTGAAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 203  
Db 121 CATCTGAGGTGTTTCCCTGGCTCTGAAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 180  
QY 204 GTGTTGCTTCTCACTTCATCTGGACACAGAGGCTCTGTGTCGAAGGCTCTTTCGCGTGA 263  
Db 181 GTGTTGCTTCTCACTTCATCTGGACACAGAGGCTCTGTGTCGAAGGCTCTTTCGCGTGA 240  
QY 264 GAAGAGCTTTCATCTCAGGTGTCTATGAGAAATATGGGATCAACCTTGTGAGCAAAAG 323  
Db 241 GAAGAGCTTTCATCTCAGGTGTCTATGAGAAATATGGGATCAACCTTGTGAGCAAAAG 300  
QY 324 GCGAAACGAGCTGAATTTTCAAGAGCTTAAGGAGGCTGTAGGCTGTGGGACTAAGT 383  
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Db 1561 GCTCTGAAAGAGAAAAACCGTATCCCACTGACATGTCCTTCTGAGCCGCTAAGAGCAAA 1620  
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Db 1621 AGAATGGCAGAAAAGTTTAGCCCCCTGAAAAGCCATGGAGATTTCTATAAATCTGAGACCTAA 1680  
QY 1704 TCTCTGAAAGCTTAAATAAAGAAATAGAACAGGCTGAGGATACCAAGTACACAGTGTCA 1763  
Db 1681 TCTCTGAAAGCTTAAATAAAGAAATAGAACAGGCTGAGGATACCAAGTACACAGTGTCA 1740  
QY 1764 GCAGGACTGTAAACACAGACAGGCTCAAAGTGTCTCTGAAACATTTAGTGTGAAT 1823  
Db 1741 GCAGGACTGTAAACACAGACAGGCTCAAAGTGTCTCTGAAACATTTAGTGTGAAT 1800  
QY 1824 CACTGTTTGAACACACACACTTACTTTTCTGCTCTACCACTGCTGATATTTCTCT 1883  
Db 1801 CACTGTTTGAACACACACACTTACTTTTCTGCTCTACCACTGCTGATATTTCTCT 1860  
QY 1884 AGGAAATATACCTTTTCAAGTAAACAAAATAAAACTCTTATAAAATTTCTATTTTATCT 1943  
Db 1861 AGGAAATATACCTTTTCAAGTAAACAAAATAAAACTCTTATAAAATTTCTATTTTATCT 1920  
QY 1944 GAGTTACAGAAATGATTTACTAAGGAGATTTACTCAGTAATTTGTTTAAAGGTAATAAAA 2003  
Db 1921 GAGTTACAGAAATGATTTACTAAGGAGATTTACTCAGTAATTTGTTTAAAGGTAATAAAA 1980  
QY 2004 TTCAACAACATTTAAAAAAA 2025  
Db 1981 TTCAACAACATTTGCTGAATA 2002

## RESULT 10

BD172711

LOCUS

DEFINITION

SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING

THE SAME.

ACCESSION

BD172711.1

VERSION

GI:28414015

KEYWORDS

JP 2002238586-A/165

SOURCE

HOMO SAPIENS (HUMAN)

ORGANISM

HOMO SAPIENS

EUKARYOTA; METAZOA; CHORDATA; CRANIATA; VERTEBRATA; EUTELEOSTOMI;

MAMMALIA; EUTHERIA; PRIMATES; CATARRHINI; HOMINIDAE; HOMO.





QY	1284	TCAGGAGTCGCATTGGACTATGAGATGACCAAAAGAGAAATGCCCTTCTCCTTATTGTAAC	1343
DB	1261	TCAGGACTGCCATTGGACTATGAGATGACCAAAAGAGAAATGCCCTTCTCCTTATTGTAAC	1320
QY	1344	CCTGTCCTGGATCCCTATCCCTCTCCTCCAAAGCTTCCACGGCCCTTTCTAGCCTGGCTAT	1403
DB	1321	CCTGTCCTGGATCCCTATCCCTCTCCTCCAAAGCTTCCACGGCCCTTTCTAGCCTGGCTAT	1380
QY	1404	GTCCTAATAATATCCCACTGGGAGAAAGAGGTTTGTCAAAGTGTCAAGAGACCTTAACAATC	1463
DB	1381	GTCCTAATAATATCCCACTGGGAGAAAGAGGTTTGTCAAAGTGTCAAGAGACCTTAACAATC	1440
QY	1464	TCATCAGTATCCAGTGTGTAAAGAGCCCTCTGGCTGTCTGAGGCTAGGTGGGTTGAAAGC	1523
DB	1441	TCATCAGTATCCAGTGTGTAAAGAGCCCTCTGGCTGTCTGAGGCTAGGTGGGTTGAAAGC	1500
QY	1524	CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTTCCGAGCTCAGACCTTTCTTCA	1583
DB	1501	CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTTCCGAGCTCAGACCTTTCTTCA	1560
QY	1584	GCTCTGAAAGAGAAACAGTATCCCACTGCATGTCTCTCTGAGCCCGGTAAAGAGCAA	1643
DB	1561	GCTCTGAAAGAGAAACAGTATCCCACTGCATGTCTCTCTGAGCCCGGTAAAGAGCAA	1620
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QY	1704	TCTCTGTAAAGCTTAAATAAAGAAATAGAACCAAGGCTGAGGATACGACGTACACTGTCA	1763
DB	1681	TCTCTGTAAAGCTTAAATAAAGAAATAGAACCAAGGCTGAGGATACGACGTACACTGTCA	1740
QY	1764	GCAGGAGCTGTAAACACAGACAGGGTCAAAGTGTCTCTGTGAACACATTGAGTGGAAAT	1823
DB	1741	GCAGGAGCTGTAAACACAGACAGGGTCAAAGTGTCTCTGTGAACACATTGAGTGGAAAT	1800
QY	1824	CAGTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT	1883
DB	1801	CAGTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT	1860
QY	1884	AGGAAATATACTTTTACAGTAAACAAAATAAAGCTTTATAAATTTCTATTTTATCT	1943
DB	1861	AGGAAATATACTTTTACAGTAAACAAAATAAAGCTTTATAAATTTCTATTTTATCT	1920
QY	1944	GAGTTACAGAAATGATTACTTAAGGAAGATTTACTCAGTAAATTTCTTTTAAAAAGTAATAAA	2003
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QY	2004	TTCAACAAACATTTTAAAAAAA 2025	
DB	1981	TTCAACAAACATTTTAAAGTAA 2002	

RESULT	11
LOCUS	BD173030
DEFINITION	Secreted and transmembrane polypeptides and nucleic acids encoding the same.
ACCESSION	BD173030
VERSION	BD173030.1 GI:28414336
KEYWORDS	JP 2002238587-A/165.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL	Patent: JP 2002238587-A 165 27-AUG-2002;
COMMENT	GENENTECH INC OS Homo sapiens (human)

Db 301 GCGAACCGAGCTGAAATTTACAGAAGCTAAGGAGCCTGTAGGCTGCTGGGACTAAAGT 360  
QY 384 TTGGCCGGCAAGGACCAAGTTGAAACAGCCTTTGAAAGCTAGCTTTTGAAACTTTGCAGCTAT 443  
Db 361 TTGGCCGGCAAGGACCAAGTTGAACAGCCTTTGAAAGCTAGCTTTTGAAACTTTGCAGCTAT 420  
QY 444 GGCTGGGTTGGAGATGGATTCGTGGTCACTCTTAGGATTTAGCCCAAACCCCAAGTGTGGG 503  
Db 421 GGCTGGGTTGGAGATGGATTCGTGGTCACTCTTAGGATTTAGCCCAAACCCCAAGTGTGGG 480  
QY 504 AAAATGGGTGGGTGCTGATTTGGAGGTTCCAGTGAGCCGACAGTTTCAGCCTAT 563  
Db 481 AAAATGGGTGGGTGCTGATTTGGAGGTTCCAGTGAGCCGACAGTTTCAGCCTAT 540  
QY 564 TGTTCAACTCATCTGATCTTGGACTAACTCGTGCAATTCAGAAATATCAACCACCAA 623  
Db 541 TGTTCAACTCATCTGATCTTGGACTAACTCGTGCAATTCAGAAATATCAACCACCAA 600  
QY 624 GATCCCATATCAACACTCAAACTGCAACACAAAACAAAGAAATTTATTGTAGTGACAGT 683  
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QY 684 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTACTACTACTCTCTCTGCT 743  
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Db 721 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATGATTTGTGTACAGAAGTTTTATG 780  
QY 804 GAAACTAGCACCATGTCTACAGAACTGAACCATTTGTTGAAAAAATAAGCAGCATTCAG 863  
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Db 1981 TTCAACAAACATTTGCTGAATA 2002

RESULT 12  
BD173349  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BD173349 2372 bp DNA linear PAT 18-FEB-2003  
Secreted and transmembrane polypeptides and nucleic acids encoding the same.  
BD173349.1 GI:28414660  
JP 2002238588-A/165.  
Homo sapiens (human).  
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 2372)  
Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.  
Secreted and transmembrane polypeptides and nucleic acids encoding the same  
Patent: JP 2002238588-A 165 27-AUG-2002;  
GENENTECH INC  
OS Homo sapiens (human)  
PN JP 2002238588-A/165  
PD 27-AUG-2002  
PF 18-DEC-2001 JP 2001385315  
PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR  
17-SEP-1997 US 60/059122,17-SEP-1997 US 60/059117 PR  
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17-SEP-1997 US 60/059119,18-SEP-1997 US 60/059263 PR  
18-SEP-1997 US 60/059266,15-OCT-1997 US 60/062125 PR  
17-OCT-1997 US 60/062287,17-OCT-1997 US 60/062285 PR  
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24-NOV-1997 US	60/066453,25-NOV-1997 US	60/066840 PI
WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI		
JIAN ZHENG,		
PI	JEAN YUAN	
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PC	C12P21/02/C12P21/08, (C12N1/19, C12R1:645), (C12N1/21, C12R1:19),	
PC	(C12N5/10, C12R1:91), C12N15/00, C12N5/00, (C12N5/00, C12R1:91) CC	
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FEATURES	Location/Qualifiers	
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ORIGIN		
Query Match	98.3%; Score 1994; DB 6; Length 2372;	
Best Local Similarity	99.8%; Pred. No. 0;	
Matches 1997; Conservative	0; Mismatches 5; Indels 0; Gaps 0;	
QY	24 AGCAGGAAATCGGATGTCGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 83	
Db	1 AGCAGGAAATCGGATGTCGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 60	
QY	84 GTTCCAGAACTCCATCGGACTAGTTATTGAGCATCTGCTCTCATATCACAGTGGC 143	
Db	61 GTTCCAGAACTCCATCGGACTAGTTATTGAGCATCTGCTCTCATATCACAGTGGC 120	
QY	144 CATCTGAGTGTTCCCTGGCTCTGAAGGGGTAGGCATGGCCAGGTGCTTCAGCCTG 203	
Db	121 CATCTGAGTGTTCCCTGGCTCTGAAGGGGTAGGCATGGCCAGGTGCTTCAGCCTG 180	
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Db	541 TGTTTAAACATCATCTGATACCTTCGACATTAACCTCGTGATTCACAGAAATTAACACACAAA 600	
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Db	781 GAAACTAGACCATGCTCTACAGAACTGAACCAATTTGTTGAAATAAAGCAGCATTCAG 840	
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LOCUS BD175383  
DEFINITION Secretary and transmembrane polypeptide and nucleic acid encoding the same.  
ACCESSION BD175383  
VERSION BD175383.1 GI:29121079  
KEYWORDS JP 2002253280-A/165.  
SOURCE Homo sapiens (human)  
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REFERENCE 1 (bases 1 to 2372)  
AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.  
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COMMENT GENENTECH INC  
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PP 18-DEC-2001 JP 2001385319  
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PI JEAN YUAN  
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ACCESSION AY358925
VERSION AY358925.1 GI:37182967
KEYWORDS FLI_CDNA.
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ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2372)
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
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Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
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Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
JOURNAL Genome Res. 13 (10), 2285-2270 (2003)
PUBMED 12975309
REFERENCE 2 (bases 1 to 2372)
AUTHORS Clark,H.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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QY	2004	TTCAACAAAACATTTAAAAAAA 2025	
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 15, 2004, 06:39:12 ; Search time 5287 Seconds  
(without alignments)  
11460.254 Million cell updates/sec

Title: US-10-079-111-2

Perfect score: 2029

Sequence: 1 ccttgacaagtcagaagctt.....aaacatttaaaaaaaaaa 2029

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estm:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_mam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_phg:\*

27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	1053.4	51.9	1143	9	AL574194
C 2	1043.8	51.4	1154	9	AL550279
C 3	991.6	48.9	1201	9	AL550621
C 4	954.6	47.0	1073	9	AL552625

C 5	954.4	47.0	1201	9	AL546590
C 6	943.8	46.5	1015	9	AL552299
C 7	937.8	46.2	1157	9	AL575514
C 8	936	46.1	1201	13	AL575514
C 9	933	46.0	1007	9	AL575633
C 10	932.8	46.0	1201	9	AL547774
C 11	925.8	45.6	1201	9	AL546669
C 12	924.2	45.5	1172	9	AL552127
C 13	914	45.0	1116	9	AL552661
C 14	907.6	44.7	973	9	AL574433
C 15	907.2	44.7	1201	9	AL546623
C 16	905.4	44.6	1201	9	AL544430
C 17	899.8	44.3	978	9	AL573693
C 18	893.4	44.0	1151	9	AL550829
C 19	891.6	43.9	1074	9	AL552777
C 20	890.4	43.9	1201	13	AL552777
C 21	885.4	43.6	1201	9	AL5402505
C 22	881	43.4	970	9	AL571928
C 23	878.6	43.3	1172	9	AL550615
C 24	877.2	43.2	1201	9	AL550911
C 25	872.8	43.0	1014	9	AL551020
C 26	854.4	42.1	1161	9	AL553858
C 27	850.4	41.9	972	9	AL550876
C 28	848.4	41.8	1201	9	AL549512
C 29	838	41.3	911	9	AL570563
C 30	834.8	41.1	913	13	AL543874
C 31	831.2	41.0	1201	9	AL549046
C 32	826.8	40.7	1201	13	AL553712
C 33	813.8	40.1	1201	9	AL550911
C 34	791.2	39.0	865	14	AL571871
C 35	790.8	39.0	864	9	AL545331
C 36	788.4	38.9	1066	13	AL545331
C 37	789	38.8	863	12	AL545331
C 38	785.6	38.7	840	9	AL545331
C 39	774.4	38.2	839	9	AL571644
C 40	755	37.2	960	9	AL546217
C 41	733.6	36.2	743	9	AL553920
C 42	730.2	36.0	1201	9	AL598709
C 43	728	35.9	987	13	AL541927
C 44	721.4	35.6	746	14	AL541927
C 45	713.2	35.2	758	14	AL541927

ALIGNMENTS

RESULT 1

AL574194/c

LOCUS

DEFINITION

AL574194 Homo sapiens

Clone CSODI039Y06 3-PRIME, mRNA sequence.

ACCESSION

AL574194

VERSION

EST

KEYWORDS

EST

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 1143)

AUTHORS

Li.W.B., Gruber.C., Jessee.J. and Polayes.D.

TITLE

Full-length cDNA libraries and normalization

JOURNAL

Unpublished (2001)

COMMENT

On Feb 16, 2001 this sequence version replaced gi:12934166.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 5952.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CSODI039PE03NP1&cluster=5952.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CS0DI039DE03NP1.  
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/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

Query Match 51.4%; Score 1053.4; DB 9; Length 1143;  
Best Local Similarity 97.3%; Pred. No. 1.6e-202;  
Matches 1083; Conservative 8; Mismatches 20; Indels 2; Gaps 2;  
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QY 889 TCCCAACGGCTCTGCTAGTGTCTGCTCCCTCTCTTTGTTGGTGTGCTGACGTGCTGTGAT 948  
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QY 949 TTTCTATGTCAAAGGTATGTGAAGGCTTCCCTTTTACAAAACAAGATCAGCAGAGG 1008  
DB 965 TTTGCTATGTCAAAGGTATGTGAAGGCTTCCCTTTTACAAAACAAGATCAGCAGAGG 906  
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DB 785 GATGCTGGAAGCTGAAGTTTAGATGAGACAGAAAATGAGGAGACACACCTGAGGCTGTT 726  
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LOCUS AL550279 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
DEFINITION clone CS0DI039YJ06 5-PRIME, mRNA sequence.  
ACCESSION AL550279  
VERSION AL550279.2 GI:31272096  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
JOURNAL 1 (bases 1 to 1154)  
COMMENT Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
On Feb 15, 2001 this sequence version replaced gi:12887098.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 5952.r For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0DI039DE03QP1&cluster=5952.r. Contact :  
Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CS0DI039DE03QP1.

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primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

Query Match 51.4%; Score 1043.8; DB 9; Length 1154;  
Best Local Similarity 98.9%; Pred. No. 1.4e-200;  
Matches 1057; Conservative 4; Mismatches 6; Indels 2; Gaps 1;  
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Db 485 GGGGTGGGTGCTCTGATTTGGAGGTTCCAGTCAGCCGACAGTTTCAGCCATTGTTAC 544
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QY 630 ATATTCAACACTCAAACTGCAACACAAACAAAGATTTATTTGTCAGTCAGTACTAC 689
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clone CS0D1067YG15 3-PRIME, mRNA sequence.
AL552625
VERSION
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1073)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12891706.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D1067AD08NP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0D1067AD08NP1.
Location/Qualifiers
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Best Local Similarity 94.7%; Pred. No. 1.4e-182;
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Db	109	AGTTGGAATCAGTGTGTAACACACACACTTACTTTTCTGCTCTCTCTCTCTCTCTCTCTCTCT	50						
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DEFINITION	clone CS0D1040YD03 5-PRIME, mRNA sequence.				
ACCESSION	BX366718				
VERSION	BX366718.1 GI:30451557				
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ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Li W.B., Gruber C., Jessee J. and Pollayes D.				
TITLE	Full-length cDNA libraries and normalization				
COMMENT	Unpublished (2001)				
CONTACT	Genoscope - Centre National de Sequencage				
BP	191 91006 EVRY cedex - France				
EMAIL	Email: secref@genoscope.cns.fr, Web: www.genoscope.cns.fr				
LIBRARY	Library was constructed by Life Technologies, a division of				
INVITROGEN	Invitrogen. This sequence belongs to sequence cluster 5952.r For				
MORE INFORMATION	about this cluster, see				
CGI-BIN/CLUSTER	cgi-bin/cluster.cgi?seq=CS0A1040CB02QP1&cluster=5952.r. Contact :				
FENG LIANG	Email: fliang@lifetech.com URL :				
HTTP://FULLLENGTH	http://fulllength.invitrogen.com/ InvitroGen Corporation 1600				
PARADAY AVENUE	Genoscope sequence ID : CS0A1040CB02QP1.				
LOCATION/QUALIFIERS	1. .1201				
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ORIGIN	/organism="Homo sapiens"				
Query Match	46.1%; Score 936; DB 13; Length 1201;				
Best Local Similarity	97.6%; Pred No. 8.2e-179;				
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QY	155	TTTCCTCGCTCTGAAGGGTGGAGCAGTGGCCAGGTGCTTTCAGCTGGTGTGCTTCT	214		
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QY	215	CATTTCCATCTGGACCAAGAGCTCTGTGTCGAGGCTTTTTCGTCGAGAGAGCTTTTC	274		
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QY	275	CATCCAGGTGTCAGCAATTTATGGGATCACCTTGTGAGCAAAAGGCGAACACGA	334		
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QY	395	GGACCAAGTTGAAACAGCCTTGAAGAGCTAGCTTTGAAACTTTGAGCTATGGCTGGTGG	454		
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clone CS0DI069YN02 3-PRIME, mRNA sequence.
ACCESSION
AL575633
VERSION
EST.
SOURCE
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ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 1007)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:12936986.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5952.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI069D01NP1&cluster=5952.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue Genoscope sequence ID : CS0DI069D01NP1.
Location/Qualifiers
1..1007
/organism="Homo sapiens"
/mol_type="mRNA"

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FEATURES

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Source

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/Note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match
Best Local Similarity 46.0%; Score 933; DB 9; Length 1007;
Matches 974; Conservative 19; Mismatches 12; Indels 5; Gaps 4;
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QY 1152 ATGACACAGAAATGAGGAGACACCTGAGGCTGTTTCTTTCATGCTCTCTTACCCTGCC 1211
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REFERENCE  
 AUTHORS Li W.B., Gruber, C., Jessee, J. and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 5952.r For  
 more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgi-bin/cluster.cgi?seq=CSODI029CE05QP1&cluster=5952.r. Contact :  
 Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CSODI029CE05QP1.  
 Location/Qualifiers  
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 /note="1st strand cDNA was primed with a NotI-oligo (dT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and cloned into the Not I and EcoR V  
 sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES  
 source  
 1 (bases 1 to 1201)  
 Li W.B., Gruber, C., Jessee, J. and Polayes, D.  
 Full-length cDNA libraries and normalization  
 Unpublished (2001)  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 5952.r For  
 more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgi-bin/cluster.cgi?seq=CSODI029CE05QP1&cluster=5952.r. Contact :  
 Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CSODI029CE05QP1.  
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 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and cloned into the Not I and EcoR V  
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN  
 Query Match 45.6%; Score 925.8; DB 9; Length 1201;  
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 Matches 983; Conservative 4; Mismatches 36; Indels 8; Gaps 3;  
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 QY 168 GAAGGGGTAGGACGATGCGCAGGTGCTTACGCTGGTGTCTCTCTCATCTTCATCTGG 227  
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 AL552127  
 AL552127.2 GI:31273943  
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 Homo sapiens (human)  
 Homo sapiens  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 1172)  
 Li W.B., Gruber, C., Jessee, J. and Polayes, D.  
 Full-length cDNA libraries and normalization  
 Unpublished (2001)  
 On Feb 15, 2001 this sequence version replaced gi:12890728.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 5952.r For  
 more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgi-bin/cluster.cgi?seq=CSODI059BA06QP1&cluster=5952.r. Contact :  
 Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CSODI059BA06QP1.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
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FEATURES  
 source





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QY 1932 CTATTTTATCTGAGTACAGAAATGATTACTA-AGGAAGATTAC-TCAGTAAATTTGTTT 1989  
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VERSION AL546623.2 GI:31268456  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1201)  
AUTHORS Li W.B., Gruber,C., Jessee,J. and Polayes,D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT On Feb 15, 2001 this sequence version replaced gi:12879917.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 5952.r For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CSODI029AG12QPl&cluster=5952.r. Contact :  
Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CSODI029AG12QPl.  
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primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES  
source  
1. 1201  
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sites of the pCMVSPORT 6 vector. Library was normalized."

Query Match 44.7%; Score 907.2; DB 9; Length 1201;  
Best Local Similarity 96.8%; Pred. No. 5.4e-173;  
Matches 976; Conservative 11; Mismatches 14; Indels 7; Gaps 6;

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Db 347 TGGTCCAAAGGCTCTTTGGCTGAGAGAGGCTTTCCATCCAGGTGTCATCGAATATTAG 406  
QY 301 GGATCACCTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTTTCAGAAAGCTAAGGAGG 360  
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QY 361 CCTGTAGGCTGCTGGGACTAAGTTTGGCGGCAAGCAAGCTTGAAGCCTTGAAG 420  
Db 467 CCTGTAGGCTGCTGGGACTAAGTTTGGCGGCAAGCAAGCTTGAAGCCTTGAAG 526  
QY 421 CTAGCTTTTGAAGCTTTCAGCCTTATGTTTGAAGTGGGTGCTCTGATTTTGAAGGTTCCAG 540  
Db 527 CTAGCTTTTGAAGCTTTCAGCCTTATGTTTGAAGTGGGTGCTCTGATTTTGAAGGTTCCAG 586  
QY 481 TTAGCCCCAAACCCCAAGTGTGGGAAATTTGGGTTGGGTGCTCTGATTTTGAAGGTTCCAG 540  
Db 587 TTAGCCCCAAACCCCAAGTGTGGGAAATTTGGGTTGGGTGCTCTGATTTTGAAGGTTCCAG 546  
QY 541 TGAGCCGACAGTTTTCAGCCTTATGTTTGAAGTGGGTGCTCTGATTTTGAAGGTTCCAG 600  
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QY 601 TTCCAGAAATTTATCACCAACCAAGTCCATATTTCAACACTCAAACTGCAACACAAACAA 660  
Db 707 TTCCAGAAATTTATCACCAACCAAGTCCATATTTCAACACTCAAACTGCAACACAAACAA 766  
QY 661 CAGAAATTTATGTCAGTCAAGTACTACTCGTGGCATCCCTTACTCTCAATACCTG 720  
Db 767 CAGAAATTTATGTCAGTCAAGTACTACTCGTGGCATCCCTTACTCTCAATACCTG 826  
QY 721 CCCCTACTACTCTCTCTCTGCTCCAGTTCACCTTCTATTTCCAGGAGAAAAAATTGA 780  
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QY 841 TTGAAAAATAAGCAGCATTTCAAGAAATGAAGTGTGGGTTTGGAGGTTCCCCACGGCTC 900  
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QY 901 TGCTAGTGTGCTCTCTCTCTTCTTTGGTGTGAGCTGCTTGGATTTTGGCTATGTCA 960  
Db 1005 TGCTAGTGTGCTCTCTCTCTTCTTTGGTGTGAGCTGCTTGGATTTTGGCTATGTCA 1061  
QY 961 AAAGGTATGTGAAGGCTTCCCTTTTACAACAGAAATCAGCAGAAAG 1008  
Db 1062 AAAGK--AKGRAGGCTTCCCTTTTMAAAGAAATATATCYGAGGGATG 1107

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Job time : 5297 secs

B/ank



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OM nucleic - nucleic search, using sw model

Run on: September 15, 2004, 09:52:54 ; Search time 964 Seconds

(without alignments)  
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Title: US-10-079-111-2

Perfect score: 2029

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 6608766

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2029	100.0	2029	15	US-10-079-111-2
2	2005	98.8	2404	9	US-09-833-381-849
3	2005	98.8	2404	9	US-09-833-381-853
4	1994	98.3	2372	9	US-09-903-320-200
5	1994	98.3	2372	9	US-09-903-088B-200
6	1994	98.3	2372	9	US-09-905-291A-200
7	1994	98.3	2372	9	US-09-902-853-200
8	1994	98.3	2372	9	US-09-907-824-200
9	1994	98.3	2372	9	US-09-907-841-200
10	1994	98.3	2372	10	US-09-904-011-200
11	1994	98.3	2372	10	US-09-906-742-200
12	1994	98.3	2372	10	US-09-906-838-200
13	1994	98.3	2372	10	US-09-907-613-200
14	1994	98.3	2372	10	US-09-907-942-200

15	1994	98.3	2372	10	US-09-904-859-200	Sequence 200, App
16	1994	98.3	2372	10	US-09-909-204-200	Sequence 200, App
17	1994	98.3	2372	10	US-09-904-820-200	Sequence 200, App
18	1994	98.3	2372	10	US-09-904-786-200	Sequence 200, App
19	1994	98.3	2372	10	US-09-906-646-200	Sequence 200, App
20	1994	98.3	2372	10	US-09-906-700-200	Sequence 200, App
21	1994	98.3	2372	10	US-09-903-786-200	Sequence 200, App
22	1994	98.3	2372	10	US-09-902-903-200	Sequence 200, App
23	1994	98.3	2372	10	US-09-903-749A-200	Sequence 200, App
24	1994	98.3	2372	10	US-09-904-119-200	Sequence 200, App
25	1994	98.3	2372	10	US-09-904-956-200	Sequence 200, App
26	1994	98.3	2372	10	US-09-902-736-200	Sequence 200, App
27	1994	98.3	2372	10	US-09-907-794-200	Sequence 200, App
28	1994	98.3	2372	10	US-09-903-943-200	Sequence 200, App
29	1994	98.3	2372	10	US-09-904-462-200	Sequence 200, App
30	1994	98.3	2372	10	US-09-907-925-200	Sequence 200, App
31	1994	98.3	2372	10	US-09-902-692-200	Sequence 200, App
32	1994	98.3	2372	10	US-09-903-520-200	Sequence 200, App
33	1994	98.3	2372	10	US-09-905-056-200	Sequence 200, App
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35	1994	98.3	2372	10	US-09-904-553-200	Sequence 200, App
36	1994	98.3	2372	10	US-09-905-381-200	Sequence 200, App
37	1994	98.3	2372	10	US-09-905-088-200	Sequence 200, App
38	1994	98.3	2372	10	US-09-907-575-200	Sequence 200, App
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40	1994	98.3	2372	10	US-09-902-759-200	Sequence 200, App
41	1994	98.3	2372	10	US-09-902-634-200	Sequence 200, App
42	1994	98.3	2372	10	US-09-902-713-200	Sequence 200, App
43	1994	98.3	2372	10	US-09-907-979-200	Sequence 200, App
44	1994	98.3	2372	10	US-09-902-615-200	Sequence 200, App
45	1994	98.3	2372	10	US-09-903-925-200	Sequence 200, App

#### ALIGNMENTS

#### RESULT 1

US-10-079-111-2  
; Sequence 2, Application US/10079111  
; Publication No. US20030124543A1  
; GENERAL INFORMATION:  
; APPLICANT: Stuart, Susan G.  
; APPLICANT: Streeter, David G.  
; TITLE OF INVENTION: BREAST CANCER MARKER  
; FILE REFERENCE: PC-0053 CIP  
; CURRENT APPLICATION NUMBER: US/10/079,111  
; CURRENT FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: 09/232,160  
; PRIOR FILING DATE: 1999-01-15  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PERL Program  
; SEQ ID NO 2  
; LENGTH: 2029  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; OTHER INFORMATION: Incyte ID No. US20030124543A1 3044710CB1  
US-10-079-111-2

Query Match	100.0%;	Score 2029;	DB 15;	Length 2029;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2029;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Oy	1	CCTTGACAAGTCGAGAGCTTGAAAGCAGGAGAAATCCGATGCTCTCGGTATGAAAGTGAG 60		
Db	1	CCTTGACAAGTCGAGAGCTTGAAAGCAGGAGAAATCCGATGCTCTCGGTATGAAAGTGAG 60		
Oy	61	CAGTGAGTGAGGCTCAACATAGTTCGAGAACTCTCCATCCGACTAGTTATTGAGCAT 120		
Db	61	CAGTGAGTGAGGCTCAACATAGTTCGAGAACTCTCCATCCGACTAGTTATTGAGCAT 120		
Oy	121	CTGCTCTCATATCACCAGTGCGCATCTGAGGTGTTTCCCTGGCTCTGAAAGGGGTAGCA 180		

Db 121 |||||CTGCTCTCATATCAACAGTGGCCATCTGAGGTGTTCCCTGGCTCTGAAGGGTAGGCA 180  
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Db 181 CGATGGCCAGGTGCTTTCAGCTGGTGTGCTTCTCTCACTTCCATCTGGACCAAGGCTCC 240  
QY 241 TGGTCCAAAGGCTTTTGGGTGAGAAAGAGCTTTTCCATCCAGGTGTCAGAGAAATATGG 300  
Db 241 TGGTCCAAAGGCTTTTGGGTGAGAAAGAGCTTTTCCATCCAGGTGTCAGAGAAATATGG 300  
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Db 301 GGATCACCTTGTGAGCAAAAAGCGAACCAGCAGCTGAATTTACAGAGCTTAAGGAGG 360  
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Db 361 CCGTAGGCTGTGGGACTTAAGTTTGGCCGGCAAGGACCAAGTTGAAAACAGCCTTTGAAAG 420  
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Db 421 CTAGCTTTGAAACTTGGCAGCTATGGCTGGGTTGGAGATGGATTCCGTGGTCACTCTAGGA 480  
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QY 601 TTCCAGAAATTAACAGCAAAAGATCCCATATTCAAGCTCAACTGCAACAGCAACAA 560  
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QY 781 TTTGTGTACAGAGTTTATGGAACCTAGCACCATGCTACAGAACTGACCACTTTG 840  
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QY 901 TGCTAGTGTCTGCT 960  
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QY 1141 CTGAAGTTTAGACACAGAAATGAGGACACACTGAGGCTGTTCTTTCATGCTC 1200  
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QY 1201 CTTTACCTGCTCCCGAGTGGGAAATCAAAGGCGCAAGAACCAAGAGAAAGTCCACC 1260

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Db 1261 CTTGGTTCTTAATCGGAATCAGCTCAGACTGCCATTCGACTATCGACTATCGACTGACCAAGAG 1320  
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Db 1321 AATGCCCTTCTCTTATTGTAACCTGCTGTGATCCTATCCTCTTACCTCCAAAGCTTCC 1380  
QY 1381 CACGCCCTTCTAGCTGGCTATGCTTAATAATATCCACTGGAGAAAGAGTTTGC 1440  
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QY 1441 AAAGTGAAGGACCTTAAACATCTCATCAGTATCCAGTGGTAAAGGCTCCTGGCTGT 1500  
Db 1441 AAAGTGAAGGACCTTAAACATCTCATCAGTATCCAGTGGTAAAGGCTCCTGGCTGT 1500  
QY 1501 CTGAGGCTAGGTGGGTTGAAAGCCAAAGAGTCACTGAGACCAAGGCTTCTCTACTGATT 1560  
Db 1501 CTGAGGCTAGGTGGGTTGAAAGCCAAAGAGTCACTGAGACCAAGGCTTCTCTACTGATT 1560  
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Db 1561 CGCAGCTCAGACCTTTCTCAGCTCTGAAAGAGAAACACATATCCCACTGACATGTC 1620  
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Db 1621 CTTCTGAGCCCGGTAAGAGCAAAAGATGGCGAAAGTTTAGCCCTGAAAGCCATGGA 1680  
QY 1681 GATTTCTCAATCTGAGACCTAATCTCTGTAAGGCTTAAATTAAGAAATAGAACAGGCT 1740  
Db 1681 GATTTCTCAATCTGAGACCTAATCTCTGTAAGGCTTAAATTAAGAAATAGAACAGGCT 1740  
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QY 1861 CTACACCTGCTGATATTTCTTAGGAATATACITTTTACAGTAACCAAAATAAAACT 1920  
Db 1861 CTACACCTGCTGATATTTCTTAGGAATATACITTTTACAGTAACCAAAATAAAACT 1920  
QY 1921 CTTTAAATTTCTATTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATTACTCAGT 1980  
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QY 1981 AATTTGTTTAAAGTAATAAATTCACAAACATTTTAAAAAATAAAAAA 2029  
Db 1981 AATTTGTTTAAAGTAATAAATTCACAAACATTTTAAAAAATAAAAAA 2029

## RESULT 2

US-09-833-381-849  
; Sequence 849, Application US/09833381  
; Patent No. US20020132090A1  
; GENERAL INFORMATION:  
; APPLICANT: Robison, Keith E.  
; TITLE OF INVENTION: No. US20020132090A1el Nucleic Acid and Protein Homologs  
; FILE REFERENCE: 5800-119  
; CURRENT APPLICATION NUMBER: US/09/833,381  
; CURRENT FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: 09/516,448  
; PRIOR FILING DATE: 2000-02-29  
; NUMBER OF SEQ ID NOS: 2050  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 849  
; LENGTH: 2404  
; TYPE: DNA  
; ORGANISM: Homo sapiens

US-09-833-381-849

Query Match 98.8%; Score 2005; DB 9; Length 2404;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2019; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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DB	68	CAGTGAGTGTGAGCCTCAACATAGTCTCCAGAACTCTCCATCCGGACTAGTTATTAGCAT	127
QY	121	CTGGCTCTCATATCACAGTGGCCATCTGAGGTGTTTCCCTGGCTCTGAAAGGGTAGGCA	180
DB	128	CTGGCTCTCATATCACAGTGGCCATCTGAGGTGTTTCCCTGGCTCTGAAAGGGTAGGCA	187
QY	181	CGATGGCCAGGTGCTTCAGCCTGCTGTTGCTTCTCACTTCCATCTGGACCAAGGCTCC	240
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QY	241	TGGTCCAAAGGCTCTTTGGCTGCAGAAAGCTTTCCATCCAGGTGTCATGCAGAAATTATGG	300
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DB	488	TTAGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTGATTTTGAAGTTCCAG	547
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DB	548	TGAGCCGACAGTTTGACGCTATGCTTACACTCATCTGATCTGACTTGGACTAAGTTCG	607
QY	601	TTCCAGAAATTTATCACCAACCAAGATCCCATATTTCAACACTCAAACTGCAACACAA	660
DB	608	TTCCAGAAATTTATCACCAACCAAGATCCCATATTTCAACACTCAAACTGCAACACAA	667
QY	661	CAGAAATTTATGTCAGTGACAGTACTACTCGTGGGATCCCTTACTCTCAATACCTG	720
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QY	721	CCCCTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCAGGAGAAAAAATTGA	780
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QY	781	TTTGTGTCACAGAAAGTTTTATGGAACCTAGCACCATGCTCTACAGAAACTGAACCATTTG	840
DB	788	TTTGTGTCACAGAAAGTTTTATGGAACCTAGCACCATGCTCTACAGAAACTGAACCATTTG	847
QY	841	TTGAAATTAAGCAGCATTTCAAGATGAAGTGTGAGGTGTGGAGGTGCTCCCGGCTC	900
DB	848	TTGAAATTAAGCAGCATTTCAAGATGAAGTGTGAGGTGTGGAGGTGCTCCCGGCTC	907
QY	901	TGCTAGTCTGCTCTCTCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	960
DB	908	TGCTAGTCTGCTCTCTCTCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	967
QY	961	AAAGTATGTGAAGGCTTCCCTTTTACAAAACAAAGATCAGCAGAGGAAATGATCGAAA	1020
DB	968	AAAGTATGTGAAGGCTTCCCTTTTACAAAACAAAGATCAGCAGAGGAAATGATCGAAA	1027

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QY	1081	CTGATAAAACCCAGAGAGTCCAGAGTCCAAAGCAAAACTACCTGCGATGCTTGGAG	1140
DB	1088	CTGATAAAACCCAGAGAGTCCAGAGTCCAAAGCAAAACTACCTGCGATGCTTGGAG	1147
QY	1141	CTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGTTTCTTTTCTGCTC	1200
DB	1148	CTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGTTTCTTTTCTGCTC	1207
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QY	1261	CTTGGTTCCTAACTGGAATCAGCTCAGGACTGCCATTCGACTATGAGTGCACCAAGAG	1320
DB	1268	CTTGGTTCCTAACTGGAATCAGCTCAGGACTGCCATTCGACTATGAGTGCACCAAGAG	1327
QY	1321	AATGCCCTTCTCCTTATTGTAAACCTGTCTGGATCCTATCCTTACCTCCTCAAAAGCTTCC	1380
DB	1328	AATGCCCTTCTCCTTATTGTAAACCTGTCTGGATCCTATCCTTACCTCCTCAAAAGCTTCC	1387
QY	1381	CACGGCTTTTAGCCTGGCTATGCTCTAAATAATATCCACTGGGAGAAAGAGTGTTCG	1440
DB	1388	CACGGCTTTTAGCCTGGCTATGCTCTAAATAATATCCACTGGGAGAAAGAGTGTTCG	1447
QY	1441	AAAGTGCAAGGACCTTAAACATCTCATCAGTATCAGTGTGTAAAGGCTCTCGGCTGT	1500
DB	1448	AAAGTGCAAGGACCTTAAACATCTCATCAGTATCAGTGTGTAAAGGCTCTCGGCTGT	1507
QY	1501	CTGAGGCTTAGTGGGTTTGAAGCCAAAGAGTCACTGAGACCAAGGCTTTCTCTACTGATT	1560
DB	1508	CTGAGGCTTAGTGGGTTTGAAGCCAAAGAGTCACTGAGACCAAGGCTTTCTCTACTGATT	1567
QY	1561	CCGAGCTCAGACCCCTTTCTTTCAGCTCTGAAAGGAAACACGATATCCACCTGACATGTC	1620
DB	1568	CCGAGCTCAGACCCCTTTCTTTCAGCTCTGAAAGGAAACACGATATCCACCTGACATGTC	1627
QY	1621	CTTCTGAGCCCGGTAAAGCAAAAGATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGA	1680
DB	1628	CTTCTGAGCCCGGTAAAGCAAAAGATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGA	1687
QY	1681	GATTCTCATAACTTGAACCTTAATCTCTGTAAAGCTAAATATAAGAAATAGAACGCT	1740
DB	1688	GATTCTCATAACTTGAACCTTAATCTCTGTAAAGCTAAATATAAGAAATAGAACGCT	1747
QY	1741	GAGGATACGACAGTACACTGTGAGGAGCTGTAAACACAGACAGGCTCAAGTGTGTTT	1800
DB	1748	GAGGATACGACAGTACACTGTGAGGAGCTGTAAACACAGACAGGCTCAAGTGTGTTT	1807
QY	1801	CTCTGAACACATTCAGTTGGAAATCACTGTTTAGAACACACACTTACTTTCTGCTCT	1860
DB	1808	CTCTGAACACATTCAGTTGGAAATCACTGTTTAGAACACACACTTACTTTCTGCTCT	1867
QY	1861	CTACCCTGCTGATTTTCTCTAGGAAATATATCTTTTACAAAGTAAACAAAATAAAACT	1920
DB	1868	CTACCCTGCTGATTTTCTCTAGGAAATATATCTTTTACAAAGTAAACAAAATAAAACT	1927
QY	1921	CTTATAAATTTCTATTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATTACTCAGT	1980
DB	1928	CTTATAAATTTCTATTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATTACTCAGT	1987
QY	1981	AATTGTTTAAAAAGTAATAAATTTCAACAACTTTTAAAAAAA	2025
DB	1988	AATTGTTTAAAAAGTAATAAATTTCAACAACTTTTAAAAAAA	2032

RESULT 3  
US-09-833-381-853  
; Sequence 853, Application US/09833381

; Patent No. US20020132090A1  
; GENERAL INFORMATION:  
; APPLICANT: Robison, Keith E.  
; TITLE OF INVENTION: No. US20020132090A1el Nucleic Acid and Protein Homologs  
; FILE REFERENCE: 5800-119  
; CURRENT APPLICATION NUMBER: US/09/833,381  
; CURRENT FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: 09/516,448  
; PRIOR FILING DATE: 2000-02-29  
; NUMBER OF SEQ ID NOS: 2050  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 853  
; LENGTH: 2404  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-833-381-853

Query Match 98.8%; Score 2005; DB 9; Length 2404;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2019; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY	2	CTTGACAGTCAGAA-GCTTGAAGCAGGGAATCCGGATGCTCGGTTATGAAGTGGAG	60
Db	8	CTTGACAGTCAGAAACGGCTTGAAGCAGGGAATCCGGATGCTCGGTTATGAAGTGGAG	67
QY	61	CAGTCAGTGTGAGCCTCAACATAGTTCAGAACTCTCCATCCGGACTAGTTATTGAGCAT	120
Db	68	CAGTCAGTGTGAGCCTCAACATAGTTCAGAACTCTCCATCCGGACTAGTTATTGAGCAT	127
QY	121	CTGCCCTCTCATATCACAGTGGCCATCTGAGGTGTTCCCTGGCTCTGAAGGGTAGGCA	180
Db	128	CTGCCCTCTCATATCACAGTGGCCATCTGAGGTGTTCCCTGGCTCTGAAGGGTAGGCA	187
QY	181	CGATGGCAGAGTGTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCAAGGCTCC	240
Db	188	CGATGGCAGAGTGTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCAAGGCTCC	247
QY	241	TGGTCCAGGCTCTTGGCTGAGAGAGCTTTCATCCAGGTGCATGACAGAAATTGG	300
Db	248	TGGTCCAGGCTCTTGGCTGAGAGAGCTTTCATCCAGGTGCATGACAGAAATTGG	307
QY	301	GGATCACCCCTGTGACAAAAAGGGGAAACAGCAGCTGAATTTACAGAACTAAGGAGG	360
Db	308	GGATCACCCCTGTGACAAAAAGGGGAAACAGCAGCTGAATTTACAGAACTAAGGAGG	367
QY	361	CCTGTAGGTGTGGGACATAAGTTTGGCGGCAAGGACCAAGTGAAGCAGCTTGAAG	420
Db	368	CCTGTAGGTGTGGGACATAAGTTTGGCGGCAAGGACCAAGTGAAGCAGCTTGAAG	427
QY	421	CTAGCTTTGAACTTGCAGCTATGCTGGTGGAGATGGATTCGTGGTCACTCTTAGGA	480
Db	428	CTAGCTTTGAACTTGCAGCTATGCTGGTGGAGATGGATTCGTGGTCACTCTTAGGA	487
QY	481	TTAGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCTCTGATTTGGAAAGTTCCAG	540
Db	488	TTAGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCTCTGATTTGGAAAGTTCCAG	547
QY	541	TGAGCCGACAGTTTGAGCCTATTGTACACTCATCTGATACCTTGGACTAATCGTGCA	600
Db	548	TGAGCCGACAGTTTGAGCCTATTGTACACTCATCTGATACCTTGGACTAATCGTGCA	607
QY	601	TTCCAGAAATATACACCAAGATCCCATATTCACACTCAAACTGCAACACAAACAA	660
Db	608	TTCCAGAAATATACACCAAGATCCCATATTCACACTCAAACTGCAACACAAACAA	667
QY	661	CAGAAATTTATGTCAGTGAAGTACTACTCGGTGGCATGCCCTTACTCTCAAACTCTG	720
Db	668	CAGAAATTTATGTCAGTGAAGTACTACTCGGTGGCATGCCCTTACTCTCAAACTCTG	727
QY	721	CCCCCTACTACTCTCTCTGCTCCAGCTTCCACTTCTATCCACGGAGAAAAATTGA	780
Db	728	CCCCCTACTACTCTCTCTGCTCCAGCTTCCACTTCTATCCACGGAGAAAAATTGA	787

QY	781	TTTGTGTCACAGAACTTTTATGGAACTAGCACCATGCTACAGAACTGAACCATTTG	840
Db	788	TTTGTGTCACAGAACTTTTATGGAACTAGCACCATGCTACAGAACTGAACCATTTG	847
QY	841	TTGAAAAATAAGCAGCACTTCAAGATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTC	900
Db	848	TTGAAAAATAAGCAGCACTTCAAGATGAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTC	907
QY	901	TGCTAGTGTGCTCTCTCTCTCTTTGGTGTGAGCTGGTCTTGATTTTGTCTATGCA	960
Db	908	TGCTAGTGTGCTCTCTCTCTCTTTGGTGTGAGCTGGTCTTGATTTTGTCTATGCA	967
QY	961	AAAGTATGTGAAGGCTTCCCTTTTACAAACAAGATCAGCAGAAAGAAATGATCGAAA	1020
Db	968	AAAGTATGTGAAGGCTTCCCTTTTACAAACAAGATCAGCAGAAAGAAATGATCGAAA	1027
QY	1021	CCAAAGTAGTAAAGGAGGAGGCAATGATAGCAACCTTAATGAGGAATCAAGAAAA	1080
Db	1028	CCAAAGTAGTAAAGGAGGAGGCAATGATAGCAACCTTAATGAGGAATCAAGAAAA	1087
QY	1081	CTGATAAAAAACCCAGAGAGTCCAGAGTCCNAAGCAAACTACCGTGCATGCTGGAG	1140
Db	1088	CTGATAAAAAACCCAGAGAGTCCAGAGTCCNAAGCAAACTACCGTGCATGCTGGAG	1147
QY	1141	CTGAAATTTAGATGAGACAGAAATCAGGAGACACACCTGAGGCTGGTTCCTTTCATGCTC	1200
Db	1148	CTGAAATTTAGATGAGACAGAAATCAGGAGACACACCTGAGGCTGGTTCCTTTCATGCTC	1207
QY	1201	CTTACCCTGCCCCAGCTGGGGAATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACC	1260
Db	1208	CTTACCCTGCCCCAGCTGGGGAATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACC	1267
QY	1261	CTTGGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAG	1320
Db	1268	CTTGGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAG	1327
QY	1321	AATGCCCTTCTCTTTATTGTAACCTGCTGGATCCTATCCTCTACCTCCAAAGCTCC	1380
Db	1328	AATGCCCTTCTCTTTATTGTAACCTGCTGGATCCTATCCTCTACCTCCAAAGCTCC	1387
QY	1381	CACGCCCTTTCTAGCCTGGCTATGCTTAATAATATCCACCTGGGAGAAAGGAGTTTGC	1440
Db	1388	CACGCCCTTTCTAGCCTGGCTATGCTTAATAATATCCACCTGGGAGAAAGGAGTTTGC	1447
QY	1441	AAAGTGAAGNACCTTAAACATCTCATCAGTATCCAGTGGTAAAGGCTCCTGGCTGT	1500
Db	1448	AAAGTGAAGNACCTTAAACATCTCATCAGTATCCAGTGGTAAAGGCTCCTGGCTGT	1507
QY	1501	CTGAGGCTAGGTGGGTTGAAAGCCAAAGAGTCACTGAGACCAAGGCTTTCTCTACTGAT	1560
Db	1508	CTGAGGCTAGGTGGGTTGAAAGCCAAAGAGTCACTGAGACCAAGGCTTTCTCTACTGAT	1567
QY	1561	CCGACAGTCAAGCCCTTTCTCAGCTCTGAAGAGAGAAACAGTATCCCACTGCAATGTC	1620
Db	1568	CCGACAGTCAAGCCCTTTCTCAGCTCTGAAGAGAGAAACAGTATCCCACTGCAATGTC	1627
QY	1621	CTTCTGAGCCCGGTAAAGAGCAAAAGATGGCAGAAAGTTTAGCCCTTGAAAGCCATGA	1680
Db	1628	CTTCTGAGCCCGGTAAAGAGCAAAAGATGGCAGAAAGTTTAGCCCTTGAAAGCCATGA	1687
QY	1681	GATTCCTATACTTGAAGACCTTAATCTCTGTAAGCTTAAATTAAGAAATAGAACAGGT	1740
Db	1688	GATTCCTATACTTGAAGACCTTAATCTCTGTAAGCTTAAATTAAGAAATAGAACAGGT	1747
QY	1741	GAGGATACAGATACACTGTCCAGGAGGACTGTAAACACAGACAGGCTCAAGTGTTTT	1800
Db	1748	GAGGATACAGATACACTGTCCAGGAGGACTGTAAACACAGACAGGCTCAAGTGTTTT	1807
QY	1801	CTCTCAACACATTTAGTTGGAATCACTGTTTGAAGACACACACTTACTTTTTCTGGTCT	1860
Db	1808	CTCTCAACACATTTAGTTGGAATCACTGTTTGAAGACACACACTTACTTTTTCTGGTCT	1867
QY	1861	CTACCACTGCTGATATTTTCTCTAGGAAATATATCTTTTACAAAGTACAAAAATAAACT	1920

Db 1868 CTACACACGTCGATATTTCTCTAGAAATATATCTTTTCAAGTACAAAAATAAAACT 1927  
QY 1921 CTTATAAATTTCTATTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATTACTCAGT 1980  
Db 1928 CTTATAAATTTCTATTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATTACTCAGT 1987  
QY 1981 AATTGGTTTAAAGTAATAAATTCACAAACATTTAAAAAAA 2025  
Db 1988 AATTGGTTTAAAGTAATAAATTCACAAACATTTGTGTGAATA 2032

RESULT 4

US-09-909-320-200  
; Sequence 200, Application US/09909320  
; Patent No. US20020132240A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/909,320  
; CURRENT FILING DATE: 2002-01-04  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 200  
; LENGTH: 2372  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-909-320-200  
Query Match 98.3%; Score 1994; DB 9; Length 2372;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 24 AGCAGGAAATCCGGATGTCGCGTTATGAAGTGAGCAGTGAGTGTGAGCCTCAACATA 83  
Db 1 AGCAGGAAATCCGGATGTCGCGTTATGAAGTGAGCAGTGAGTGTGAGCCTCAACATA 60  
QY 84 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCTCTCATATCACCAGTGGC 143  
Db 61 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCTCTCATATCACCAGTGGC 120  
QY 144 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTTCAGCCTG 203  
Db 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTTCAGCCTG 180  
QY 204 GTGTTGCTTCTCACTTCCATCTGGAACACGAGGCTCTGGTCCAAAGGCTCTTTGGGTGCA 263  
Db 181 GTGTTGCTTCTCACTTCCATCTGGAACACGAGGCTCTGGTCCAAAGGCTCTTTGGGTGCA 240  
QY 264 GAAGAGCTTTCATCCAGGTGTCATGCAAGATTATGGGGATCACCCCTTGTGAGCAAAAG 323  
Db 241 GAAGAGCTTTCATCCAGGTGTCATGCAAGATTATGGGGATCACCCCTTGTGAGCAAAAG 300  
QY 324 GCGAACACGAGCTGAATTTACAGAACTAAGGAGGCTGTAGGCTGCTGGGACTAAGT 383  
Db 301 GCGAACACGAGCTGAATTTACAGAACTAAGGAGGCTGTAGGCTGCTGGGACTAAGT 360  
QY 384 TTGGCCGCAAGACCAAGTTGAAACAGCCTTGAAGTAGCTTTGAAACTTTGACGTAT 443  
Db 361 TTGGCCGCAAGACCAAGTTGAAACAGCCTTGAAGTAGCTTTGAAACTTTGACGTAT 420  
QY 444 GCTGGGTTGGAGATGGATTCTGTCATCTCTAGGATTAGCCCAACCCCAAGTGTGG 503  
Db 421 GCTGGGTTGGAGATGGATTCTGTCATCTCTAGGATTAGCCCAACCCCAAGTGTGG 480  
QY 504 AAAAATGGGGTGGGTGCTCTGATTGGAAGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 563  
Db 481 AAAAATGGGGTGGGTGCTCTGATTGGAAGTTCCAGTGAGCCGACAGTTTGCAGCCTAT 540  
QY 564 TGTTACAACTCATCTGATCTTGGACTTGAACCTCGTGCATTCAGAAATTTATCACCACAAA 623  
Db 541 TGTTACAACTCATCTGATCTTGGACTTGAACCTCGTGCATTCAGAAATTTATCACCACAAA 600  
QY 624 GATCCCATATTCAACACTCAAACTGCAACACAAACAGAAATTTATGTCAGTGACAGT 683  
Db 601 GATCCCATATTCAACACTCAAACTGCAACACAAACAGAAATTTATGTCAGTGACAGT 660  
QY 684 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTACTACTCTCTCTCTGCT 743  
Db 661 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTACTACTCTCTCTCTGCT 720  
QY 744 CCAGCTTCCACTTCTATTCCACGAGAAAAAATTTGATTGTTGTGTCACAGAAATTTTATG 803  
Db 721 CCAGCTTCCACTTCTATTCCACGAGAAAAAATTTGATTGTTGTGTCACAGAAATTTTATG 780  
QY 804 GAAACTAGCACCATGTCTACAGAACTGAACCATTTCTTGAATAAATGAAGCAGCATTCAG 863







Db 1921 GAGTTACAAAGATGATTACTAGGAGATTAATTCAGTAATTTGTTTAAAAAGTAATAAAA 1980  
QY 2004 TTCAACAAACATTTAAAAAAA 2025  
Db 1981 TTCAACAAACATTTGCTGAATA 2002

RESULT 6

US-09-905-291A-200  
; Sequence 200, Application US/09905291A  
; Patent No. US20020160374A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/905,291A  
; CURRENT FILING DATE: 2001-07-12  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 200  
; LENGTH: 2372  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-905-291A-200  
Query Match 98.3%; Score 1994; DB 9; Length 2372;  
Best Local Similarity 99.8%; Pred No. 0;  
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 24 AGCAGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAAGTGTGAGCCTCAACATA 83  
Db 1 AGCAGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAAGTGTGAGCCTCAACATA 60  
QY 84 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCCTCTCATATCACCAGTGGC 143  
Db 61 GTTCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCCTCTCATATCACCAGTGGC 120  
QY 144 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGCCAGGTGCTTCAGCCTG 203  
Db 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGCCAGGTGCTTCAGCCTG 180  
QY 204 GTGTTGCTTCTCATCTCCATCTGGACACGAGGCTCTGGTCCAAAGGCTCTTTGGCGTGA 263  
Db 181 GTGTTGCTTCTCATCTCCATCTGGACACGAGGCTCTGGTCCAAAGGCTCTTTGGCGTGA 240  
QY 264 GAAGAGCTTTCCATCCAGGTGTCATGAGAAATATGGGGATCACCCCTTGTGAGCAAAAAG 323  
Db 241 GAAGAGCTTTCCATCCAGGTGTCATGAGAAATATGGGGATCACCCCTTGTGAGCAAAAAG 300  
QY 324 GCGAAACACGACGCTGAAATTTCAAGAAAGCTAAGGAGGCTGTAGGCTGTGGGACTAACT 383  
Db 301 GCGAAACACGACGCTGAAATTTCAAGAAAGCTAAGGAGGCTGTAGGCTGTGGGACTAACT 360  
QY 384 TTGGCGGCAAGGACCAAGTTGAAACAGGCTTTGAAAGCTAGCTTTGAAACTTTGCGACTAT 443  
Db 361 TTGGCGGCAAGGACCAAGTTGAAACAGGCTTTGAAAGCTAGCTTTGAAACTTTGCGACTAT 420  
QY 444 GCGTGGTGGAGATGGATTCGTGCTCATCTAGATTTAGCCCAACCCCAAGTGTGG 503  
Db 421 GCGTGGTGGAGATGGATTCGTGCTCATCTAGATTTAGCCCAACCCCAAGTGTGG 480  
QY 504 AAAAAATGGGGTGGGTGTCCTGATTTGGAAAGGTTCCAGTGAGCCGACAGTTTGAGCCTAT 563  
Db 481 AAAAAATGGGGTGGGTGTCCTGATTTGGAAAGGTTCCAGTGAGCCGACAGTTTGAGCCTAT 540  
QY 564 TGTTCACACTCATCTGATTAATTTGGACTAACTCGTGATTTCCAGAAATATATCACCACAAA 623  
Db 541 TGTTCACACTCATCTGATTAATTTGGACTAACTCGTGATTTCCAGAAATATATCACCACAAA 600  
QY 624 GATCCCATTTCAACACTCAAACTCAACACAAACAAAGAAATTTATTCAGTGACAGT 683  
Db 601 GATCCCATTTCAACACTCAAACTCAACACAAACAAAGAAATTTATTCAGTGACAGT 660  
QY 684 ACCTACTCGGTGGCATCCCTTTACTCTACAATACCTGCCCTTACTACTCTCTCTGCT 743  
Db 661 ACCTACTCGGTGGCATCCCTTTACTCTACAATACCTGCCCTTACTACTCTCTCTGCT 720  
QY 744 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTTGATTTGTTCACAGAAATTTTATG 803  
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QY 804 GAAACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAAATAAAGCAGCATTTCAAG 863  
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QY 864 AATGAAGTGTGGGTTGGAGGTGTCCCAAGGCTCTGCTAGTGGTGTCTCTCTCTCTTC 923



Db 841 AATGAAGCTGCTGGGTTTGGAGGTGCTCCCAACGGCTCTGCTAGTGGCTGCTCTCTCTTC 900  
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QY 1164 TGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTCCTTACCTGCCCTGCCAGCTGGGAA 1223  
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Db 1321 CCGTGTCTGGATCCTATCCTCTACCTCCAAAGCTTCCAGAGCTTCCAGCGGCTTCTAGCCTGGCTAT 1380  
QY 1404 GTCCTAATAATATCCACTGGGAGAAAGAGTGTTCGAAAGTGCAGAGACCTTAAACATC 1463  
Db 1381 GTCCTAATAATATCCACTGGGAGAAAGAGTGTTCGAAAGTGCAGAGACCTTAAACATC 1440  
QY 1464 TCATCAGTATCAGTGGTTAAAGGCTCTCGGTGTCTGAGGCTAGGTGGGTTGAAAGC 1523  
Db 1441 TCATCAGTATCAGTGGTTAAAGGCTCTCGGTGTCTGAGGCTAGGTGGGTTGAAAGC 1500  
QY 1524 CAAGAGTCACTGAGACCAAGCTTCTCTACTGATCCGAGCTCAGACCCCTTTCTTCA 1583  
Db 1501 CAAGAGTCACTGAGACCAAGCTTCTCTACTGATCCGAGCTCAGACCCCTTTCTTCA 1560  
QY 1584 GCTCTGAAAGAGAAACACGTATCCACCTGCATGTCCTTCTGAGCCCGGTAAGAGCAA 1643  
Db 1561 GCTCTGAAAGAGAAACACGTATCCACCTGCATGTCCTTCTGAGCCCGGTAAGAGCAA 1620  
QY 1644 AGAATGGCAGAAAAGTTAGCCCTGAAAGCCATGGAGATTCTCATTAATTGAGACCTAA 1703  
Db 1621 AGAATGGCAGAAAAGTTAGCCCTGAAAGCCATGGAGATTCTCATTAATTGAGACCTAA 1680  
QY 1704 TCTCTGTAAGCTAAAAATAAGAAATAGAACCAAGCTGAGGATACGACGTACACTGTCA 1763  
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QY 1884 AGGAAATATCTTTTACAGTAAACAAATAAAACTCTTATAATTTCTATTTTACT 1943  
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QY 1944 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAA 2003  
Db 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAA 1980

QY 2004 TTCAACAAACATTTTAAAAAAA 2025  
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RESULT 7

US-09-902-853-200  
; Sequence 200, Application US/09902853  
; Publication No. US20020192659A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Borstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/902,853  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US/09/665,350  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US00/00219  
 ; PRIOR FILING DATE: 2000-01-05  
 ; NUMBER OF SEQ ID NOS: 423  
 ; SEQ ID NO 200  
 ; LENGTH: 2372  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 US-09-902-853-200

Query Match		98.3%;	Score 1994;	DB 9;	Length 2372;
Best Local Similarity		99.8%;	Pred. No. 0;		
Matches 1997;		Conservative	0;	Mismatches	5; Indels 0; Gaps 0;
QY	24	ACGCGGAAATCCGATGCTCGGTTATGAAGTGGAGCAGTGAAGTGGAGCTTCAACATA	83		
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QY	84	GTTCAGAACTCTCCATCCGAGTCTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC	143		
DB	61	GTTCAGAACTCTCCATCCGAGTCTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC	120		
QY	144	CATCTGAGTGTTCCTGGCTCTGAAGGGTAGGCAAGATGGCCAGGTGCTTCAGCCTG	203		
DB	121	CATCTGAGTGTTCCTGGCTCTGAAGGGTAGGCAAGATGGCCAGGTGCTTCAGCCTG	180		
QY	204	GTGTTGCTTCTCACTTCCATCTGACACGAGGCTCCTGGTCCAGGCTCTTTGGTGCA	263		
DB	181	GTGTTGCTTCTCACTTCCATCTGACACGAGGCTCCTGGTCCAGGCTCTTTGGTGCA	240		
QY	264	GAAGAGCTTTCATCCAGTGTCTATGAGAAATATGGGATCACCCCTGTGAGCAAAAAG	323		
DB	241	GAAGAGCTTTCATCCAGTGTCTATGAGAAATATGGGATCACCCCTGTGAGCAAAAAG	300		
QY	324	GGAAACAGCAGCTGAATTTCAAGAGCTAAGAGGCTGTAGGCTGTGGGACTAAGT	383		
DB	301	GGAAACAGCAGCTGAATTTCAAGAGCTAAGAGGCTGTAGGCTGTGGGACTAAGT	360		
QY	384	TTGGCCGGCAGGACCAAGTTCAGACAGCTTTGAAAGCTAGCTTTGAACTTTCAGCTAT	443		
DB	361	TTGGCCGGCAGGACCAAGTTCAGACAGCTTTGAAAGCTAGCTTTGAACTTTCAGCTAT	420		
QY	444	GGCTGGTGGAGATGGATTCGTGGTCACTCTAGGATTAGCCCAACCCCAAGTGTGGG	503		
DB	421	GGCTGGTGGAGATGGATTCGTGGTCACTCTAGGATTAGCCCAACCCCAAGTGTGGG	480		
QY	504	AAAAATGGGTTGGAGTGGATTCGTGGTCACTCTAGGATTAGCCCAACCCCAAGTGTGGG	563		
DB	481	AAAAATGGGTTGGAGTGGATTCGTGGTCACTCTAGGATTAGCCCAACCCCAAGTGTGGG	540		
QY	564	TGTTACAACTCATCTGATCTGGACTAACTCGTGATTCAGAAATATACACCCAAA	623		
DB	541	TGTTACAACTCATCTGATCTGGACTAACTCGTGATTCAGAAATATACACCCAAA	600		
QY	624	GATCCCATTTCAACACTCAAACTGCAACACAAACACAGAAATTTATGTCAGTGACAGT	683		
DB	601	GATCCCATTTCAACACTCAAACTGCAACACAAACACAGAAATTTATGTCAGTGACAGT	660		
QY	684	ACCTACTCGGTGGATTCCTTACTTCAATACCTGCCCCCTACTACTCTCTCTGCT	743		
DB	661	ACCTACTCGGTGGATTCCTTACTTCAATACCTGCCCCCTACTACTCTCTCTCTGCT	720		
QY	744	CCAGCTTCCACTTCTATTCCAGGAGAAAAAATGATTTGTGTCAGAGATTTTATG	803		
DB	721	CCAGCTTCCACTTCTATTCCAGGAGAAAAAATGATTTGTGTCAGAGATTTTATG	780		
QY	804	GAACCTAGCAGCATGTCTACAGAACTGAACCATTTGTTGAAAAATAAGCAGCATCAAG	863		
DB	781	GAACCTAGCAGCATGTCTACAGAACTGAACCATTTGTTGAAAAATAAGCAGCATCAAG	840		
QY	864	AATGAAGCTGCTGGGTTGGAGGTGTCCCGCAGGCTCTGCTAGTGTCTCTCTCTTC	923		
DB	841	AATGAAGCTGCTGGGTTGGAGGTGTCCCGCAGGCTCTGCTAGTGTCTCTCTCTTC	900		

QY	924	TTTGGTGTGTCAGCTGGTCTTGGATTTTGTCTATGTCAAAAGGTATGTGAGGCTTCCCT	983
DB	901	TTTGGTGTGTCAGCTGGTCTTGGATTTTGTCTATGTCAAAAGGTATGTGAGGCTTCCCT	960
QY	984	TTTACAAACAGAATCAGCAGAAAGAAATGATCGAAACCAAAAGTAGTAAAGGAGGAGAAG	1043
DB	961	TTTACAAACAGAATCAGCAGAAAGAAATGATCGAAACCAAAAGTAGTAAAGGAGGAGAAG	1020
QY	1044	GCCATATGATAGCAACCTTAATGAGGAATCAAGAAATCTGATAAAACCCAGAGAGTCC	1103
DB	1021	GCCATATGATAGCAACCTTAATGAGGAATCAAGAAATCTGATAAAACCCAGAGAGTCC	1080
QY	1104	AGAGTCCCAAGCAAAACTACCTGCGATGCTGGAAGCTGAAGTTTAGATGACAGAGAA	1163
DB	1081	AGAGTCCCAAGCAAAACTACCTGCGATGCTGGAAGCTGAAGTTTAGATGACAGAGAA	1140
QY	1164	TCAGGAGACACACCTGAGGCTGTTTCTTTCATGTCTCTTACCTGCCCCAGCTGGGAA	1223
DB	1141	TCAGGAGACACACCTGAGGCTGTTTCTTTCATGTCTCTTACCTGCCCCAGCTGGGAA	1200
QY	1224	ATCAAAAGGCCAAAGAACCAAGAAAGTCCACCTTGGTTCCTAACTGGAATCAGC	1283
DB	1201	ATCAAAAGGCCAAAGAACCAAGAAAGTCCACCTTGGTTCCTAACTGGAATCAGC	1260
QY	1284	TCAGAGCTGCCATTCGACTATGAGTGCACCAAGAGAGTCCCTTCTCTTTATTGTAAC	1343
DB	1261	TCAGAGCTGCCATTCGACTATGAGTGCACCAAGAGAGTCCCTTCTCTTTATTGTAAC	1320
QY	1344	CCTGTCTGATCTTCTCTTACCTCCAAAGCTTCCACGGCTTCTTAGCTGCTAT	1403
DB	1321	CCTGTCTGATCTTCTCTTACCTCCAAAGCTTCCACGGCTTCTTAGCTGCTAT	1380
QY	1404	GTCTTAATAATCCACTGGGAGAAAGAGTTTTCMAAGTGAAGGACCTAAACATC	1463
DB	1381	GTCTTAATAATCCACTGGGAGAAAGAGTTTTCMAAGTGAAGGACCTAAACATC	1440
QY	1464	TCATCAGTATCCAGTGGTAAAGGCTCTCTGGTGTCTGAGGCTAGTGGTGTGAAGC	1523
DB	1441	TCATCAGTATCCAGTGGTAAAGGCTCTCTGGTGTCTGAGGCTAGTGGTGTGAAGC	1500
QY	1524	CAAGAGTCACTGAGACCAAGGCTTCTTCTACTGATTCGCGAGCTCAGACCTTTCTCA	1583
DB	1501	CAAGAGTCACTGAGACCAAGGCTTCTTCTACTGATTCGCGAGCTCAGACCTTTCTCA	1560
QY	1584	GCTCTGAAGAGAAACAGTATCCACCTGACATGCTCTCTGAGCCCGGTGAAGCAAA	1643
DB	1561	GCTCTGAAGAGAAACAGTATCCACCTGACATGCTCTCTGAGCCCGGTGAAGCAAA	1620
QY	1644	AGAATGGCAGAAAAGTTTGGCCCTGAAAGCCATGGAGATTCCTATACTGAGACCTAA	1703
DB	1621	AGAATGGCAGAAAAGTTTGGCCCTGAAAGCCATGGAGATTCCTATACTGAGACCTAA	1680
QY	1704	TCTCTGTAAGCTAAATAAGAAATAGAACCAAGCTGAGGATACGACAGTACATGTCA	1763
DB	1681	TCTCTGTAAGCTAAATAAGAAATAGAACCAAGCTGAGGATACGACAGTACATGTCA	1740
QY	1764	GCAGGAGCTGTAAACACAGACAGGCTCAAGGTTTCTCTGAAACACATTGTTGGAT	1823
DB	1741	GCAGGAGCTGTAAACACAGACAGGCTCAAGGTTTCTCTGAAACACATTGTTGGAT	1800
QY	1824	CACTCTTTAGAACACACACACTTACTTTTCTGGTCTCTACACCTGCTGATATTTCTCT	1883
DB	1801	CACTCTTTAGAACACACACACTTACTTTTCTGGTCTCTACACCTGCTGATATTTCTCT	1860
QY	1884	AGGAATATATCTTTTACAGTAAACAAATAAATACTCTTATAAATTTCTATTTTATCT	1943
DB	1861	AGGAATATATCTTTTACAGTAAACAAATAAATACTCTTATAAATTTCTATTTTATCT	1920
QY	1944	GAGTTTACAGAAATGATTTACTAGGAGAGATTTACTCAGTAAATTTGTTTAAAGTAATAAAA	2003
DB	1921	GAGTTTACAGAAATGATTTACTAGGAGAGATTTACTCAGTAAATTTGTTTAAAGTAATAAAA	1980
QY	2004	TTCAACAAACATTTTAAAAAAA 2025	



QY 924 TTTGGTGTGCTGAGCTGGTCTTGGATTTTGGCTATGTCMAAAGGTATGCTGAAGGCTTCCCT 983  
DB 901 TTTGGTGTGCTGAGCTGGTCTTGGATTTTGGCTATGTCMAAAGGTATGCTGAAGGCTTCCCT 960  
QY 984 TTTTCAAAACAAGATCAGCAGAGGAATGATCGAAACCAAAAGTAGTAAAGGAGGAGAAG 1043  
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QY 1884 AGAATATATCTTTTACAGTAAACAAAATTAATAAATCTTTATTAATTTCTATTTATCT 1943  
DB 1861 AGAATATATCTTTTACAGTAAACAAAATTAATAAATCTTTATTAATTTCTATTTATCT 1920  
QY 1944 GAGTTACAGAAATGATTACTAGGAGATTTACTCAGTAATTTGTTTAAAAAGTAATAAA 2003  
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DB 1981 TTCACAAAACATTTGCTGAATA 2002  
RESULT 9  
US-09-907-841-200  
; Sequence 200, Application US/09907841  
; Publication No. US20020198366A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/907,841  
; CURRENT FILING DATE: 2001-11-20  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 200  
; LENGTH: 2372  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-907-841-200  
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Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
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QY 144 CATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGGCACGATGCCAGGTGCTTTCAGCCTG 203  
Db 121 CATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGGCACGATGCCAGGTGCTTTCAGCCTG 180  
QY 204 GTGTTGCTTCTCACTTCATCTGGACCAAGAGCTCCTGGTCCAAAGCTCTTTGGGTGCA 263  
Db 181 GTGTTGCTTCTCACTTCATCTGGACCAAGAGCTCCTGGTCCAAAGCTCTTTGGGTGCA 240  
QY 264 GAAGAGCTTTCATCCAGTGTCAATGAGCAATATGGGATCACCTTGTGAGCAAAAAG 323  
Db 241 GAAGAGCTTTCATCCAGTGTCAATGAGCAATATGGGATCACCTTGTGAGCAAAAAG 300  
QY 324 GCGAACCCAGCAGCTGAATTTACAGAACTAAGGAGGCTGTAGGCTGCTGGCACTAAGT 383  
Db 301 GCGAACCCAGCAGCTGAATTTACAGAACTAAGGAGGCTGTAGGCTGCTGGCACTAAGT 360  
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Db 361 TTGGCCGGCAAGGACCAAGTTGAAACAGCTTTGAAAGCTAGCTTTGAAACTTTGCAGCTAT 420  
QY 444 GGCTGGTGGAGATGGATTCGTGTCTCTAGGATTTAGCCAAACCCCAAGTGTGGG 503  
Db 421 GGCTGGTGGAGATGGATTCGTGTCTCTAGGATTTAGCCAAACCCCAAGTGTGGG 480  
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QY 864 AATGAAGTCTGCTGGTGTGGAGGTGCTCCAGCGCTCTGCTAGTGTGCTCTCTCTTC 923  
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Db 1561 GCTCTGAAAGAGAAACAGTATCCACCTGACATGCTCTGAGCCCGTGAAGAGCAA 1620  
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Db 1621 AGAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCTATAACTTGGAGACCTAA 1680  
QY 1704 TCTCTGTAAGCTAAATAAAGAAATAGAACAGGCTGAGGATAGCAGATACACTGTCA 1763  
Db 1681 TCTCTGTAAGCTAAATAAAGAAATAGAACAGGCTGAGGATAGCAGATACACTGTCA 1740  
QY 1764 GCAGGACTGTAAACACAGACAGGCTCAAGTGTCTCTGAAACACATTTGAGTTGGAAT 1823  
Db 1741 GCAGGACTGTAAACACAGACAGGCTCAAGTGTCTCTGAAACACATTTGAGTTGGAAT 1800  
QY 1824 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACACCTGCTGATATTTCTCT 1883  
Db 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACACCTGCTGATATTTCTCT 1860  
QY 1884 AGGAATATACTTTTACAGTAAGCAAAATAAAACTCTTATAAATTTCTATTTTATCT 1943  
Db 1861 AGGAATATACTTTTACAGTAAGCAAAATAAAACTCTTATAAATTTCTATTTTATCT 1920  
QY 1944 GAGTTACAGAAATGATTTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAA 2003  
Db 1921 GAGTTACAGAAATGATTTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAA 1980  
QY 2004 TTCAACAAACATTTAAAAAAA 2025  
Db 1981 TTCAACAAACATTTGCTGAATA 2002

RESULT 10  
US-09-904-011-200  
; Sequence 200, Application US/09904011  
; Publication No. US20030003530A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, A.  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, Christopher J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth, J.  
 ; APPLICANT: Klijavin, Ivar J.  
 ; APPLICANT: Mather, Jennie P.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William, I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; TITLE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: 10466-14  
 ; CURRENT APPLICATION NUMBER: US/09/904,011  
 ; CURRENT FILING DATE: 2001-07-11  
 ; PRIOR APPLICATION NUMBER: 09/665,350  
 ; PRIOR FILING DATE: 2000-09-18  
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414  
 ; PRIOR FILING DATE: 2000-02-22  
 ; PRIOR APPLICATION NUMBER: US 60/143,048  
 ; PRIOR FILING DATE: 1999-07-07  
 ; PRIOR APPLICATION NUMBER: US 60/145,698  
 ; PRIOR FILING DATE: 1999-07-26  
 ; PRIOR APPLICATION NUMBER: US 60/146,222  
 ; PRIOR FILING DATE: 1999-07-28  
 ; PRIOR APPLICATION NUMBER: PCT/US99/20594  
 ; PRIOR FILING DATE: 1999-09-08  
 ; PRIOR APPLICATION NUMBER: PCT/US99/20944  
 ; PRIOR FILING DATE: 1999-09-13  
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090  
 ; PRIOR FILING DATE: 1999-09-15  
 ; PRIOR APPLICATION NUMBER: PCT/US99/21547  
 ; PRIOR FILING DATE: 1999-09-15  
 ; PRIOR APPLICATION NUMBER: PCT/US99/23089  
 ; PRIOR FILING DATE: 1999-10-05  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28214  
 ; PRIOR FILING DATE: 1999-11-29  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313  
 ; PRIOR FILING DATE: 1999-11-30  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28564  
 ; PRIOR FILING DATE: 1999-12-02  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28565  
 ; PRIOR FILING DATE: 1999-12-02  
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095  
 ; PRIOR FILING DATE: 1999-12-16  
 ; PRIOR APPLICATION NUMBER: PCT/US99/30911  
 ; PRIOR FILING DATE: 1999-12-20  
 ; PRIOR APPLICATION NUMBER: PCT/US99/30999  
 ; PRIOR FILING DATE: 1999-12-20  
 ; PRIOR APPLICATION NUMBER: PCT/US00/00219  
 ; PRIOR FILING DATE: 2000-01-05  
 ; NUMBER OF SEQ ID NOS: 423  
 ; SEQ ID NO 200  
 ; LENGTH: 2372  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 ; US-09-904-011-200

Query Match 98.3%; Score 1994; DB 10; Length 2372;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 24 AGCAGGAAATCCGATGTCCTCGGTATGAAAGTGAGCGAGTGAGTGTGAGCCCTCAACATA 83  
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Db QY 1 AGCAGGAAATCCGATGTCCTCGGTATGAAAGTGAGCGAGTGAGTGTGAGCCCTCAACATA 60  
 84 GTTCCAGAACTCTCCATCCGAGTATGTTATGAGCATCTGCCTCTCAATACCAAGTGGC 143  
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 Db QY 61 GTTCCAGAACTCTCCATCCGAGTATGTTATGAGCATCTGCCTCTCAATACCAAGTGGC 120  
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 QY 204 GTGTTGCTTCTCACTTCCATCTGGACACGAGGCTCTTGCTGTCACAGGCTCTTTGGCTGCA 263  
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 Db QY 181 GTGTTGCTTCTCACTTCCATCTGGACACGAGGCTCTTGCTGTCACAGGCTCTTTGGCTGCA 240  
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 QY 264 GAAAGCTTTCCATCCAGGTGTCATGAGAAATATGGGATCACCTTGTGAGCAAAAG 323  
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 Db QY 241 GAAAGCTTTCCATCCAGGTGTCATGAGAAATATGGGATCACCTTGTGAGCAAAAG 300  
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 Db QY 481 AAAAATGGGTTGGGTTGCTGCTGANTTTGGAAGGTTCCAGTGAGCGGACAGTTTTCAGGCTAT 540  
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 QY 624 GATCCCATATTCACACTCAAACTGCAACACAAACAGAGATTTATGTCAGTACAGT 683  
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 Db QY 601 GATCCCATATTCACACTCAAACTGCAACACAAACAGAGATTTATGTCAGTACAGT 660  
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 QY 684 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCCCTACTACTCTCTCTGCT 743  
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 Db QY 661 ACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCCCTACTACTCTCTCTGCT 720  
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 QY 804 GAACTAGCACCATCTCTACAGAAACTGAACCATTTGTTGAAATTAAGACAGATTCAG 863  
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 Db QY 781 GAACTAGCACCATCTCTACAGAAACTGAACCATTTGTTGAAATTAAGACAGATTCAG 840  
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 QY 864 AATGAAGCTGCTGGGTTTGGAGGTGTCGCCACGGCTCTGCTAGTGTGCTCTCTCTCTTC 923  
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 QY 924 TTTGCTGCTGAGCTGGCTTGGATTTTGTGTCATGTCACAAAGATGTCGAGGCTTCCCT 983  
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 Db QY 1021 GCCAATGATAGCAACCTTAATGAGGAATCAAGAAAACTGTATATAAAACCCAGAGAGTCC 1080  
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 QY 1104 AAGAGTCCAGCAAAACTACCGTGGAGTCCCTGGAGCTGGAAGTGAAGTTAGTGTAGACAGAAA 1163  
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 Db QY 1081 AAGAGTCCAGCAAAACTACCGTGGAGTCCCTGGAGTCCCTGGAGTGAAGTTAGTGTAGACAGAAA 1140  
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QY 1164 TGAGGAGACACACCTGAGCTGGTTCTTTCTATGCTCCTTACCTGCCCGAGCTGGGAA 1223  
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 QY 1224 ATCAAAGGGCCAAAGAACAAAGAGAAAGTCCACCTTGGTTCCTAACTGGAATCAGC 1283  
 Db 1201 ATCAAAGGGCCAAAGAACAAAGAGAAAGTCCACCTTGGTTCCTAACTGGAATCAGC 1260  
 QY 1284 TCAGGACTGCCATTGCACTATGAGTGCACCAAGAGAAATGCCCTTCTCTTATTTGTAAC 1343  
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 Db 1381 GTCTTAATAATATCCACCTGGGAGAAAGAGATTTTGCAAAGTGCAGGACCTAAACATC 1440  
 QY 1464 TCATCAGTATCAGTGGTAAAGGCTCTCTGCTGTCTGAGCTAGGTGGGTGAAAGC 1523  
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 QY 1524 CAAGGAGTCACTGAGACCAAGCTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1583  
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 QY 1764 GCAGGAGCTGTAACACACAGACAGGCTCAAGTGTCTTCTGAAACACATGAGTTGGAAT 1823  
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 QY 1824 CACTCTTTAGAACACACACACTTCTTTCTGCTCTTACCACTGCTGATTTTCTCT 1883  
 Db 1801 CACTCTTTAGAACACACACACTTCTTTCTGCTCTTACCACTGCTGATTTTCTCT 1860  
 QY 1884 AGGAATATATCTTTTACAGTAAACAAATAAAACTCTTATAAAATTTCTATTTTATCT 1943  
 Db 1861 AGGAATATATCTTTTACAGTAAACAAATAAAACTCTTATAAAATTTCTATTTTATCT 1920  
 QY 1944 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAGTAATAAAA 2003  
 Db 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAGTAATAAAA 1980  
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 Db 1981 TTCACAAACATTTTCTGAATA 2002

RESULT 11

US-09-906-742-200  
 ; Sequence 200, Application US/09906742  
 ; Publication No. US20030023054A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Genentech, Inc.  
 ; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone

Query Match 98.3%; Score 1994; DB 10; Length 2372;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 24 AGCAGGAAATCCGATCTCTCGGTATGAAAGTCGAGCAGTGAGTGCAGCTCAACATA 83  
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; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, A.  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, Christopher J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth, J.  
 ; APPLICANT: Kljavin, Ivar J.  
 ; APPLICANT: Mather, Jennie P.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William, I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE REFERENCE: 10466-14  
 ; CURRENT APPLICATION NUMBER: US/09/906,742  
 ; CURRENT FILING DATE: 2001-07-16  
 ; PRIOR APPLICATION NUMBER: 09/665,350  
 ; PRIOR FILING DATE: 2000-09-18  
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414  
 ; PRIOR FILING DATE: 2000-02-22  
 ; PRIOR APPLICATION NUMBER: US 60/143,048  
 ; PRIOR FILING DATE: 1999-07-07  
 ; PRIOR APPLICATION NUMBER: US 60/145,698  
 ; PRIOR FILING DATE: 1999-07-26  
 ; PRIOR APPLICATION NUMBER: US 60/146,222  
 ; PRIOR FILING DATE: 1999-07-28  
 ; PRIOR APPLICATION NUMBER: PCT/US99/20594  
 ; PRIOR FILING DATE: 1999-09-08  
 ; PRIOR APPLICATION NUMBER: PCT/US99/20944  
 ; PRIOR FILING DATE: 1999-09-13  
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090  
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 ; PRIOR APPLICATION NUMBER: PCT/US99/21547  
 ; PRIOR FILING DATE: 1999-09-15  
 ; PRIOR APPLICATION NUMBER: PCT/US99/23089  
 ; PRIOR FILING DATE: 1999-10-05  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28214  
 ; PRIOR FILING DATE: 1999-11-29  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313  
 ; PRIOR FILING DATE: 1999-11-30  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28564  
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 ; PRIOR FILING DATE: 1999-12-20  
 ; PRIOR APPLICATION NUMBER: PCT/US99/30999  
 ; PRIOR FILING DATE: 1999-12-20  
 ; PRIOR APPLICATION NUMBER: PCT/US00/00219  
 ; PRIOR FILING DATE: 2000-01-05  
 ; NUMBER OF SEQ ID NOS: 423  
 ; SEQ ID NO 200  
 ; LENGTH: 2372  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 ; US-09-906-742-200



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Db 61 GTTCCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCTTCATATCAACAGTGGC 120  
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QY 204 GTGTGCTTCTCACCTCCATCTGGACCAAGGCTCCTGGTCCAGAGCTCTTTGGGTGCA 263  
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Db 421 GGTGGGTTGGAGATGGATTCGTGGTCTCTAGGATTTAGCCAAACCCCAAGTGGG 480  
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QY 864 AATGAAGCTGCTGGGTTTGGAGGTGTCGCCAGGGCTCTGCTAGTGCTGCTCTCTCTTC 923  
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Db 1501 CAGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGAGCTCAGACCTTCTTCTCA 1560  
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Db 1801 CACTGTTTGAACACACACATTTACTTTTCTGGTCTCTTACCCTGCTGATATTTTCTCT 1860  
QY 1884 AGGAAATATACCTTTTACAGTAACAAAAATAAAACTTATAAAATTTCTATTTTATCT 1943  
Db 1861 AGGAAATATACCTTTTACAGTAACAAAAATAAAACTTATAAAATTTCTATTTTATCT 1920  
QY 1944 GAGTTACAGAAATGATTACTAAGGAGATTTACTCAGTAAATTTGTTTAAAAAGTAAATAA 2003  
Db 1921 GAGTTACAGAAATGATTACTAAGGAGATTTACTCAGTAAATTTGTTTAAAAAGTAAATAA 1980  
QY 2004 TTCAACAAACATTTAAAAAAA 2025  
Db 1981 TTCAACAAACATTTGCTGAATA 2002

RESULT 12  
US-09-906-838-200  
; Sequence 200, Application US/09906838  
; Publication No. US20030027143A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desrochers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone



APPLICANT: Filvaroff, Ellen  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, A.  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, Christopher J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Hillan, Kenneth, J.  
 APPLICANT: Kijavlin, Ivar J.  
 APPLICANT: Mather, Jennie P.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William, I.  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 TITLE OF INVENTION: Acids Encoding the Same  
 FILE REFERENCE: 10466-14  
 CURRENT APPLICATION NUMBER: US/09/906,838  
 CURRENT FILING DATE: 2001-07-16  
 PRIOR APPLICATION NUMBER: 09/665,350  
 PRIOR FILING DATE: 2000-09-18  
 PRIOR APPLICATION NUMBER: PCT/US00/04414  
 PRIOR FILING DATE: 2000-02-22  
 PRIOR APPLICATION NUMBER: US 60/143,048  
 PRIOR FILING DATE: 1999-07-07  
 PRIOR APPLICATION NUMBER: US 60/145,698  
 PRIOR FILING DATE: 1999-07-26  
 PRIOR APPLICATION NUMBER: US 60/146,222  
 PRIOR FILING DATE: 1999-07-28  
 PRIOR APPLICATION NUMBER: PCT/US99/20594  
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 PRIOR APPLICATION NUMBER: PCT/US99/20944  
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 PRIOR APPLICATION NUMBER: PCT/US99/21090  
 PRIOR FILING DATE: 1999-09-15  
 PRIOR APPLICATION NUMBER: PCT/US99/21547  
 PRIOR FILING DATE: 1999-09-15  
 PRIOR APPLICATION NUMBER: PCT/US99/23089  
 PRIOR FILING DATE: 1999-10-05  
 PRIOR APPLICATION NUMBER: PCT/US99/28214  
 PRIOR FILING DATE: 1999-11-29  
 PRIOR APPLICATION NUMBER: PCT/US99/28313  
 PRIOR FILING DATE: 1999-11-30  
 PRIOR APPLICATION NUMBER: PCT/US99/28564  
 PRIOR FILING DATE: 1999-12-02  
 PRIOR APPLICATION NUMBER: PCT/US99/28565  
 PRIOR FILING DATE: 1999-12-02  
 PRIOR APPLICATION NUMBER: PCT/US99/30095  
 PRIOR FILING DATE: 1999-12-16  
 PRIOR APPLICATION NUMBER: PCT/US99/30911  
 PRIOR FILING DATE: 1999-12-20  
 PRIOR APPLICATION NUMBER: PCT/US99/30999  
 PRIOR FILING DATE: 1999-12-20  
 PRIOR APPLICATION NUMBER: PCT/US00/00219  
 PRIOR FILING DATE: 2000-01-05  
 NUMBER OF SEQ ID NOS: 423  
 SEQ ID NO 200  
 LENGTH: 2372  
 TYPE: DNA  
 ORGANISM: Homo Sapien  
 US-09-906-838-200

Query Match 98.3%; Score 1994; DB 10; Length 2372;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

24 AGCAGGAAATCCGGATGTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 83  
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1	AGCAGGAAATCCGGATGTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA	60	Db
84	GTTCAGAACTCTCCATCCGGACTAGTTATTAGCACTCTGCTCTCATATCAGCTGGC	143	Qy
61	GTTCAGAACTCTCCATCCGGACTAGTTATTAGCACTCTGCTCTCATATCAGCTGGC	120	Db
144	CATCTGAGGTGTTCCCTGGCTCTGAAGGGTAGGACGATGCCAGGTGCTTCAGCCTG	203	Qy
121	CATCTGAGGTGTTCCCTGGCTCTGAAGGGTAGGACGATGCCAGGTGCTTCAGCCTG	180	Db
204	GTGTTGCTTCTCACTTCCATCTGGACACAGAGCTCTGCTCAAGGCTCTTTGGTGCA	263	Qy
181	GTGTTGCTTCTCACTTCCATCTGGACACAGAGCTCTGCTCAAGGCTCTTTGGTGCA	240	Db
264	GAAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGGATCACCTCTTGAGCAAAAAG	323	Qy
241	GAAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGGATCACCTCTTGAGCAAAAAG	300	Db
324	CGAACCAGCAGCTGAATTTACAGAGCTAAGGAGGCTGTAGGCTGCTGGAGCTAAGT	383	Qy
301	CGAACCAGCAGCTGAATTTACAGAGCTAAGGAGGCTGTAGGCTGCTGGAGCTAAGT	360	Db
384	TTGGCCGGCAAGCAACAAAGTTCAAAACAGCTTTGAAAGCTAGCTTTGAAACTTTGAGCTAT	443	Qy
361	TTGGCCGGCAAGCAACAAAGTTCAAAACAGCTTTGAAAGCTAGCTTTGAAACTTTGAGCTAT	420	Db
444	GGCTGGTTGGAGATGGATTTCGTGTCATCTCTAGGATTAGCCCAACCCCAAGTGTGGG	503	Qy
421	GGCTGGTTGGAGATGGATTTCGTGTCATCTCTAGGATTAGCCCAACCCCAAGTGTGGG	480	Db
504	AAAAATGGGTGGGTGCTCTGATTTTGGAAAGTTTCAGTGAGCCGACAGTTTCAGGCTAT	563	Qy
481	AAAAATGGGTGGGTGCTCTGATTTTGGAAAGTTTCAGTGAGCCGACAGTTTCAGGCTAT	540	Db
564	TGTTACAACTCATCTGATACCTTGGACTAATCGTGCTATTCAGAAATATACACCAAA	623	Qy
541	TGTTACAACTCATCTGATACCTTGGACTAATCGTGCTATTCAGAAATATACACCAAA	600	Db
624	GATCCCATATTCAACTCAACTCAAACTCAAACTCAAACTCAAACTCAAACTCAAACT	683	Qy
601	GATCCCATATTCAACTCAACTCAAACTCAAACTCAAACTCAAACTCAAACTCAAACT	660	Db
684	ACCTACTCGGTGGGATCCCTTACTCTCAATACCTGCCCCCTACTACTCTCTCTGCT	743	Qy
661	ACCTACTCGGTGGGATCCCTTACTCTCAATACCTGCCCCCTACTACTCTCTCTGCT	720	Db
744	CCAGCTTCCACTTCTATTCCACGAGAAAAAATGATTGTGTGTCAGAAAGTTTATG	803	Qy
721	CCAGCTTCCACTTCTATTCCACGAGAAAAAATGATTGTGTGTCAGAAAGTTTATG	780	Db
804	GAACTAGACCATGTCATACAGAACTGAACTGAACTGAACTGAACTGAACTGAACT	863	Qy
781	GAACTAGACCATGTCATACAGAACTGAACTGAACTGAACTGAACTGAACTGAACT	840	Db
864	AATGAAGCTGCTGGTTTGGAGGTGTCCTCCAGGCTCTGCTAGTGTCTCTCTCTCT	923	Qy
841	AATGAAGCTGCTGGTTTGGAGGTGTCCTCCAGGCTCTGCTAGTGTCTCTCTCTCT	900	Db
924	TTTGTGCTGAGCTGCTTTGGATTTTGGATTTTGGATTTTGGATTTTGGATTTTGG	983	Qy
901	TTTGTGCTGAGCTGCTTTGGATTTTGGATTTTGGATTTTGGATTTTGGATTTTGG	960	Db
984	TTTACAAACAAAGATACAGCAAGAAATGATCGAAACCAAGTAGTAAAGAGGAGAG	1043	Qy
961	TTTACAAACAAAGATACAGCAAGAAATGATCGAAACCAAGTAGTAAAGAGGAGAG	1020	Db
1044	GCCATGATAGCAACCTTAATGAGAACTCAAGAAACTGATAAAACCCAGAGAGTCC	1103	Qy
1021	GCCATGATAGCAACCTTAATGAGAACTCAAGAAACTGATAAAACCCAGAGAGTCC	1080	Db
1104	AAGAGTCCAAAGCAAACTACCGTGGATGCTCGGAGCTGAAGTTTACATGAGACAGAA	1163	Qy
1081	AAGAGTCCAAAGCAAACTACCGTGGATGCTCGGAGCTGAAGTTTACATGAGACAGAA	1140	Db

Qy	1164	TGAGGACACACCTGAGGTGGTTTCTTTTCATGCTCTTTACCGTGCCCGCAGCTGGGGAA	1223
Db	1141	TGAGGACACACCTGAGGTGGTTTCTTTTCATGCTCTTTACCGTGCCCGCAGCTGGGGAA	1200
Qy	1224	ATCAAAAGGCGCAAAGAACCAAAGAAGTAGTCCACCCTTGGTTCTCTAACCTGGAATCAGC	1283
Db	1201	ATCAAAAGGCGCAAAGAACCAAGAAGAAAGTCCACCCTTGGTTCTTAATCTGNATCAGC	1260
Qy	1284	TCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAGAAATGCCCTTCTCTTAATTGPAAC	1343
Db	1261	TCAGGACTGCCAATTGGACTATGGAGTGCACCAAGAGAGAAATGCCCTTCTCTTAATTGTAAC	1320
Qy	1344	CCTGTCTGGATCCTATCCTCTACTCTCCAAGCTTCCCACGGCTTCTPAGCCCTGGCTAT	1403
Db	1321	CCTGTCTGGATCCTATCCTCTACTCTCCAAGCTTCCCACGGCTTCTPAGCCCTGGCTAT	1380
Qy	1404	GTCCTAAATAATATCCCCACTGCGGAGAAAGGAGTTTTGCAAAAGTGCAGAGCACTAAAACATC	1463
Db	1381	GTCCTAAATAATATCCCCACTGCGGAGAAAGGAGTTTTGCAAAAGTGCAGAGCACTAAAACATC	1440
Qy	1464	TCATCAGTATCCAGTGGTAAAAGGCCCTCTGGCTGTCTGAGGCTAGGTGGGTGAAAGC	1523
Db	1441	TCATCAGTATCTCAGTGGTAAAAGGCCCTCTGGCTGTCTGAGGCTAGGTGGGTGAAAGC	1500
Qy	1524	CAAGGAGTCACTGAGACAAGAGCTTTCTCTACTGATTTCCGCGAGCTCAGAGCCCTTTCCTCA	1583
Db	1501	CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTTCCGCGAGCTCAGAGCCCTTTCCTCA	1560
Qy	1584	GCTCTGAAAGAGAAACACGTATCCCACTGACATGTCTTCTGAGCCCGGTAAAGACAAA	1643
Db	1561	GCTCTGAAAGAGAAACACGTATCCCACTGACATGTCTTCTGAGCCCGGTAAAGACAAA	1620
Qy	1644	AGANTGCAGAAAGTTTAGCCCTGAGAACCATCGAGAGTTCTCATAACTTGAGACCTAA	1703
Db	1621	AGANTGCAGAAAGTTTAGCCCTGAGAACCATCGAGAGTTCTCATAACTTGAGACCTAA	1680
Qy	1704	TCTCTGTAAGCTAAAAATAAGAAATAAGAACCAAGGCTGAGGATACGACAGTACACTGTCA	1763
Db	1681	TCTCTGTAAGCTAAAAATAAGAAATAAGAACCAAGGCTGAGGATACGACAGTACACTGTCA	1740
Qy	1764	GCAGGACTGTAAACACAGACAGAGGTCAAGTGTTTTCTCTGAACACATTTGAGTTGGAAT	1823
Db	1741	GCAGGACTGTAAACACAGACAGAGGTCAAGTGTTTTCTCTGAACACATTTGAGTTGGAAT	1800
Qy	1824	CACCTGTTTAGAACACACACACTTACTTTTTCTGTGCTCTACCACTGCTGATATTTTCTCT	1883
Db	1801	CACCTGTTTAGAACACACACACTTACTTTTTCTGTGCTCTACCACTGCTGATATTTTCTCT	1860
Qy	1884	AGGAAATATATCTTTTACAGTAAACAAAATAAAACTCTTATAAAATTTCTATTTTTTATCT	1943
Db	1861	AGGAAATATATCTTTTACAGTAAACAAAATAAAACTCTTATAAAATTTCTATTTTTTATCT	1920
Qy	1944	GAGTTTACAGAAATGATTACTTAAGGAAGTACTCAGTAAATTTGTTTAAAAAGTAATAAAA	2003
Db	1921	GAGTTTACAGAAATGATTACTTAAGGAAGTACTCAGTAAATTTGTTTAAAAAGTAATAAAA	1980
Qy	2004	TTCAACAAACATTTAAAAAAA 2025	
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RESULT 13

RESULTS IS  
US-09-907-613-200

US-09-907-613-200  
; Sequence 200, Application US/09907613  
; Publication No. US20030027145A1

Publication No: US20060106441A1

; GENERAL INFORMATION:  
: APPLICANT: Genentech Inc

APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.

Query Match	98.3%;	Score 1994;	DB 10;	Length 2372;
Best Local Similarity	99.8%;	Pred. No. 0;		

**Qy** 24 AGCAGGGAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 83  
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**Dp** 1 ACAGGGGAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATA 60

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; APPLICANT: Pilvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Thomas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same

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QY 84 GTTCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 143  
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QY 61 GTTCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120  
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QY 144 CATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTTCAGCCTG 203  
DB |||||  
QY 121 CATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTTCAGCCTG 180  
DB |||||  
QY 204 GTGTTGCTTCTCATTCCATCTTGACACGAGGCTCTGGTCAAGGCTCTTTGGGTGCA 263  
DB |||||  
QY 181 GTGTTGCTTCTCATTCCATCTGGACACGAGGCTCTGGTCAAGGCTCTTTGGGTGCA 240  
DB |||||  
QY 264 GAAAGACTTTCATCCAGGTGTCATSCAGAAATTATGGGGATCACCTCTGTGAGCAAAAG 323  
DB |||||  
QY 241 GAAAGACTTTCATCCAGGTGTCATGCGAAATTATGGGGATCACCTCTGTGAGCAAAAG 300  
DB |||||  
QY 324 GCGAACCGAGCTGAATTTTCAGAACTTAAGGAGGCTGTAGGCTGTGGGACTTAAGT 383  
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QY 361 TTGGCGGCAAGGACCAAGTTGAAACAGGCTTGAAGCTAGCTTTGAAACTTTCAGCTAT 420  
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QY 684 ACCTACTCGTGGGCACTCCCTTACTCTACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 743  
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QY 721 CCAGTTCCTACTCTTATCCAGGAGAAATAATTTGATTTGTGTACAGAAATTTTATG 780  
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QY 841 AATGAAGCTGTGGTGTGGAGGTGCCCCAGGCTCTGCTAGTCTGCTCTCTCTCTCTCT 900  
DB |||||  
QY 924 TTTGTGCTGAGCTGTGCTTGGATTTGCTATGTGCAAAAGTATGTGAAGCCTTCCCT 983  
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QY 901 TTTGTGCTGAGCTGTGCTTGGATTTGCTATGTGCAAAAGTATGTGAAGCCTTCCCT 960  
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QY 984 TTTCAAAACAAGATCAGCAGAGGAAATGATCGAAACCAAGTAGTAAAGAGGAGAG 1043  
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QY 961 TTTCAAAACAAGATCAGCAGAGGAAATGATCGAAACCAAGTAGTAAAGAGGAGAG 1020  
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QY 1021 GCCAATGATAGCAACCTTAATGAGGAATCAAGAAAACTGATAAAAAACCCAGAGAGTCC 1080  
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QY 1104 AAGAGTCCAGCAAACTTACCGTGGGATGCTGGAGCTGAAGTTAGATGAGACAGAAA 1163  
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QY 1081 AAGAGTCCAGCAAACTTACCGTGGGATGCTGGAGCTGAAGTTAGATGAGACAGAAA 1140  
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QY 1164 TGAGGAGACACACTGAGGCTGGTTTCTTTCATGCTTACCTTACCTGCCCGAGCTGGGAA 1223  
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DB 1141 TGAGGAGACACACTGAGGCTGGTTCTTTCATGCTCTTACCTGCCCGACGCTGGGAA 1200  
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QY 1284 TCAGGACTGCCATTGGACTATGAGGTGACCAAAAGAGATGCCCTTCTCTTATTGTAAAC 1343  
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QY 1261 TCAGGACTGCCATTGGACTATGAGGTGACCAAAAGAGATGCCCTTCTCTTATTGTAAAC 1320  
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QY 1344 CTTGTCTGATCCTATCCTCTTACCTCCAAAGCTTCCCGAGGCTTCTAGCCTGGCTAT 1403  
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QY 1321 CTTGTCTGATCCTATCCTCTTACCTCCAAAGCTTCCCGAGGCTTCTAGCCTGGCTAT 1380  
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QY 1404 GTCTTAATAATATCCACTGGGAGAAAGGAGTTTTCGCAAGTGCAAGGACCTTAAACATC 1463  
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QY 1381 GTCTTAATAATATCCACTGGGAGAAAGGAGTTTTCGCAAGTGCAAGGACCTTAAACATC 1440  
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QY 1464 TCATCAGTATCCAGTGGTAAAGGCTTCTGGCTGTCTGAGGCTAGTGGGTGAAAGC 1523  
DB |||||  
QY 1441 TCATCAGTATCCAGTGGTAAAGGCTTCTGGCTGTCTGAGGCTAGTGGGTGAAAGC 1500  
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QY 1681 TCTCTGAAAGCTAAATATAAGAAATAGAAAGGCTGAGGATTCCTATCTGAGACCTTAA 1740  
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QY 1824 CACTGTTAGAACACACACTTACTTTTCTGCTCTACACCTGCTGATATTTCTCT 1883  
DB |||||  
QY 1801 CACTGTTAGAACACACACTTACTTTTCTGCTCTACACCTGCTGATATTTCTCT 1860  
DB |||||  
QY 1884 AGGAATATCTTTTACAAAGTAAACAAATAAARACTCTTATAATTTCTATTTTATCT 1943  
DB |||||  
QY 1861 AGGAATATCTTTTACAAAGTAAACAAATAAARACTCTTATAATTTCTATTTTATCT 1920  
DB |||||  
QY 1944 GAGTTACAGAAATGATTACTAAGGAGATTAAGTAAATTTGTTTAAAAAGTAAATAAA 2003  
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DB |||||

## RESULT 14

US-09-907-942-200

; Sequence 200, Application US/09907942

; Publication No. US20030027146A1

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

```
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,942
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
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; PRIOR APPLICATION NUMBER: PCT/US99/23089
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; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-907-942-200

Query Match      98.3%; Score 1994; DB 10; Length 2372;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      24  AGCAGGAAATCCGATGCTCGGTTATGAAGTGAGCAGTCAGTGTGAGCCTCAACATA 83
Db      1  AGCAGGAAATCCGATGCTCGGTTATGAAGTGAGCAGTCAGTGTGAGCCTCAACATA 60
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Db      121 CATCTGAGGTGTTCCCTGGCTCTGAAGGGTAGGACGATGGCCAGGTGCTTACGCTTG 180
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QY      204 GTGTTGCTTCTCACTTCCATCTGGACACGAGGCTCTGGTCCMAGGCTCTTTGGCTGCA 263
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QY      264 GAAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGGATCACCCCTGTGAGCAAAAAG 323
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Db      241 GAAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGGATCACCCCTGTGAGCAAAAAG 300
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QY      324 GCGAACACGACGCTGAAATTTCAAGAGCTAAGAGGCTCTGAGGCTGTGGGACTAAAGT 383
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QY      384 TTGGCCGGCAAGGACCAAGTTGAAACAGCTTTGAAAGCTAGCTTTGAAACTTTGCAGCTAT 443
          |||||
Db      361 TTGGCCGGCAAGGACCAAGTTGAAACAGCTTTGAAAGCTAGCTTTGAAACTTTGCAGCTAT 420
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QY      444 GGTGGGTTGGAGATGGATTCGTGTCATCTCTAGGATTAGCCCAACCCCAAGTGGG 503
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Db      421 GGTGGGTTGGAGATGGATTCGTGTCATCTCTAGGATTAGCCCAACCCCAAGTGGG 480
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QY      504 AAAAATGGGTTGGGTCCTGATTTGGAAAGGTTCCAGTGAGCGGACAGTTTGGAGCCTAT 563
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Db      541 TGTTCACACTCATCTGATCTTGGACTAACTCGTGATTTCCAGAAATTTATTTGTCAGTGACAGT 600
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QY      624 GATCCCATATTCAACACTCAAACTGCACACACAAACACAGAAATTTATTTGTCAGTGACAGT 683
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QY      744 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTTGATTTGTTGTCACAGAAATTTTATG 803
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DB 1561 GCTCTGAAGAGAAACACGATATCCCACTGACATGCTCTCTGAGCCGGTGAAGACAA 1620
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DB 1801 CACTGTTTAGAACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT 1860
QY 1884 AGGAAATATACTTTACAGTAAACAAAAATAAAAACTCTTATAAATTTCTATTTTATCT 1943
DB 1861 AGGAAATATACTTTACAGTAAACAAAAATAAAAACTCTTATAAATTTCTATTTTATCT 1920
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DB 1981 TTCAACAAACATTTGCTGATA 2002
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## RESULT 15

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US-09-904-859-200
; Sequence 200, Application US/09904859
; Publication No. US20030036060A1
; GENERAL INFORMATION:
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; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter

Query Match 98.3%; Score 1994; DB 10; Length 2372;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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DB 1 AGCAGGGAATCCGGATGTCCTCGGTTATGAAGTGAGCAGTGTGAGCCTCAACATA 60
QY 84 GTTCCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCTCTCATATCACCAGTGGC 143
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; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,859
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
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; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 200
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-904-859-200
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 Db 241 GAAGAGCTTTCCATCCAGGTGTGATCGAGAAATATAGGGATCACCCCTTGTGAGCAAAAAG 300  
 Qy 324 GGAACACGACGTGAATTTACAGAGCTAAGAGGCTGTAGGCTGTGGGACTAAGT 383  
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 Qy 1884 AGGAATATATCTTTTACAGTAAACAAATAAAAACTCTTTATAAATTTCTATTTTATCT 1943  
 Db 1861 AGGAATATATCTTTTACAGTAAACAAATAAAAACTCTTTATAAATTTCTATTTTATCT 1920  
 Qy 1944 GAGTTACAGAAATGATTACTAAGGAGATTAAGTAAATTTGTTTAAAGTAATAAAA 2003  
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 Qy 2004 TTCAACAAACATTTAAAAAAA 2025  
 Db 1981 TTCAACAAACATTTGCTGAATA 2002

Search completed: September 15, 2004, 14:11:36  
 Job time : 973 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 15, 2004, 01:53:03 ; Search time 819 Seconds

(without alignments)

10524.535 Million cell updates/sec

Title: US-10-079-111-2

Perfect score: 2029

Sequence: 1 cctgacagtcagaagctt.....aacatttaaaaaaaaaa 2029

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq 29Jan04:\*

1: geneseqn1980s:\*

2: geneseqn1990s:\*

3: geneseqn2000s:\*

4: geneseqn2001as:\*

5: geneseqn2001bs:\*

6: geneseqn2002s:\*

7: geneseqn2003as:\*

8: geneseqn2003bs:\*

9: geneseqn2003cs:\*

10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2029	100.0	2029	3	AAZ98172	AAZ98172 Human sig
2	2029	100.0	2029	10	ADE71445	Ade71445 Human cDN
3	2027	99.9	2027	10	ADE71449	Ade71449 Human cDN
4	1994	98.3	2372	2	AAZ52250	AAZ52250 Protein P
5	1994	98.3	2372	3	ADC78520	Adc78520 Human PRO
6	1994	98.3	2372	4	AAZ72408	Aaf72408 Human PRO
7	1994	98.3	2372	4	AAZ92060	Aaf92060 Human PRO
8	1994	98.3	2372	6	ABZ74380	Abz74380 Human cDN
9	1994	98.3	2372	6	ABL88087	Abi88087 Human PRO
10	1994	98.3	2372	6	ABL95576	Abi95576 Human ang
11	1994	98.3	2372	7	ACA59060	ACA59060 Human PRO
12	1994	98.3	2372	7	ACA58457	ACA58457 cDNA enco
13	1994	98.3	2372	7	ACA60164	ACA60164 Human cDN
14	1994	98.3	2372	7	ACD07564	ACD07564 Novel hum
15	1994	98.3	2372	7	ACA91166	ACA91166 Novel hum
16	1994	98.3	2372	7	ACD81543	ACD81543 Human cDN
17	1994	98.3	2372	7	ACA60365	ACA60365 Novel hum
18	1994	98.3	2372	7	ABX71612	Abx71612 Human cDN
19	1994	98.3	2372	7	ACH06944	ACH06944 Human sec
20	1994	98.3	2372	7	ACA58812	ACA58812 cDNA enco
21	1994	98.3	2372	7	ACA63988	ACA63988 cDNA enco
22	1994	98.3	2372	7	ACA91252	ACA91252 cDNA enco
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27	1994	98.3	2372	7	ACD20169	ACD20169 Human sec
28	1994	98.3	2372	7	ACA67273	ACA67273 cDNA enco
29	1994	98.3	2372	7	ACH66246	ACH66246 Novel hum
30	1994	98.3	2372	7	ACD02300	ACD02300 Novel hum
31	1994	98.3	2372	7	ACA89291	ACA89291 Novel hum
32	1994	98.3	2372	7	ACA68928	ACA68928 Novel hum
33	1994	98.3	2372	7	ACA54972	ACA54972 Novel hum
34	1994	98.3	2372	7	ACA98450	ACA98450 Human PRO
35	1994	98.3	2372	8	ACA63375	ACA63375 cDNA enco
36	1994	98.3	2372	8	ACD19807	ACD19807 Human sec
37	1994	98.3	2372	8	ADB29405	ADB29405 Human cDN
38	1994	98.3	2372	8	ADB17062	ADB17062 Human cDN
39	1994	98.3	2372	8	ACH03578	ACH03578 Human sec
40	1994	98.3	2372	8	ADA18261	ADA18261 Human sec
41	1994	98.3	2372	8	ACD66954	ACD66954 Human cDN
42	1994	98.3	2372	8	ADA19867	ADA19867 Novel hum
43	1994	98.3	2372	8	ADB17250	ADB17250 Human cDN
44	1994	98.3	2372	8	ACD83115	ACD83115 Human PRO
45	1994	98.3	2372	8	ADA16236	ADA16236 Human sec

#### ALIGNMENTS

##### RESULT 1

AAZ98172

ID AAZ98172 standard; cDNA; 2029 BP.

XX AAZ98172;

AC AAZ98172;

XX AAZ98172;

DT 11-MAY-2000 (first entry)

DE Human signal peptide containing protein HSP-64 cDNA SEQ ID NO:198.

XX Human; signal peptide-containing protein; HSP; diagnosis; cancer;

KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;

KW antimicrobial; nontropic; neuroprotective; cardiovascular; hepatotropic;

KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;

KW reproductive disorder; developmental disorder; arteriosclerosis;

KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;

KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;

KW Parkinson's disease; Huntington's disease; muscular dystrophy; ss.

XX Homo sapiens.

OS Homo sapiens.

XX WO200000610-A2.

PN 06-JAN-2000. -

XX 25-JUN-1999; 99WO-US014484.

PF 26-JUN-1998; 98US-0090762P.

XX 31-JUL-1998; 98US-0094983P.

PR 01-OCT-1998; 98US-0102686P.

PR 11-DEC-1998; 98US-0112129P.

XX (INCY-) INCYTE PHARM INC.

PA Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;

XX Akerblom JE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;

PI Bandman O;

XX WPI; 2000-160673/14.

DR P-PSDB; AAY87287.

DR New human signal peptide-containing proteins useful in treatment,

XX prevention and diagnosis of e.g. cancer, inflammation and cardiovascular

PT disease.

PT

XX

PS Claim 9; Page 288-289; 327pp; English.

XX AAZ98109 to AAZ98242 encode AA87224 to AA87357 which represent the

CC human signal peptide-containing proteins HSPB-1 to HSPB-134. HSPBs have

CC anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic,

CC neuroprotective, cardiovascular and antiasthmatic activities, and can be

CC used in gene therapy. HSPBs can be used to treat or prevent disorders

CC associated with decreased activity or function of HSPB. Antagonists of

CC HSPB are used to treat or prevent disorders associated with increased

CC activity or function of HSPB. Such diseases include cell proliferation

CC (including cancer), inflammation, cardiovascular, neurological,

CC reproductive or developmental disorders, (e.g. arteriosclerosis,

CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,

CC asthma, Crohn's disease, microbial or other infections, congestive or

CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's

CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPB

CC nucleic acids can be used for the recombinant production of HSPB, for

CC detecting HSPB in standard hybridisation and amplification assays (for

CC diagnosis and monitoring), in gene therapy, as antisense, triplex-forming

CC or ribozyme therapeutics, for detecting related sequences or genetic

CC variations, and for chromosomal mapping. HSPB are also used to raise

CC specific antibodies (Ab) and to screen for agonists and antagonists

CC (potential therapeutic agents). Ab are used to diagnose, or monitor, HSPB

CC -related diseases (in usual immunoassays), as therapeutic antagonists, in

CC competitive drug screens, and for purification of HSPB from natural

CC sources

XX

SQ Sequence 2029 BP; 612 A; 463 C; 445 G; 509 T; 0 U; 0 Other;

Query Match 100.0%; Score 2029; DB 3; Length 2029;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2029; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGACAGTCAGAGCTTGAACGAGGAAATCCGATGCTCGGTTATGAAGTGGAG 60

DB 1 CCTTGACAAGTCAGAGCTTGAACGAGGAAATCCGATGCTCGGTTATGAAGTGGAG 60

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DB 61 CAGTGAGTCGAGCTCAACATAGTTCAGAACTCTCCATCCGACTAGTATTGAGCAT 120

QY 121 CTGCTCTCATATACAGTGGCCATCTGAGGTGTTCCCTGGCTCTGAAGGGTAGGCA 180

DB 121 CTGCTCTCATATACAGTGGCCATCTGAGGTGTTCCCTGGCTCTGAAGGGTAGGCA 180

QY 181 CGATGCCAGGTGCTTACGCTGCTGTTCTTCTCATCTCCATCTGGACCAAGGCTCC 240

DB 181 CGATGCCAGGTGCTTACGCTGCTGTTCTTCTCATCTCCATCTGGACCAAGGCTCC 240

QY 241 TGGTCCAAAGGCTCTTGGGTGCAGAAAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGG 300

DB 241 TGGTCCAAAGGCTCTTGGGTGCAGAAAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGG 300

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DB 301 GGATCACCTTGTGAGCAAAAAGGGCAACACAGAGCTGAATTCACAGAGCTTAAGGAGG 360

QY 361 CCTGTAGGCTGCTGGAGCTAAGTTTGGCGGCAAGCAAGTTCGAAACAGCTTGAAG 420

DB 361 CCTGTAGGCTGCTGGAGCTAAGTTTGGCGGCAAGCAAGTTCGAAACAGCTTGAAG 420

QY 421 CTAGCTTTGAAACTTTGCAGCTATGCTGGGTTGGAGATGCAATTCGTGTCATCTCTAGGA 480

DB 421 CTAGCTTTGAAACTTTGCAGCTATGCTGGGTTGGAGATGCAATTCGTGTCATCTCTAGGA 480

QY 481 TTAGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCTGATTTGGAAGGTTCCAG 540

DB 481 TTAGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCTGATTTGGAAGGTTCCAG 540

QY 541 TGAGCCGACAGTTTGAGGCTTATGTTACAACTCATCTGATCTGGACTTAAGTCTGTCGA 600

DB 541 TGAGCCGACAGTTTGAGGCTTATGTTACAACTCATCTGATCTGGACTTAAGTCTGTCGA 600

QY 601 TTCCAGAAATTATCACCACCAAGATGCCCATATTCACAACTCAAACTGCAACACAAACAA 660

DB 601 TTCCAGAAATTATCACCACCAAGATGCCCATATTCACAACTCAAACTGCAACACAAACAA 660

QY 661 CAGAATTATTCTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTTG 720

DB 661 CAGAATTATTCTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTTG 720

QY 721 CCCCTACTACTCTCTCGTCCAGCTTCCACTTCTATCCACGAGAAAAAATTGA 780

DB 721 CCCCTACTACTCTCTCGTCCAGCTTCCACTTCTATCCACGAGAAAAAATTGA 780

QY 781 TTGTGTACACAGATTTTATGGAACCTAGCACCATGCTACAGAACTGAACCAATTG 840

DB 781 TTGTGTACACAGATTTTATGGAACCTAGCACCATGCTACAGAACTGAACCAATTG 840

QY 841 TTGAAAAATAAGCAGCATTCAGAATGAAGCTGGTGGTGGAGGTGTCACACGGCTC 900

DB 841 TTGAAAAATAAGCAGCATTCAGAATGAAGCTGGTGGTGGAGGTGTCACACGGCTC 900

QY 901 TCGTAGTCTTCT 960

DB 901 TCGTAGTCTTCT 960

QY 961 AAAGGTATGTGAAGGCTTCCCTTTTACAAACAAGAACTCAGCAGAGGAAATGATCGAAA 1020

DB 961 AAAGGTATGTGAAGGCTTCCCTTTTACAAACAAGAACTCAGCAGAGGAAATGATCGAAA 1020

QY 1021 CCAAGTAGTAAAGGAGGAGGCAATGATAGCAACCTTAATGAGGAATCAAGAAAA 1080

DB 1021 CCAAGTAGTAAAGGAGGAGGCAATGATAGCAACCTTAATGAGGAATCAAGAAAA 1080

QY 1081 CTGATAAAACCCAGAGAGTCCAGAGTCCAAAGCTCAAGCAAACTACCGTCCGATCGTGAAG 1140

DB 1081 CTGATAAAACCCAGAGAGTCCAAAGCTCCAAAGCTCAAGCAAACTACCGTCCGATCGTGAAG 1140

QY 1141 CTGAGTTTAGATGAGACAGAAATCAGGAGACACACCTGAGGCTGGTCTTCTTCTCATGCTC 1200

DB 1141 CTGAGTTTAGATGAGACAGAAATCAGGAGACACACCTGAGGCTGGTCTTCTTCTCATGCTC 1200

QY 1201 CTTACCTTCCCTCCAGCTGGGAAATCAAAGGGCCAAAGAACCAAGAGAAAGTCCACC 1260

DB 1201 CTTACCTTCCCTCCAGCTGGGAAATCAAAGGGCCAAAGAACCAAGAGAAAGTCCACC 1260

QY 1261 CTTGGTCTCTAACTGGAATCAGTCCAGGCTCCGATTCGACTTGGAGTGCACCAAGAG 1320

DB 1261 CTTGGTCTCTAACTGGAATCAGTCCAGGCTCCGATTCGACTTGGAGTGCACCAAGAG 1320

QY 1321 AATGCCCTTCTCTTATTGTAACCTGCTGGATCCTATCTCTCTACCTCCAAAGCTTCC 1380

DB 1321 AATGCCCTTCTCTTATTGTAACCTGCTGGATCCTATCTCTCTACCTCCAAAGCTTCC 1380

QY 1381 CACGCCCTTTCTAGCCTGGCTATGCTCTTAATAATATCCACCTGGGAGAAAGGAGTTTGC 1440

DB 1381 CACGCCCTTTCTAGCCTGGCTATGCTCTTAATAATATCCACCTGGGAGAAAGGAGTTTGC 1440

QY 1441 AAGTGCAGGAGCTTAAACATCTCATCAGTATCCAGTGGTAAAGGGCTCTCTGGCTGT 1500

DB 1441 AAGTGCAGGAGCTTAAACATCTCATCAGTATCCAGTGGTAAAGGGCTCTCTGGCTGT 1500

QY 1501 CTGAGCTAGGTGGGTTGAAAGCCCAAGAGTCACTGAGACCAAGGCTTCTCTACTGATT 1560

DB 1501 CTGAGCTAGGTGGGTTGAAAGCCCAAGAGTCACTGAGACCAAGGCTTCTCTACTGATT 1560

QY 1561 CGCAGCTCAGACCTTTCTTCTAGCTCTGAAGAGAAACAGATATCCCACTGACATGTC 1620

DB 1561 CGCAGCTCAGACCTTTCTTCTAGCTCTGAAGAGAAACAGATATCCCACTGACATGTC 1620

QY 1621 CTTCTGAGCCGGTAAAGAGCAAAAAGATGGCAGAAAGTTTAGCCCCCTGAAAGCCATGA 1680

DB 1621 CTTCTGAGCCGGTAAAGAGCAAAAAGATGGCAGAAAGTTTAGCCCCCTGAAAGCCATGA 1680

QY 1681 GATTCCTATAAGTTGAGAGCTTAATCTCTGTAAGAGCTAAAAATAAGAAATAGAACAGGCT 1740



Db 1681 GATTCTCACTAGACCTAATCTCTGAAGCTAAATAGAAATAGACAGGCT 1740  
QY 1741 GAGGATACAGACAGTACACTGTGACAGGACTGTAAACACAGACAGGGTCAAGTGT 1800  
Db 1741 GAGGATACAGACAGTACACTGTGACAGGACTGTAAACACAGACAGGGTCAAGTGT 1800  
QY 1801 CTCTGAACACATTGAGTGGATCACTGTTAGAACACACACTTACTTTCTGGTCT 1860  
Db 1801 CTCTGAACACATTGAGTGGATCACTGTTAGAACACACACTTACTTTCTGGTCT 1860  
QY 1861 CTACCACTGCTGATATTTTCTCTAGGAATATATCTTTTACAAAGTAAACAAAATAA 1920  
Db 1861 CTACCACTGCTGATATTTTCTCTAGGAATATATCTTTTACAAAGTAAACAAAATAA 1920  
QY 1921 CTTATAAATTTCTATTTTATCTGAGTACAGAAATGATTAAGGAAGATTA 1980  
Db 1921 CTTATAAATTTCTATTTTATCTGAGTACAGAAATGATTAAGGAAGATTA 1980  
QY 1981 AATTTGTTTAAAGTAAATAAATTCACAAACATTTAAATAAATAA 2029  
Db 1981 AATTTGTTTAAAGTAAATAAATTCACAAACATTTAAATAAATAA 2029

RESULT 2

AD71445  
ID ADE71445 standard; cDNA; 2029 BP.

XX ADE71445;

XX 29-JAN-2004 (first entry)

DE Human cDNA encoding PDEBC Incyte 3044710CB1.

XX breast cancer; PDEBC; metastatic; human; ss; gene.

OS Homo sapiens.

XX Key Location/Qualifiers

FT 183..1151

FT /\*tag= a

FT /product= "PDEBC"

XX US2003124543-A1.

XX 03-JUL-2003.

XX 20-FEB-2002; 2002US-00079111.

XX 15-JAN-1999; 99US-00232160.

XX (STUA/) STUART S G.

XX (STRE/) STREETER D G.

XX Stuart SG, Streeter DG;

XX MPI; 2004-009141/01.

XX P-PSDB; ADE71444.

XX A new cDNA encoding a protein differentially expressed in breast cancer designated PCBC is useful to stage, treat, and monitor progression or treatment of breast cancer, particularly an invasive, metastatic stage of the disease.  
PS Claim 2; SEQ ID NO 2; 31pp; English.  
XX The invention relates to an isolated cDNA encoding a protein that is differentially expressed in breast cancer, designated PDEBC. The invention is useful to diagnose breast cancer. The invention is also useful to stage, treat, and monitor progression or treatment of breast cancer, particularly an invasive, metastatic stage of the disease. The present sequence represents cDNA encoding human PDEBC Incyte 3044710CB1. Note: There are two sequences that have been assigned SEQ ID 2 in the

CC specification, the present sequence represents the sequence given in the CC sequence listing.

XX

SQ Sequence 2029 BP; 612 A; 463 C; 445 G; 509 T; 0 U; 0 Other;

Query Match 100.0%; Score 2029; DB 10; Length 2029;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2029; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGACAGTTCAGAAAGCTTGAAGCAGGAAATCCGATGTCTCGGTTATCAAGTGGAG 60

Db 1 CTTGACAGTTCAGAAAGCTTGAAGCAGGAAATCCGATGTCTCGGTTATCAAGTGGAG 60

QY 61 CAGTGAAGTGTGAGCCTCAACATAGTTCAGAACTCTCCATCCGGACTAGTATTAGCAT 120

Db 61 CAGTGAAGTGTGAGCCTCAACATAGTTCAGAACTCTCCATCCGGACTAGTATTAGCAT 120

QY 121 CTGCTCTCATATACCAAGTGGCCATCTGAGTGTTCCCTGGCTCTGAAGGGTAGGCA 180

Db 121 CTGCTCTCATATACCAAGTGGCCATCTGAGTGTTCCCTGGCTCTGAAGGGTAGGCA 180

QY 181 CGATGCCAGGTGCTTCAGCCTGTGTCTTCTCATTCCATCTGGACACGAGGCTCC 240

Db 181 CGATGCCAGGTGCTTCAGCCTGTGTCTTCTCATTCCATCTGGACACGAGGCTCC 240

QY 241 TGGTCAAGGCTCTTTGGTGCAGAAAGAGCTTCCATCCAGGTGTATGCAATATATGG 300

Db 241 TGGTCAAGGCTCTTTGGTGCAGAAAGAGCTTCCATCCAGGTGTATGCAATATATGG 300

QY 301 GGATCACCTTGTGAGCAAAAGCGCAACAGCAGCTGAATTTTCAGAAAGCTAAGGAGG 360

Db 301 GGATCACCTTGTGAGCAAAAGCGCAACAGCAGCTGAATTTTCAGAAAGCTAAGGAGG 360

QY 361 CCTGTAGGCTGCTGGGACTTAAGTTTGGCGGCAAGGACCAAGTTGAAACAGCCTTGAAG 420

Db 361 CCTGTAGGCTGCTGGGACTTAAGTTTGGCGGCAAGGACCAAGTTGAAACAGCCTTGAAG 420

QY 421 CTAGCTTTGAAACTTTCAGCTATGCTGGTGGAGATGGATTCGTGTCATCTCTAGGA 480

Db 421 CTAGCTTTGAAACTTTCAGCTATGCTGGTGGAGATGGATTCGTGTCATCTCTAGGA 480

QY 481 TTAGCCCAAAACCCCAAGTGTGGGAAATGGGTTGGGTTGGAGGTTCCAG 540

Db 481 TTAGCCCAAAACCCCAAGTGTGGGAAATGGGTTGGGTTGGAGGTTCCAG 540

QY 541 TGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTTGGACTAATCGTGCA 600

Db 541 TGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTTGGACTAATCGTGCA 600

QY 601 TTCAGAAATTTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAA 660

Db 601 TTCAGAAATTTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCAACACAA 660

QY 661 CAGAAATTTATGTCAGTCACAGTACTACTCGGTGGCATCCCTTACTCTCAATACCTG 720

Db 661 CAGAAATTTATGTCAGTCACAGTACTACTCGGTGGCATCCCTTACTCTCAATACCTG 720

QY 721 CCCCTACTACT 780

Db 721 CCCCTACTACT 780

QY 781 TTTGTGTACAGAAAGTTTTATGAAACTAGACACATGTCTACAGAACTGAACTGAT 840

Db 781 TTTGTGTACAGAAAGTTTTATGAAACTAGACACATGTCTACAGAACTGAACTGAT 840

QY 841 TTGAAATTAAGCAGCATTTCAAGATGAAGTGTGGTGGGTTGGAGGTTGCCACGGCTC 900

Db 841 TTGAAATTAAGCAGCATTTCAAGATGAAGTGTGGTGGGTTGGAGGTTGCCACGGCTC 900

QY 901 TGCTAGTCTTGTCT 960

Db 901 TGCTAGTCTTGTCT 960

QY 961 AAAGTATGTGAAGGCTTCCCTTTTACAAACAAGATCAGCAGAGGAATGATCGAAA 1020  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
961 AAAGTATGTGAAGGCTTCCCTTTTACAAACAAGATCAGCAGAGGAATGATCGAAA 1020  
QY 1021 CCAAAGTAGTAAAGGAGGAGGCGCAATGATAGCAACCTAATGAGGAATCAAGAAAA 1080  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1021 CCAAAGTAGTAAAGGAGGAGGCGCAATGATAGCAACCTAATGAGGAATCAAGAAAA 1080  
QY 1081 CTGATAAAACCAGAGAGTCAAGAGTCCAGAGCAAACTACCGTGCATCGCTGGAAG 1140  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1081 CTGATAAAACCAGAGAGTCCAGAGTCCAGAGCAAACTACCGTGCATCGCTGGAAG 1140  
QY 1141 CTGAAGTTTAGATGACAGAGAATGAGGAGACACCTGAGGTGGTTCTTTCATGCTC 1200  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1141 CTGAAGTTTAGATGACAGAGAATGAGGAGACACCTGAGGTGGTTCTTTCATGCTC 1200  
QY 1201 CTTACCTCCCGCAGCTGGGGAATCAAAAGGCGCCAAAGAACCAAGAGAAAGTCCACC 1260  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1201 CTTACCTCCCGCAGCTGGGGAATCAAAAGGCGCCAAAGAACCAAGAGAAAGTCCACC 1260  
QY 1261 CTTGGTTCTTAAGTCAAGTCAAGGCTGAGGCTGAGGATGAGGATGAGGATGAGGATGAGG 1320  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1261 CTTGGTTCTTAAGTCAAGTCAAGGCTGAGGCTGAGGATGAGGATGAGGATGAGGATGAGG 1320  
QY 1321 AATGCCCTTCTCTTATTTGTAACCTCTGCTGATCCTATCCTCTTACCTCCAAAGCTCC 1380  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1321 AATGCCCTTCTCTTATTTGTAACCTCTGCTGATCCTATCCTCTTACCTCCAAAGCTCC 1380  
QY 1381 CACGGCTCTTCTAGCTGCTGCTATGCTTAATATATCCCACTGGGAGAAAGGATTTGTC 1440  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1381 CACGGCTCTTCTAGCTGCTGCTATGCTTAATATATCCCACTGGGAGAAAGGATTTGTC 1440  
QY 1441 AAAGTGCAAGGACTAAACATCTCATAGTATCCAGTGGTAAAGGCGCTCTGCTGT 1500  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1441 AAAGTGCAAGGACTAAACATCTCATAGTATCCAGTGGTAAAGGCGCTCTGCTGT 1500  
QY 1501 CTGAGCTAGTGGTGGTGAAGCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGAT 1560  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1501 CTGAGCTAGTGGTGGTGAAGCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGAT 1560  
QY 1561 CCGAGCTCAGACCCCTTCTTCTAGCTCTGAAAGAGAAACACGATATCCCACTGACATGTC 1620  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1561 CCGAGCTCAGACCCCTTCTTCTAGCTCTGAAAGAGAAACACGATATCCCACTGACATGTC 1620  
QY 1621 CTTCTGAGCCGGTAGACCAAAAGATGCGAGAAAGTTTAGCCCTGAAAGCCATGGA 1680  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1621 CTTCTGAGCCGGTAGACCAAAAGATGCGAGAAAGTTTAGCCCTGAAAGCCATGGA 1680  
QY 1681 GATTTCTAATCTGAGACCTAATCTCTGTAAGCTAAATAAAGAAATAGAACAGGCT 1740  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1681 GATTTCTAATCTGAGACCTAATCTCTGTAAGCTAAATAAAGAAATAGAACAGGCT 1740  
QY 1741 GAGGATACGACAGTACACTGTGAGCAGGACTGTAAACACAGACAGGGTCAAAGTGT 1800  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1741 GAGGATACGACAGTACACTGTGAGCAGGACTGTAAACACAGACAGGGTCAAAGTGT 1800  
QY 1801 CTTGACACATGAGTGGATCACTGTTAGACACACACACTTACTTTTTCTGGTCT 1860  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1801 CTTGACACATGAGTGGATCACTGTTAGACACACACACTTACTTTTTCTGGTCT 1860  
QY 1861 CTACCACTGCTGATATTTCTCTAGGAAATATATCTTTTACCAAGTAAACAAATATAAACT 1920  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1861 CTACCACTGCTGATATTTCTCTAGGAAATATATCTTTTACCAAGTAAACAAATATAAACT 1920  
QY 1921 CTTATAAATTTCTATTTTATCTGAGTTACAGAAATGATTAAGGAAAGATTACTCAGT 1980  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1921 CTTATAAATTTCTATTTTATCTGAGTTACAGAAATGATTAAGGAAAGATTACTCAGT 1980  
QY 1981 AATTGTTTAAAAGTAATAAATTTCAACAACATTTTAAAAAATAAAAA 2029  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1981 AATTGTTTAAAAGTAATAAATTTCAACAACATTTTAAAAAATAAAAA 2029

RESULT 3  
ADE71449  
ID ADE71449 standard; cDNA; 2027 BP.  
XX  
AC ADE71449;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human cDNA encoding PDEBC #2.  
XX  
KW breast cancer; PDEBC; metastatic; human; ss; gene.  
XX  
OS Homo sapiens.  
XX  
PN US200324543-A1.  
XX  
PD 03-JUL-2003.  
XX  
PF 20-FEB-2002; 2002US-00079111.  
XX  
PR 15-JAN-1999; 99US-00232160.  
XX  
PA (STUA/) STUART S G.  
PA (STRE/) STREETER D G.  
XX  
PI Stuart SG, Streeter DG;  
XX  
DR WPI; 2004-009141/01.  
DR P-PSDB; ADE71444.  
XX  
PT A new cDNA encoding a protein differentially expressed in breast cancer designated PCBC is useful to stage, treat, and monitor progression or treatment of breast cancer, particularly an invasive, metastatic stage of the disease.  
XX  
PS Claim 2; Fig 1; 3lpp; English.  
XX  
CC The invention relates to an isolated cDNA encoding a protein that is differentially expressed in breast cancer, designated PDEBC. The invention is useful to diagnose breast cancer. The invention is also useful to stage, treat, and monitor progression or treatment of breast cancer, particularly an invasive, metastatic stage of the disease. The present sequence represents cDNA encoding human PDEBC Incyte 3044710CB1.  
CC Note: There are two sequences that have been assigned SEQ ID 2 in the specification, the present sequence represents the sequence given in figure 1.  
XX  
SQ Sequence 2027 BP; 612 A; 461 C; 445 G; 509 T; 0 U; 0 Other;  
  
Query Match 99.9%; Score 2027; DB 10; Length 2027;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 TTGCAAGTCAGAAGCTTGAAAGCAGGAGAAATCCGGATGCTCGGTTATGAAGTGAGCA 62  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1 TTGCAAGTCAGAAGCTTGAAAGCAGGAGAAATCCGGATGCTCGGTTATGAAGTGAGCA 60  
QY 63 GTGAGTGTGAGCCTCAACATAGTTCAGAACTCTCCATCCGACATGATTATTGAGCATCT 122  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
61 GTGAGTGTGAGCCTCAACATAGTTCAGAACTCTCCATCCGACATGATTATTGAGCATCT 120  
QY 123 GCCTCTCATATCAGCAGTGGCCATCTGAGGTGTTTCCCTGGCTCGAAGGGTAGGCAG 182  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
121 GCCTCTCATATCAGCAGTGGCCATCTGAGGTGTTTCCCTGGCTCGAAGGGTAGGCAG 180  
QY 183 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCCAGGGTCTCTG 242  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
181 ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACCCAGGGTCTCTG 240  
QY 243 GTCCAAAGGCTCTTTGGTGCAGAAAGCTTTCCATCCAGGTGTCTCATGCAATATTGGGG 302  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
241 GTCCAAAGGCTCTTTGGTGCAGAAAGCTTTCCATCCAGGTGTCTCATGCAATATTGGGG 300

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QY 303 ATCACCCCTTGAGCAAAAAGCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGAGGCC 362
Db 301 ATCACCCCTTGAGCAAAAAGCGAACCCAGCAGCTGAATTTACAGAAAGCTAAGAGGCC 360
QY 363 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAGGACCAAGTTGAAACAGCCCTTGAAGCT 422
Db 361 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAGGACCAAGTTGAAACAGCCCTTGAAGCT 420
QY 423 AGCTTTGAAACTTGAGCACTATGGCTGGGTTGGAGATGGAATCGTGCTCATCTCTAGGATT 482
Db 421 AGCTTTGAAACTTGAGCACTATGGCTGGGTTGGAGATGGAATCGTGCTCATCTCTAGGATT 480
QY 483 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCTGATTTGGAAGCTTCCAGTG 542
Db 481 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCTGATTTGGAAGCTTCCAGTG 540
QY 543 AGCCGACAGTTTGCAGCCCTATTGTTTACAACTCATCTGATACCTTGGACTAACTCGTGCATT 602
Db 541 AGCCGACAGTTTGCAGCCCTATTGTTTACAACTCATCTGATACCTTGGACTAACTCGTGCATT 600
QY 603 CCAGAAATATCACCAACCAAGATCCATATTAACACTCAAACTGAACTGAAACAAACA 662
Db 601 CCAGAAATATCACCAACCAAGATCCATATTAACACTCAAACTGAACTGAAACAAACA 660
QY 663 GAATTTATTGTGAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAAATACCTGCC 722
Db 661 GAATTTATTGTGAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAAATACCTGCC 720
QY 723 CCTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 782
Db 721 CCTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
QY 783 TGTGTACAGAAAGTTTATGGAACCTAGCAGCATGTCTACAGAACTGAACCATTTGTT 842
Db 781 TGTGTACAGAAAGTTTATGGAACCTAGCAGCATGTCTACAGAACTGAACCATTTGTT 840
QY 843 GAAATAAAGCAGCAATCAAGAATCAAGCTGCTGGTTTGGAGGTGCCCCAGCCTCTG 902
Db 841 GAAATAAAGCAGCAATCAAGATGAGCTGCTGGTTTGGAGGTGCCCCAGCCTCTG 900
QY 903 CTAGTGCTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 962
Db 901 CTAGTGCTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
QY 963 AGTATGTGAAGGCTTCCCTTTTACAAACAGAAATCAGCAGAGAAATGATCGAAACC 1022
Db 961 AGTATGTGAAGGCTTCCCTTTTACAAACAGAAATCAGCAGAGAAATGATCGAAACC 1020
QY 1023 AAAAGTAGTAAAGGAGGAGGCAATGATAGCAACCTTAATGAGGAATCAAGAAAGCT 1082
Db 1021 AAAAGTAGTAAAGGAGGAGGCAATGATAGCAACCTTAATGAGGAATCAAGAAAGCT 1080
QY 1083 GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAACTACCGTCGATGCTGGAAGCT 1142
Db 1081 GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAACTACCGTCGATGCTGGAAGCT 1140
QY 1143 GAAAGTTAGATGAGACAAATAGGAGACACACCTGAGGCTGGTTCTTCTCATGCTCTCT 1202
Db 1141 GAAAGTTAGATGAGACAAATAGGAGACACACCTGAGGCTGGTTCTTCTCATGCTCTCT 1200
QY 1203 TACCTGCCCCAGCTGGGGAATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCT 1262
Db 1201 TACCTGCCCCAGCTGGGGAATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCT 1260
QY 1263 TGGTTCTTAATCGGAACTCAGGCTCAGGACTGCGCAATTTGGACTATGGAGTGCACCAAGAGAA 1322
Db 1261 TGGTTCTTAATCGGAACTCAGGCTCAGGACTGCGCAATTTGGACTATGGAGTGCACCAAGAGAA 1320
QY 1323 TGCCCTTCTCTCTATTGTAACCTGTCTGGATCTCTATCTCTCTCTCTCTCTCTCTCTCTCT 1382
Db 1321 TGCCCTTCTCTCTATTGTAACCTGTCTGGATCTCTATCTCTCTCTCTCTCTCTCTCTCTCT 1380
QY 1383 CGGCCCTTTCTAGCTGGCTATGTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTCGAA 1442
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Db 1381 CGGCCCTTTCTAGCTGGCTATGTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTCGAA 1440
QY 1443 AGTCAAGGACCTAAAAACATCTCATCTCAGTATCCAGTGGTAAAAAGGCCCTCTCTGGCTGTCT 1502
Db 1441 AGTCAAGGACCTAAAAACATCTCATCTCAGTATCCAGTGGTAAAAAGGCCCTCTCTGGCTGTCT 1500
QY 1503 GAGGCTAGGTTGGTTGAAAGCCAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCC 1562
Db 1501 GAGGCTAGGTTGGTTGAAAGCCAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCC 1560
QY 1563 GCAGCTCAGACCCCTTTCTTTCAGCTCTGAAAGAGAAAACAGTATCCACCTGACATGTCTCT 1622
Db 1561 GCAGCTCAGACCCCTTTCTTTCAGCTCTGAAAGAGAAAACAGTATCCACCTGACATGTCTCT 1620
QY 1623 TCTGAGCCCGTAAAGAGCAAAAGAAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGA 1682
Db 1621 TCTGAGCCCGTAAAGAGCAAAAGAAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGA 1680
QY 1683 TTCTCATTAACCTTGAGACCTTAATCTCTGTAAGCTTAAATAAAGAAATAGAACAGGCTGA 1742
Db 1681 TTCTCATTAACCTTGAGACCTTAATCTCTGTAAGCTTAAATAAAGAAATAGAACAGGCTGA 1740
QY 1743 GGATACGACAGCTACACTGTCAGCAGGGACTCTGTAACACAGACAGGTCCTCAAGTGTCTCT 1802
Db 1741 GGATACGACAGCTACACTGTCAGCAGGGACTCTGTAACACAGACAGGTCCTCAAGTGTCTCT 1800
QY 1803 CTGAACACATTTGAGTTGGAATCACTGTTTAGAACACACACACTTTACTTTTCTGCTCTCT 1862
Db 1801 CTGAACACATTTGAGTTGGAATCACTGTTTAGAACACACACACTTTACTTTTCTGCTCTCT 1860
QY 1863 ACCACTGCTGATATTTCTCTAGGAAATATATTCTTACAGTAACAAAAATAAAACTCT 1922
Db 1861 ACCACTGCTGATATTTCTCTAGGAAATATATTCTTACAGTAACAAAAATAAAACTCT 1920
QY 1923 TATAAATTTCTATTTTATCTGAGTTACAGAAATGATTACTTAAGAAAGATTACTCAGTAA 1982
Db 1921 TATAAATTTCTATTTTATCTGAGTTACAGAAATGATTACTTAAGAAAGATTACTCAGTAA 1980
QY 1983 TTTGTTTAAAAAGTAATAAAATTCAACAAACATTTTAAAAAATAAAAAA 2029
Db 1981 TTTGTTTAAAAAGTAATAAAATTCAACAAACATTTTAAAAAATAAAAAA 2027

RESULT 4
AAAX52250
ID AAAX52250 standard; DNA; 2372 BP.
XX
AC AAAX52250;
XX
DT 25-JUN-1999 (first entry)
XX
DE Protein PRO263 cDNA clone DNA34431-1171.
XX
KW Secreted protein; transmembrane protein; human; enterocolitis;
KW Zollinger-Ellison syndrome; gastrointestinal ulceration;
KW congenital microvillus atrophy; skin disease; cell growth;
KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin;
KW dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic;
KW wound healing; tissue repair; ss.
XX
OS Homo sapiens.
XX
PN WO9914328-A2.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98MO-US019330.
XX
PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
```



QY 924 TTTTGTGCTGCAGTGGTCTTGGATTTTCTATGTCAAAGGTATGCTGAAGCCCTTCCCT 983  
Db 901 TTTTGTGCTGCAGTGGTCTTGGATTTTCTATGTCAAAGGTATGCTGAAGCCCTTCCCT 960

QY 984 TTTTACAAACAAGATCAGCAGAGGAAATGATCGAAACCAAAAGTAGTAAAGGAGAGAG 1043  
Db 961 TTTTACAAACAAGATCAGCAGAGGAAATGATCGAAACCAAAAGTAGTAAAGGAGAGAG 1020

QY 1044 GCCATGATAGCAACCCCTAATGAGGAAATCAAGAAAACTGATAAAACCCAGAGAGTCC 1103  
Db 1021 GCCAATGATAGCAACCCCTAATGAGGAAATCAAGAAAACTGATAAAACCCAGAGAGTCC 1080

QY 1104 AAGAGTCCAAAGCAAACTACCGTGCATGCGTGGAGCTGAAGTTTAGATGAGACAGAAA 1163  
Db 1081 AAGAGTCCAAAGCAAACTACCGTGCATGCGTGGAGCTGAAGTTTAGATGAGACAGAAA 1140

QY 1164 TGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGTCTTACCTGCCGCCAGCTGGGAA 1223  
Db 1141 TGAGGAGACACACCTGAGGCTGGTTTCTTTTCATGTCTTACCTGCCGCCAGCTGGGAA 1200

QY 1224 ATCAAAGGGCCAAAGAACCAAGAAAGTCCACCTTTGGTTCTTAACCTGGAATCAGC 1283  
Db 1201 ATCAAAGGGCCAAAGAACCAAGAAAGTCCACCTTTGGTTCTTAACCTGGAATCAGC 1260

QY 1284 TCAGGACTGCCATTCGACTATGAGTGCACCAAGAGATGCCCTTCTCCTTATTGTAAC 1343  
Db 1261 TCAGGACTGCCATTCGACTATGAGTGCACCAAGAGATGCCCTTCTCCTTATTGTAAC 1320

QY 1344 CCTGTCTGATCCTATCCTCTACCTCCAAAGCTTCCCAAGCTTCTTAGGCTGGCTAT 1403  
Db 1321 CCTGTCTGATCCTATCCTCTACCTCCAAAGCTTCCCAAGCTTCTTAGGCTGGCTAT 1380

QY 1404 GTCCCTAATAATATCCACTGGAGAAAGAGTTTGGCAAAGTGCAAGGACCTTAAACATC 1463  
Db 1381 GTCCCTAATAATATCCACTGGAGAAAGAGTTTGGCAAAGTGCAAGGACCTTAAACATC 1440

QY 1464 TCATCAGTATCCAGTGGTAAAGAGCCCTCCGCTGCTGAGGCTAGGTGGGTGAAGC 1523  
Db 1441 TCATCAGTATCCAGTGGTAAAGAGCCCTCCGCTGCTGAGGCTAGGTGGGTGAAGC 1500

QY 1524 CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGGCAGCTCAGACCCCTTTCTCA 1583  
Db 1501 CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGGCAGCTCAGACCCCTTTCTCA 1560

QY 1584 GCTCTGAAGAGAAACAGTATCCACCTGACATGCTCTTCTGAGCCCGGTGAAGAGAAA 1643  
Db 1561 GCTCTGAAGAGAAACAGTATCCACCTGACATGCTCTTCTGAGCCCGGTGAAGAGAAA 1620

QY 1644 AGAATGGCAGAAAGTTTAGCCCTGAAAGCCATGGAGATTCCTATACTTGAGACCTAA 1703  
Db 1621 AGAATGGCAGAAAGTTTAGCCCTGAAAGCCATGGAGATTCCTATACTTGAGACCTAA 1680

QY 1704 TCTCTGTAAGCTAAATTAAGAAATAGAACCAAGGCTGAGGATACGACAGTACACTGTCA 1763  
Db 1681 TCTCTGTAAGCTAAATTAAGAAATAGAACCAAGGCTGAGGATACGACAGTACACTGTCA 1740

QY 1764 GCAGGACTGTAAACACAGACAGGCTCAAGTGTCTTCTGAAACATGAGTTGGAAT 1823  
Db 1741 GCAGGACTGTAAACACAGACAGGCTCAAGTGTCTTCTGAAACATGAGTTGGAAT 1800

QY 1824 CACTGTTTGAACACACACACTTACTTTTCTGCTCTCTACACCTGCTGATATTTCTCT 1883  
Db 1801 CACTGTTTGAACACACACACTTACTTTTCTGCTCTCTACACCTGCTGATATTTCTCT 1860

QY 1884 AGGAAATATCTTTTACAAGTAACAAAATAAAAACTCTTATAAATTTCTATTTTATCT 1943  
Db 1861 AGGAAATATCTTTTACAAGTAACAAAATAAAAACTCTTATAAATTTCTATTTTATCT 1920

QY 1944 GAGTTACAGAAATGATTTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 2003  
Db 1921 GAGTTACAGAAATGATTTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAA 1980

QY 2004 TTCAACAACATTAAAAAAA 2025  
Db 1981 TTCAACAACATTGCTGAATA 2002

RESULT 5  
ADC78520  
ID ADC78520 standard; cDNA; 2372 BP.  
XX  
AC ADC78520;  
XX  
DT 01-JAN-2004 (first entry)  
XX  
DE Human PRO263 cDNA.  
XX  
KW antiinflammatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian;  
KW neurotropic; neuroprotective; vasotrophic; chemotactic; angiogenic;  
KW neurotrophic; osteopathic; antiasthmatic; antiarthritic; antirheumatic;  
KW antiarteriosclerotic; cardiant; antidiabetic; cerebroprotective;  
KW thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome;  
KW gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease;  
KW Alzheimer's; ALS; neuropathy; bone; cartilage formation; wound healing;  
KW nerve repair; thrombosis; bone; cartilage formation; angiogenesis;  
KW asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder;  
KW atherosclerosis; cardiac injury; infertility; premature aging; AIDS;  
KW diabetes; stroke; gene therapy; transgenic; PRO; human; ss; gene.  
XX Homo sapiens.  
XX WO200015796-A2.  
XX  
XX 23-MAR-2000.  
XX  
PF 15-SEP-1999; 99WO-US021090.  
XX  
PR 16-SEP-1998; 98WO-US019330.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
PI Chen J, Goddard A, Gurney AL, Hillan K, Pennica D, Wood WI;  
PI Yuan J;  
XX  
XX WPI: 2000-271434/23.  
DR P-PSDB; ADC78521.  
XX  
PT Novel nucleic acids encoding secreted and transmembrane polypeptides with  
PT homology, e.g. to growth and cancer-associated antigens.  
XX  
PS Claim 2; SEQ ID NO 200; 355pp; English.  
XX  
CC The invention relates to a novel nucleic acid encoding a PRO polypeptide.  
CC The polypeptides and polymucleotides of the invention may be useful as  
CC research tools and as therapeutics for treating enterocolitis, Zollinger-  
CC Ellison syndrome, gastrointestinal ulceration, psoriasis, cancer, dermal  
CC Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal  
CC scarring and wound healing, nerve repair, thrombosis, bone and/or  
CC cartilage formation, angiogenesis, asthma, rheumatoid arthritis, multiple  
CC sclerosis, inflammatory disorders, atherosclerosis, cardiac injury,  
CC infertility, premature aging, AIDS, diabetes complications and stroke.  
CC The molecules may also be utilised during gene therapy procedures and  
CC transgenic animal production. The current sequence is that of the human  
CC PRO cDNA of the invention.  
XX  
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Query Match 98.3%; Score 1994; DB 3; Length 2372;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 24 AGCAGGGAATCCCGATGTCCTCGGTATGAAGTGGAGCAGTGAGTGGAGCTCAACATA 83  
Db 1 AGCAGGGAATCCCGATGTCCTCGGTATGAAGTGGAGCAGTGAGTGGAGCTCAACATA 60



antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes;  
ophthalmological; gene therapy; skin disease; gastrointestinal disorder;  
ischaemia; inflammation; ss.

KW	Homo sapiens.	QY	144	CATCTGAGGTGTTCCCTGGCTCTGAAAGGGTAGGCACGATGGCAGGTGCTTTCAGCCTG	203
KW	WO200104311-A1.	DB	121	CATCTGAGGTGTTCCCTGGCTCTGAAAGGGTAGGCACGATGGCAGGTGCTTTCAGCCTG	180
XX	18-JAN-2001.	QY	204	GTGTTGCTTCTCACCTTCATCTGGACACGAGGCTCCCTGGTCCAGGCTCTTTGGTGCA	263
XX	22-FEB-2000; 2000WO-US004414.	DB	181	GTGTTGCTTCTCACCTTCATCTGGACACGAGGCTCCCTGGTCCAGGCTCTTTGGTGCA	240
XX	07-JUL-1999; 99US-0143048P.	QY	264	GAAAGAGCTTTCCATCCAGGTGTCTGAGCAAAATTATGGGGATCACCTTTGTGAGCAAAAAG	323
XX	26-JUL-1999; 99US-0145698P.	DB	241	GAAAGAGCTTTCCATCCAGGTGTCTGAGCAAAATTATGGGGATCACCTTTGTGAGCAAAAAG	300
PR	28-JUL-1999; 99US-0146222P.	QY	324	GCGAACGAGCTGAATTTACAGAGCTAAGAGGCTGTAGGCTGTGGAGCTAAGT	383
PR	08-SEP-1999; 99WO-US020594.	DB	301	GCGAACGAGCTGAATTTACAGAGCTAAGAGGCTGTAGGCTGTGGAGCTAAGT	360
PR	13-SEP-1999; 99WO-US020944.	QY	384	TTGGCCGGCAAGGCAAGTTGAAACAGCTTTGAAAGCTAGCTTTGAAACCTTGCAGCTAT	443
PR	15-SEP-1999; 99WO-US021090.	DB	361	TTGGCCGGCAAGGCAAGTTGAAACAGCTTTGAAAGCTAGCTTTGAAACCTTGCAGCTAT	420
PR	15-SEP-1999; 99WO-US021547.	QY	444	GGCTGGGTTGGAGATGGATTCGTGCTCATCTCTAGGATTAGCCCAAAACCCCAAGTGTGGG	503
PR	05-OCT-1999; 99WO-US023089.	DB	421	GGCTGGGTTGGAGATGGATTCGTGCTCATCTCTAGGATTAGCCCAAAACCCCAAGTGTGGG	480
PR	29-NOV-1999; 99WO-US028214.	QY	504	AAAAATGGGGTGGGTGCTCTGATTTGGAAAGTTCCAGTGAGCCGACAGTTTGCAGCCTAT	563
PR	30-NOV-1999; 99WO-US028313.	DB	481	AAAAATGGGGTGGGTGCTCTGATTTGGAAAGTTCCAGTGAGCCGACAGTTTGCAGCCTAT	540
PR	02-DEC-1999; 99WO-US028564.	QY	564	TGTTACAACTCATCTGATCTTGGACTTAACTCGTGCATTTCAGAAATATATACCAACCAA	623
PR	02-DEC-1999; 99WO-US028565.	DB	541	TGTTACAACTCATCTGATCTTGGACTTAACTCGTGCATTTCAGAAATATATACCAACCAA	600
PR	16-DEC-1999; 99WO-US030095.	QY	624	GATCCCATATTCAACACTGCAACCTGCAACACAAACACAGAAATTTATTTGTCAGTGACAGT	683
PR	20-DEC-1999; 99WO-US030911.	DB	601	GATCCCATATTCAACACTGCAACCTGCAACACAAACACAGAAATTTATTTGTCAGTGACAGT	660
PR	20-DEC-1999; 99WO-US030999.	QY	684	ACCTACTCGGTGGCATCCCTTACTCTCAATACCTGCCCTCTACTACTCTCTCTCTCTCT	743
PR	05-JAN-2000; 2000WO-US000219.	DB	661	ACCTACTCGGTGGCATCCCTTACTCTCAATACCTGCCCTCTACTACTCTCTCTCTCTCT	720
XX	(GETH ) GENENTECH INC.	QY	744	CCAGCTCCACTCTCTATTCACGGAGAAATAATGTTGTCACAGAGTGTGTTTATG	803
XX	AShenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;	DB	721	CCAGCTCCACTCTCTATTCACGGAGAAATAATGTTGTCACAGAGTGTGTTTATG	780
XX	Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;	QY	804	GAAACTAGCACCATGTCTACAGAACTGAACCATTTGTTGAAAATAAAGACGATTCAG	863
XX	Godowski PI, Grimaldi CJ, Gurney AL, Hillan KJ, Kijavini LJ;	DB	781	GAAACTAGCACCATGTCTACAGAACTGAACCATTTGTTGAAAATAAAGACGATTCAG	840
XX	Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;	QY	864	AATGAGCTGCTGGGTTTGGAGGTGTCACAGGCTCTGCTAGTGTGCTCTCTCTCTCTCT	923
XX	Williams PM, Wood WI;	DB	841	AATGAGCTGCTGGGTTTGGAGGTGTCACAGGCTCTGCTAGTGTGCTCTCTCTCTCTCT	900
XX	WPI; 2001-081051/09.	QY	924	TTTGTGCTGAGCTGGTCTTTGGATTTTGTATGTCAAAAGTATGTGAAGGCTTCCTCT	983
XX	P-PSDB; AAB80247.	DB	901	TTTGTGCTGAGCTGGTCTTTGGATTTTGTATGTCAAAAGTATGTGAAGGCTTCCTCT	960
XX	Sixty one nucleic acids encoding PRO polypeptides which are useful in the	QY	984	TTTCAAAACAAGAATCAGCAGAGGAATAATGATCGAAACCAAAAGTAGTAAAGGAGAGAG	1043
XX	treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous	DB	961	TTTCAAAACAAGAATCAGCAGAGGAATAATGATCGAAACCAAAAGTAGTAAAGGAGAGAG	1020
XX	cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's	QY	1044	GCCATGATAGCAACCTTATGAGGAATCAAGAAACTGATATAAAACCCAGAGAGTCC	1103
XX	disease).	DB	1021	GCCATGATAGCAACCTTATGAGGAATCAAGAAACTGATATAAAACCCAGAGAGTCC	1080
XX	Claim 2; Fig 73; 393pp; English.	QY	1104	AAGAGTCCAGCAAACTTACCGTGCATGCTCGTGAAGCTGAAGTTTAGATCAGACAGAA	1163
XX	The present sequence is one of sixty one nucleic acids encoding novel	DB	1081	AAGAGTCCAGCAAACTTACCGTGCATGCTCGTGAAGCTGAAGTTTAGATCAGACAGAA	1140
XX	secreted and transmembrane PRO polypeptides. The PRO polypeptides are	QY	1164	TGAGGAGACACCTGAGGCTGGTTCCTTTCATGCTCTTACCTGCCCCAGCTGGGAA	1223
XX	useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung	DB	1141	TGAGGAGACACCTGAGGCTGGTTCCTTTCATGCTCTTACCTGCCCCAGCTGGGAA	1200
XX	squamous cell carcinoma), gastrointestinal disorders (e.g.				
XX	enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,				
XX	Parkinson's disease), wound repair, cardiovascular disorders (e.g.				
XX	cardiac disease), inflammatory disorders (e.g. asthma, rheumatoid				
XX	arthritis, multiple sclerosis), infertility, AIDS and diabetes and				
XX	renal disorders such as retinitis pigmentosa. The PRO nucleic acids				
XX	have applications in molecular biology, including use as hybridization				
XX	probes, and in chromosome and gene mapping				
XX	Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;				
XX	Query Match				
XX	Best Local Similarity 98.3%; Score 1994; DB 4; Length 2372;				
XX	Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;				
QY	24 AGCAGGAAATCCGATGCTCGGTTATGAAAGTGAGCAGTGAGTGTGAGCTCAACATA				83
DB	1 AGCAGGAAATCCGATGCTCGGTTATGAAAGTGAGCAGTGAGTGTGAGCTCAACATA				60
QY	84 GTTCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCTCTCATATCACCAGTGGC				143
DB	61 GTTCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCTCTCATATCACCAGTGGC				120



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QY 1224 ATCAAGGGCCAAAGAACCAAGAGAAAGTCCACCTTGCTGGTCTTCTAATCGAATCAGC 1283
DB 1201 ATCAAGGGCCAAAGAACCAAGAGAAAGTCCACCTTGCTGGTCTTCTAATCGAATCAGC 1260
QY 1284 TCAGAGCTGCCATTGGACTATCGAGTGCACCAAGAGATGCCCTTCTCTTATTGTAAAC 1343
DB 1261 TCAGAGCTGCCATTGGACTATCGAGTGCACCAAGAGATGCCCTTCTCTTATTGTAAAC 1320
QY 1344 CTTGTCTGATCCTATTCCTTACCTCCAAAGCTTCCACGCGCTTTCTAGCCTGGCTAT 1403
DB 1321 CTTGTCTGATCCTATTCCTTACCTCCAAAGCTTCCACGCGCTTTCTAGCCTGGCTAT 1380
QY 1404 GTCTAAATAATCCACTGGCAGAGAAAGGAGTTTGCAGAGTCAAGGACCTTAAACATC 1463
DB 1381 GTCTAAATAATCCACTGGCAGAGAAAGGAGTTTGCAGAGTCAAGGACCTTAAACATC 1440
QY 1464 TCATCAGTATCCAGTGGTAAAGGCTTCTGGCTGTCTGAGGCTAGGTGGTGAAGC 1523
DB 1441 TCATCAGTATCCAGTGGTAAAGGCTTCTGGCTGTCTGAGGCTAGGTGGTGAAGC 1500
QY 1524 CAAGAGTCACTGAGACCAAGCTTCTACTGATTCGGAGCTCAGACCTTCTTCA 1583
DB 1501 CAAGAGTCACTGAGACCAAGCTTCTACTGATTCGGAGCTCAGACCTTCTTCA 1560
QY 1584 GCTCTGAAAGAGAAACAGTATCCACCTGACATGCTTCTGAGCCGGTGAAGCAAA 1643
DB 1561 GCTCTGAAAGAGAAACAGTATCCACCTGACATGCTTCTGAGCCGGTGAAGCAAA 1620
QY 1644 AGAATGGCAAGAAAGTTTAGCCCTGAAAGCCATGGAGATTTCTAATCTGAGACCTAA 1703
DB 1621 AGAATGGCAAGAAAGTTTAGCCCTGAAAGCCATGGAGATTTCTAATCTGAGACCTAA 1680
QY 1704 TCTCTGTAAGCTAAATAAGAAATAGAACTAGAAAGCTGAGGATACGACAGTACTGTCA 1763
DB 1681 TCTCTGTAAGCTAAATAAGAAATAGAACTAGAAAGCTGAGGATACGACAGTACTGTCA 1740
QY 1764 CGAGGACTGTAAACACACAGAGGTCAAAGTGTCTCTGAAACACATTTGAGTTGGAAT 1823
DB 1741 CGAGGACTGTAAACACACAGAGGTCAAAGTGTCTCTGAAACACATTTGAGTTGGAAT 1800
QY 1824 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTTACCACTGCTGATATTTCTCT 1883
DB 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTTACCACTGCTGATATTTCTCT 1860
QY 1884 AGGAATATATCTTTTACAGTACAAATAAATAAATCTTATAATTTCTATTTATCT 1943
DB 1861 AGGAATATATCTTTTACAGTACAAATAAATAAATCTTATAATTTCTATTTATCT 1920
QY 1944 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAAATAAA 2003
DB 1921 GAGTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAAATAAA 1980
QY 2004 TTCAACAAACATTTAAAAAAA 2025
DB 1981 TTCAACAAACATTTGCTGAATA 2002
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## RESULT 7

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AAF92060
ID AAF92060 standard; cDNA; 2372 BP.
XX
AC AAF92060;
XX
DT 15-MAY-2001 (first entry)
XX
DE Human PRO263 cDNA.
XX
KW Human; PRO protein; mapping; ss.
XX
OS Homo sapiens.
XX
FN WO200116318-A2.
XX
```

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PD 08-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-US023328.
XX
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 07-DEC-1999; 99US-0169495P.
PR 09-DEC-1999; 99US-0170262P.
PR 11-JAN-2000; 2000US-0175481P.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 03-MAR-2000; 2000US-0187202P.
PR 21-MAR-2000; 2000US-0191007P.
PR 30-MAR-2000; 2000WO-US008439.
PR 25-APR-2000; 2000US-0199397P.
PR 22-MAY-2000; 2000WO-US014042.
PR 05-JUN-2000; 2000US-0209832P.
XX
(GETH ) GENENTECH INC.
PA
XX Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CU, Gurney AL, Watanabe CK, Wood WI;
XX WPI: 2001-183260/18.
DR P-PSDB; AAB87528.
XX
PT Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
PT biology, including use as hybridization probes, and in chromosome and
PT gene mapping.
XX
PS Claim 2; Fig 5; 278pp; English.
XX
CC The present sequence is the coding sequence for a human PRO polypeptide
CC (secreted and transmembrane). The PRO protein, and PRO agonists, PRO
CC antagonists or anti-PRO antibodies are useful for preparation of a
CC medicament useful in the treatment of a condition which is responsive to
CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO
CC protein may also be employed as molecular weight markers for protein
CC electrophoresis. The PRO coding sequence has applications in molecular
CC biology, including use as hybridisation probes, and in chromosome and
CC gene mapping
XX
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;
Query Match 98.3%; Score 1994; DB 4; Length 2372;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 24 AGCAGGGAATCCGGATGCTCGGTATGAAAGTGGAGCAGTGTGAGCCTCAACATA 83
DB 1 AGCAGGGAATCCGGATGCTCGGTATGAAAGTGGAGCAGTGTGAGCCTCAACATA 60
QY 84 GTTCCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGC 143
DB 61 GTTCCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGC 120
QY 144 CATCTGAGTGTTCCTGGCTCTGAAAGGGTAGGCACGATGGCAGGTCCTTCAAGCTG 203
DB 121 CATCTGAGTGTTCCTGGCTCTGAAAGGGTAGGCACGATGGCAGGTCCTTCAAGCTG 180
QY 204 GTGTTGCTTCTCAGTTCCTGACCTGGACCTGGTCCAGGCTCTTTGGTGCA 263
DB 181 GTGTTGCTTCTCAGTTCCTGACCTGGACCTGGTCCAGGCTCTTTGGTGCA 240
QY 264 GAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGATCACCTTGTGAGCAAAAAG 323
DB 241 GAAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGATCACCTTGTGAGCAAAAAG 300
QY 324 GCGAACCAGCAGCTGAATTTACAGAACTAAGAGGCTGTAGGCTGTGGGACTTAAGT 383
DB 301 GCGAACCAGCAGCTGAATTTACAGAACTAAGAGGCTGTAGGCTGTGGGACTTAAGT 360
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Qy	384	TTGGCCGCGCAAGGACCAAGTTGAAACACAGCCTTGAAAGCTAGCTTTGAAACTTGACGCTAT	443
Db	361	TTGGCCGCGCAAGGACCAAGTTGAAACACAGCCTTGAAAGCTAGCTTTGAAACTTGACGCTAT	420
Qy	444	GGCTGGGTTGGAGATGATTCGTGGTTCATCTCTAGGATTAGCCCAACACCCCAAGTGTGGG	503
Db	421	GGCTGGGTTGGAGATGATTCGTGGTTCATCTCTAGGATTAGCCCAACACCCCAAGTGTGGG	480
Qy	504	AAAAATGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGAGAGCCTAT	563
Db	481	AAAAATGGGTGGGTGTCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGAGAGCCTAT	540
Qy	564	TGTTACAACTCATCTGATATCTTGGAAGTAACTCGTGCAATCCAGNAATATCACCAACAAA	623
Db	541	TGTTACAACTCATCTGATATCTTGGAAGTAACTCGTGCAATCCAGNAATATCACCAACAAA	600
Qy	624	GATCCCATATTTCAACACTCAAACGTCACAAACAAACAGAAATTTATTTGTCAGTGACAGT	683
Db	601	GATCCCATATTTCAACACTCAAACGTCACAAACAAACAGAAATTTATTTGTCAGTGACAGT	660
Qy	684	ACCTACTCGGTGGGATCCCTTACTCTACAAATCCTGCGCCCTACTACTCTCTCTGCT	743
Db	661	ACCTACTCGGTGGGATCCCTTACTCTACAAATCCTGCGCCCTACTACTCTCTCTGCT	720
Qy	744	CCAGCTTCCACTTCTATTTCACGAGAGAAAAAATTTGATTTGTGTACAGAAATTTTATG	803
Db	721	CCAGCTTCCACTTCTATTTCACGAGAGAAAAAATTTGATTTGTGTACAGAAATTTTATG	780
Qy	804	GAACCTAGCACCATGTCTACAGAAACTGAAACCAATTTGTTGAAATAAAGCAGCAATTCAG	863
Db	781	GAACCTAGCACCATGTCTACAGAAACTGAAACCAATTTGTTGAAATAAAGCAGCAATTCAG	840
Qy	864	AATCGAGCTGCTGGTTTGGAGGTGCCACCGCTCTGCTAGTGTCTCTCTCTCTTC	923
Db	841	AATCGAGCTGCTGGTTTGGAGGTGCCACCGCTCTGCTAGTGTCTCTCTCTCTTC	900
Qy	924	TTTGGTGTCTGAGCTGTCTTTGGATTTTGCTATGTCAAAAGGTATGTGAAAGGCTTCCTCT	983
Db	901	TTTGGTGTCTGAGCTGTCTTTGGATTTTGCTATGTCAAAAGGTATGTGAAAGGCTTCCTCT	960
Qy	984	TTTACAAACAGAAATCAGCAGAGAGAAATGATCGAAACCAAGTAGTAAAGGAGGAGAAG	1043
Db	961	TTTACAAACAGAAATCAGCAGAGAGAAATGATCGAAACCAAGTAGTAAAGGAGGAGAAG	1020
Qy	1044	GCCAAATGATAGCAACCCCTAATGAGGAATCAAGAAAGAACTGATMAAAACCCAGAAAGTCC	1103
Db	1021	GCCAAATGATAGCAACCCCTAATGAGGAATCAAGAAAGAACTGATMAAAACCCAGAAAGTCC	1080
Qy	1104	AAGAGTCCAGCAAAAATACCGTGCATGCTCGGAAGTGAAGTTTAGATGAGACAGAAA	1163
Db	1081	AAGAGTCCAGCAAAAATACCGTGCATGCTCGGAAGTGAAGTTTAGATGAGACAGAAA	1140
Qy	1164	TGAGGAGACACACTGAGGCTGGTTCTTTTCATCTCTTACCTGCTGCCAGAGTGGGGAA	1223
Db	1141	TGAGGAGACACACTGAGGCTGGTTCTTTTCATCTCTTACCTGCTGCCAGAGTGGGGAA	1200
Qy	1224	ATCAAAAGGGCCAAAGAACCAAGAAAGTCCACCTCTTGTTCTCTAACTGGAATCAGC	1283
Db	1201	ATCAAAAGGGCCAAAGAACCAAGAAAGTCCACCTCTTGTTCTCTAACTGGAATCAGC	1260
Qy	1284	TCAGGAGCTGCATTGGAGTATGGAGTGCACCAAGAGAAATGCCCTTCTCTTATTGTAAC	1343
Db	1261	TCAGGAGCTGCATTGGAGTATGGAGTGCACCAAGAGAAATGCCCTTCTCTTATTGTAAC	1320
Qy	1344	CCTGTCTGGATCTCTATCCTCCTACTCCAAAGCTTCCACGGCCTTTCTAGCCTGGCTAT	1403
Db	1321	CCTGTCTGGATCTCTATCCTCCTACTCCAAAGCTTCCACGGCCTTTCTAGCCTGGCTAT	1380
Qy	1404	GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTGCAAGTGCAGAGCTATAAAATCATC	1463
Db	1381	GTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTGCAAGTGCAGAGCTATAAAATCATC	1440

Qy	1464	TCATCAGTATCCAGTGTGTAAAGGCCCTCTCGCTGTCTGAGGCTAGGTGGTTGAAAGC	1523
Db	1441	TCATCAGTATCCAGTGTGTAAAGGCCCTCTCGCTGTCTGAGGCTAGGTGGTTGAAAGC	1500
Qy	1524	CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGCAGCTCAGACCCCTTCTTCA	1583
Db	1501	CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGCAGCTCAGACCCCTTCTTCA	1560
Qy	1584	GCTCTGAAAGAGAAAAACAGTATCCCACTGACATGTCTCTCTGAGCCCGGTAAAGAGCAAA	1643
Db	1561	GCTCTGAAAGAGAAAAACAGTATCCCACTGACATGTCTCTCTGAGCCCGGTAAAGAGCAAA	1620
Qy	1644	AGAAATGCGCAGAAAGTTTAGCCCTGTAAGCCATGAGAGATTCCTCATAACTTGAGACCTAA	1703
Db	1621	AGAAATGCGCAGAAAGTTTAGCCCTGTAAGCCATGAGAGATTCCTCATAACTTGAGACCTAA	1680
Qy	1704	TCTCTGTAAGAGCTAAAAATAAGAAATAAGAACAGGCTGAGGATACGACAGTACCTGCA	1763
Db	1681	TCTCTGTAAGAGCTAAAAATAAGAAATAAGAACAGGCTGAGGATACGACAGTACCTGCA	1740
Qy	1764	GCAGGAGCTGTAAACACAGACAGGCTCAAGTGTCTCTGAAACACATTTGAGTTGGAAT	1823
Db	1741	GCAGGAGCTGTAAACACAGACAGGCTCAAGTGTCTCTGAAACACATTTGAGTTGGAAT	1800
Qy	1824	CACCTGTTTAGAACACACACACTTTACTTTTTCTGGTCTCTACCACTGCTGATATTTCTCT	1883
Db	1801	CACCTGTTTAGAACACACACACTTTACTTTTTCTGGTCTCTACCACTGCTGATATTTCTCT	1860
Qy	1884	AGGAAATATATCTTTTACAAGTAACAAAAATAAAAACTCTTATAAAATTTCTATTTTATCT	1943
Db	1861	AGGAAATATATCTTTTACAAGTAACAAAAATAAAAACTCTTATAAAATTTCTATTTTATCT	1920
Qy	1944	GAGTTTACAGAAATGATTACTTAAGGAAGATTACTCAGTAAATTTGTTTAAAAAGTAATAAAA	2003
Db	1921	GAGTTTACAGAAATGATTACTTAAGGAAGATTACTCAGTAAATTTGTTTAAAAAGTAATAAAA	1980
Qy	2004	TTCAACAAACATTTTAAAAAAA 2025	
Db	1981	TTCAACAAACATTTTGAATA 2002	
RESULT 8			
ABS74380			
ID	ABS74380	standard; cDNA; 2372 BP.	
XX	AC	ABS74380;	
XX	AC		
DT	10-DEC-2002	(first entry)	
XX	XX		
DE	Human	cDNA encoding secreted/transmembrane protein PRO263.	
XX	XX		
KW	Human; ss; gene; secreted protein; transmembrane protein; antirheumatic;		
KW	antiarthritic; osteopathic; sports-related joint problem;		
KW	articular cartilage defect; osteoarthritis; rheumatoid arthritis.		
XX	XX		
OS	Homo sapiens.		
XX	XX		
FN	US2002119130-A1.		
XX	XX		
PD	29-AUG-2002.		
XX	XX		
PF	06-DEC-2001; 2001US-00006867.		
XX	XX		
PR	29-OCT-1997;	97US-0063435P.	
PR	29-OCT-1997;	97US-0064215P.	
PR	22-APR-1998;	98US-0082797P.	
PR	29-APR-1998;	98US-0083495P.	
PR	15-MAY-1998;	98US-0085579P.	
PR	02-JUN-1998;	98US-0087759P.	
PR	04-JUN-1998;	98US-0088021P.	
PR	04-JUN-1998;	98US-0088029P.	
PR	04-JUN-1998;	98US-0088030P.	
PR	10-JUN-1998;	98US-0088734P.	

PR 10-JUN-1998; 98US-0088740P.  
 PR 10-JUN-1998; 98US-0088811P.  
 PR 10-JUN-1998; 98US-0088824P.  
 PR 10-JUN-1998; 98US-0088825P.  
 PR 11-JUN-1998; 98US-0088863P.  
 PR 12-JUN-1998; 98US-0089105P.  
 PR 16-JUN-1998; 98US-0089514P.  
 PR 17-JUN-1998; 98US-0089533P.  
 PR 19-JUN-1998; 98US-0089552P.  
 PR 22-JUN-1998; 98US-0090246P.  
 PR 24-JUN-1998; 98US-0090444P.  
 PR 25-JUN-1998; 98US-0090688P.  
 PR 25-JUN-1998; 98US-0090696P.  
 PR 26-JUN-1998; 98US-0090862P.  
 PR 02-JUL-1998; 98US-0091628P.  
 PR 10-AUG-1998; 98US-0096012P.  
 PR 17-AUG-1998; 98US-0096757P.  
 PR 18-AUG-1998; 98US-0096949P.  
 PR 18-AUG-1998; 98US-0096959P.  
 PR 26-AUG-1998; 98US-0097954P.  
 PR 26-AUG-1998; 98US-0097971P.  
 PR 26-AUG-1998; 98US-0097979P.  
 PR 01-SEP-1998; 98US-0098749P.  
 PR 10-SEP-1998; 98US-0099741P.  
 PR 10-SEP-1998; 98US-0099763P.  
 PR 10-SEP-1998; 98US-0099792P.  
 PR 10-SEP-1998; 98US-0099812P.  
 PR 16-SEP-1998; 98US-0099815P.  
 PR 16-SEP-1998; 98US-0100627P.  
 PR 16-SEP-1998; 98US-0100662P.  
 PR 17-SEP-1998; 98US-0100930P.  
 PR 17-SEP-1998; 98US-0101279P.  
 PR 23-SEP-1998; 98US-0101475P.  
 PR 24-SEP-1998; 98US-0101738P.  
 PR 24-SEP-1998; 98US-0101743P.  
 PR 30-SEP-1998; 98US-0102570P.  
 PR 06-OCT-1998; 98US-0103449P.  
 PR 08-MAR-1999; 99WO-US010731.  
 PR 14-JUN-1999; 99WO-US012252.  
 PR 01-SEP-1999; 99WO-US020111.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 15-SEP-1999; 99WO-US021194.  
 PR 22-DEC-1999; 2000WO-US030720.  
 PR 18-FEB-2000; 2000WO-US004341.  
 PR 18-FEB-2000; 2000WO-US004342.  
 PR 22-FEB-2000; 2000WO-US004414.  
 PR 01-MAR-2000; 2000WO-US005601.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 10-NOV-2000; 2000WO-US030873.  
 PR 01-DEC-2000; 2000WO-US032378.  
 PR 28-DEC-2000; 2000WO-US034956.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-MAR-2001; 2001WO-US006666.  
 PR 30-MAY-2001; 2001WO-US017443.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 20-JUN-2001; 2001WO-US019692.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 XX (GETH ) GENENTECH INC.  
 XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;  
 XX

DR WPI; 2002-731348/79.  
 DR P-PSDB; ABG95853.  
 XX  
 PT New isolated secreted and transmembrane PRO polypeptide useful for  
 PT modulating biological activity of a cell, or for treating sports-related  
 PT joint problems, osteoarthritis or rheumatoid arthritis.  
 XX  
 PS Claim 2; Fig 5; 399pp; English.  
 XX  
 CC The invention relates to an isolated secreted and transmembrane PRO  
 CC polypeptide having 80 % sequence identity to a sequence appearing as  
 CC ABG95851-ABG95934 or their associated signal peptide, or a sequence of an  
 CC extracellular domain of the proteins with their associated signal peptide  
 CC or lacking its associated signal peptide. Also included are the nucleic  
 CC acids encoding the proteins, vectors, host cells, fusion proteins and  
 CC antibodies which specifically bind to the proteins. The proteins are  
 CC useful for detecting a polypeptide designated as A, B, C or D in a sample  
 CC suspected of containing an A, B, C or D polypeptide, by contacting the  
 CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)  
 CC and determining the formation of a A/E, B/F, C/H or D/I polypeptide  
 CC conjugate in the sample, where the formation of the conjugate is  
 CC indicative of the presence of an A, B, C or D polypeptide in the sample,  
 CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a  
 CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801  
 CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a  
 CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises  
 CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,  
 CC H or I polypeptide is labeled with a detectable label or is attached to a  
 CC solid support. The proteins are useful for linking a bioactive molecule  
 CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,  
 CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.  
 CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,  
 CC or I, or antibodies against them are useful for modulating a biological  
 CC activity of a cell expressing a polypeptide designated as A, B, C or D or  
 CC E, F, G, H, or I. The cell is killed. The proteins are useful for  
 CC identifying agonists or antagonists, for the preparation of a medicament  
 CC useful in the treatment of a condition which is responsive to the  
 CC proteins, as molecular weight markers for protein electrophoresis  
 CC purposes, and as therapeutic agents for treating sports-related joint  
 CC problems, articular cartilage defects, osteoarthritis or rheumatoid  
 CC arthritis. Nucleic acids encoding the proteins are useful as  
 CC hybridisation probes, in chromosome and gene mapping, in the generation  
 CC of anti-sense RNA and DNA, for the preparation of the proteins, to  
 CC generate transgenic or knockout animals which are useful in the  
 CC development and screening of therapeutic useful reagents, for chromosome  
 CC identification, and in gene therapy. The antibody is useful as a  
 CC therapeutic agent, in a diagnostic assay and for affinity purification of  
 CC the protein from recombinant cell culture natural sources. The present  
 CC sequence encodes a novel secreted or transmembrane protein of the  
 CC invention  
 XX  
 SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;  
 Query Match 98.3%; Score 1994; DB 6; Length 2372;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 24 AGCAGGAAATCCGGATGTCCTCGGTTATGAGTGAGCAGTGAGTGTGAGCCTCAACATA 83  
 Db 1 AGCAGGAAATCCGGATGTCCTCGGTTATGAGTGAGCAGTGAGTGTGAGCCTCAACATA 60  
 QY 84 GTTCCAGAACTCTCCATCCGACCTAGTTATTGAGCATCTGCTCTCATATCACCAGTGGC 143  
 Db 61 GTTCCAGAACTCTCCATCCGACCTAGTTATTGAGCATCTGCTCTCATATCACCAGTGGC 120  
 QY 144 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGTTTCAGCCTG 203  
 Db 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGTTTCAGCCTG 180  
 QY 204 GTGTTGCTTCTCACTTCCATCTGGACACGAGGCTCTCTGGTCCCAAGGCTCTTTGGGTGCA 263  
 Db 181 GTGTTGCTTCTCACTTCCATCTGGACACGAGGCTCTCTGGTCCCAAGGCTCTTTGGGTGCA 240



PF 20-JUN-2001; 2001WO-US019692.  
XX  
PR 23-JUN-2000; 2000US-0213637P.  
PR 20-JUL-2000; 2000US-0219556P.  
PR 25-JUL-2000; 2000US-0220624P.  
PR 25-JUL-2000; 2000US-0220664P.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 02-AUG-2000; 2000US-0226959P.  
PR 17-AUG-2000; 2000US-00643657.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 07-SEP-2000; 2000US-0230978P.  
PR 18-SEP-2000; 2000US-00664610.  
PR 18-SEP-2000; 2000US-00655350.  
PR 24-OCT-2000; 2000US-0242922P.  
PR 08-NOV-2000; 2000US-00709238.  
PR 10-NOV-2000; 2000WO-US030952.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 22-JAN-2001; 2001US-00767609.  
PR 28-FEB-2001; 2001US-00796498.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 09-MAR-2001; 2001US-00802706.  
PR 14-MAR-2001; 2001US-00808689.  
PR 22-MAR-2001; 2001US-00816744.  
PR 05-APR-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 25-MAY-2001; 2001US-00866028.  
PR 25-MAY-2001; 2001US-00866034.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 30-MAY-2001; 2001US-00870574.  
PR 30-MAY-2001; 2001WO-US017443.  
PR 01-JUN-2001; 2001WO-US017800.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NP;  
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
XX  
DR WPI: 2002-090516/12.  
DR P-PSDB; ABB84832.  
XX  
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
PT infarction), endothelial or angiogenic disorders in a mammal.  
XX  
PS Claim 2; Fig 31; 565pp; English.  
XX  
CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,  
CC antiangiogenic, hypotensive, vulnerable, and antiarteriosclerotic  
CC activities, and can be used in gene therapy. The PRO polynucleotides,  
CC proteins, agonists and antagonists are useful for treating or diagnosing  
CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.  
CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,  
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
CC healing. The PRO polynucleotides have applications in molecular biology,  
CC including use as hybridisation probes, and in chromosome and gene  
CC mapping. ABL88259 to ABL88267 represent primers and probes used in the  
CC exemplification of the present invention  
XX  
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Query Match 98.3%; Score 1994; DB 6; Length 2372;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 24 AGCAGGAAATCCGATGTCGTTATGAAGTGAGCAGTGAGTGTGAGCCTCAACATA 83  
DB 1 AGCAGGAAATCCGATGTCGTTATGAAGTGAGCAGTGAGTGTGAGCCTCAACATA 60  
QY 84 GTTCCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCAACAGTGC 143  
DB 61 GTTCCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCAACAGTGC 120  
QY 144 CATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTCCTTCAGCCTG 203  
DB 121 CATCTGAGGTGTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTCCTTCAGCCTG 180  
QY 204 GTGTTGCTTCTCACTTCCATCTGGACACGAGCTCTGGTCCAGGCTCTTTGGGTGCA 263  
DB 181 GTGTTGCTTCTCACTTCCATCTGGACACGAGCTCTGGTCCAGGCTCTTTGGGTGCA 240  
QY 264 GAAGAGCTTTCCATCCAGGTGTCAGCAAAATTATGGGATCACCCCTCTGAGCAAAAAG 323  
DB 241 GAAGAGCTTTCCATCCAGGTGTCAGCAAAATTATGGGATCACCCCTCTGAGCAAAAAG 300  
QY 324 GCGAACAGCAGCTGAATTTACAGAACTAAGGAGGCTGTAGGCTGTGGGACTTAAGT 383  
DB 301 GCGAACAGCAGCTGAATTTACAGAACTAAGGAGGCTGTAGGCTGTGGGACTTAAGT 360  
QY 384 TTGGCCGGCAAGCAAGTTGAAACAGCTTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 443  
DB 361 TTGGCCGGCAAGCAAGTTGAAACAGCTTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 420  
QY 444 GGCTGGGTTGGAGATGGATTCTGTGTCATCTCTAGGATTAGCCCAAAACCCCAAGTGGG 503  
DB 421 GGCTGGGTTGGAGATGGATTCTGTGTCATCTCTAGGATTAGCCCAAAACCCCAAGTGGG 480  
QY 504 AAAAAATGGGGTGGGTGTCCTGATTTTGAAGGTTCCAGTGAGCCGACAGTTTGAGGCTAT 563  
DB 481 AAAAAATGGGGTGGGTGTCCTGATTTTGAAGGTTCCAGTGAGCCGACAGTTTGAGGCTAT 540  
QY 564 TGTACAACTCATCTGATCTTGGACTACTCGTGCATCTCCAGAAATATACCCCAA 623  
DB 541 TGTACAACTCATCTGATCTTGGACTACTCGTGCATCTCCAGAAATATACCCCAA 600  
QY 624 GATCCATATTCAACACTCAAACTGCACACAAACAAACAGAAATTTATTCAGTGACAGT 683  
DB 601 GATCCATATTCAACACTCAAACTGCACACAAACAAACAGAAATTTATTCAGTGACAGT 660  
QY 684 ACCTACTGGTGGATTCCTTACTCTACAAATACCTGCCCTTACTACTCTCTCTCTGCT 743  
DB 661 ACCTACTGGTGGATTCCTTACTCTACAAATACCTGCCCTTACTACTCTCTCTCTGCT 720  
QY 744 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTTGATTGTGTACAGAAAGTTTTATG 803  
DB 721 CCAGCTTCCACTTCTATTCCACGGAGAAAAAATTTGATTGTGTACAGAAAGTTTTATG 780  
QY 804 GAAACTAGCACCATGCTACAGAAACTGAACCATTTGTTGAAAAATAAAGCAGCATTCAG 863  
DB 781 GAAACTAGCACCATGCTACAGAAACTGAACCATTTGTTGAAAAATAAAGCAGCATTCAG 840  
QY 864 AATGAAGCTGCTGGGTTTGGAGGTGTCCACGGCTCTGCTAGTGTGCTCTCTCTCTTC 923  
DB 841 AATGAAGCTGCTGGGTTTGGAGGTGTCCACGGCTCTGCTAGTGTGCTCTCTCTCTTC 900  
QY 924 TTTGTGTGTCAGCTGCTTCTGATTTTGTCTATGTCAAAAGGTATGTGAAGGCTTCCCT 983  
DB 901 TTTGTGTGTCAGCTGCTTCTGATTTTGTCTATGTCAAAAGGTATGTGAAGGCTTCCCT 960  
QY 984 TTTCAAAACAGAAATCAGCAGAAAGAAATGTATCGAAACCAAAAGTAGTAAAGGAGAG 1043  
DB 961 TTTCAAAACAGAAATCAGCAGAAAGAAATGTATCGAAACCAAAAGTAGTAAAGGAGAG 1020  
QY 1044 GCCAATGATAGCAACCTTAATGAGGAATCAAGAAATCTGATAAAACCCAGAGAGTCC 1103  
DB 1021 GCCAATGATAGCAACCTTAATGAGGAATCAAGAAATCTGATAAAACCCAGAGAGTCC 1080





QY 1884 AGGAATATACCTTTTACAAGTACAAAATAAAAACCTCTATATAATTTCTATTTTATCT 1943  
|||||  
Db 1861 AGGAATATACCTTTTACAAGTACAAAATAAAAACCTCTATATAATTTCTATTTTATCT 1920  
|||||  
QY 1944 GAGTTACAGAAATGATTACTAAGAGAGATTACTCAGTAATTTGTTTAAAAAGTAAATAAA 2003  
|||||  
Db 1921 GAGTTACAGAAATGATTACTAAGAGAGATTACTCAGTAATTTGTTTAAAAAGTAAATAAA 1980  
|||||  
QY 2004 TTCAACAACAATTTAAAAAAA 2025  
|||||  
Db 1981 TTCAACAACAATTTGCTGAATA 2002  
|||||  
RESULT 11  
ACA59060  
ID ACA59060 standard; cDNA; 2372 BP.  
XX  
AC ACA59060;  
XX  
DT 16-JUN-2003 (first entry)  
XX  
DE Human PRO polynucleotide #36.  
XX  
KW Human; PRO; gene; ss; secreted polypeptide; transmembrane polypeptide;  
KW pathological disorder; cardiac insufficiency disorder; protein secretion;  
KW pancreas; diabetes; gastrointestinal mucosa; mucosal lesion; psoriasis;  
KW skin disease; keratinocyte differentiation; epithelial cancer; tumour;  
KW lung squamous cell carcinoma; epidermoid carcinoma; vulva; glioma;  
KW cystostatic; cardiatic; endocrine; antidiabetic; gastrointestinal;  
KW antiulcer; dermatological; vulnery.  
XX  
OS Homo sapiens.  
XX  
XX  
PN US2002146709-A1.  
XX  
PD 10-OCT-2002.  
XX  
PF 18-JUL-2001; 2001US-00909088.  
XX  
PR 17-SEP-1997; 97US-0059113P.  
PR 17-SEP-1997; 97US-0059115P.  
PR 17-SEP-1997; 97US-0059117P.  
PR 17-SEP-1997; 97US-0059119P.  
PR 17-SEP-1997; 97US-0059121P.  
PR 17-SEP-1997; 97US-0059122P.  
PR 17-SEP-1997; 97US-0059184P.  
PR 18-SEP-1997; 97US-0059263P.  
PR 18-SEP-1997; 97US-0059266P.  
PR 15-OCT-1997; 97US-0062125P.  
PR 17-OCT-1997; 97US-0062285P.  
PR 17-OCT-1997; 97US-0062287P.  
PR 21-OCT-1997; 97US-0063486P.  
PR 24-OCT-1997; 97US-0062814P.  
PR 24-OCT-1997; 97US-0062816P.  
PR 24-OCT-1997; 97US-0063045P.  
PR 24-OCT-1997; 97US-0063120P.  
PR 24-OCT-1997; 97US-0063121P.  
PR 24-OCT-1997; 97US-0063127P.  
PR 24-OCT-1997; 97US-0063128P.  
PR 27-OCT-1997; 97US-0063327P.  
PR 27-OCT-1997; 97US-0063329P.  
PR 28-OCT-1997; 97US-0063541P.  
PR 28-OCT-1997; 97US-0063542P.  
PR 28-OCT-1997; 97US-0063544P.  
PR 28-OCT-1997; 97US-0063549P.  
PR 28-OCT-1997; 97US-0063550P.  
PR 28-OCT-1997; 97US-0063564P.  
PR 29-OCT-1997; 97US-0063435P.  
PR 29-OCT-1997; 97US-0063704P.  
PR 29-OCT-1997; 97US-0063732P.  
PR 29-OCT-1997; 97US-0063734P.  
PR 29-OCT-1997; 97US-0063735P.  
PR 29-OCT-1997; 97US-0063736P.  
PR 29-OCT-1997; 97US-0063737P.  
PR 29-OCT-1997; 97US-0063738P.  
PR 29-OCT-1997; 97US-0064215P.  
PR 31-OCT-1997; 97US-0064103P.  
PR 03-NOV-1997; 97US-0064248P.  
PR 07-NOV-1997; 97US-0064809P.  
PR 12-NOV-1997; 97US-0065186P.  
PR 17-NOV-1997; 97US-0065846P.  
PR 18-NOV-1997; 97US-0065693P.  
PR 21-NOV-1997; 97US-0066120P.  
PR 24-NOV-1997; 97US-0066453P.  
PR 24-NOV-1997; 97US-0066466P.  
PR 24-NOV-1997; 97US-0066511P.  
PR 24-NOV-1997; 97US-0066770P.  
PR 24-NOV-1997; 97US-0066772P.  
PR 10-SEP-1998; 98WO-US018824.  
PR 14-SEP-1998; 98WO-US019177.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 01-DEC-1998; 98WO-US025108.  
PR 08-SEP-1999; 99WO-US020594.  
PR 13-SEP-1999; 99WO-US020944.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 05-OCT-1999; 99WO-US023089.  
PR 29-NOV-1999; 99WO-US028214.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 02-DEC-1999; 99WO-US028564.  
PR 02-DEC-1999; 99WO-US028565.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 20-DEC-1999; 99WO-US030999.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 02-JUN-2000; 2000WO-US015284.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 18-SEP-2000; 2000US-00665350.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
XX  
PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;  
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;  
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;  
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;  
PI Williams EM, Wood WI;  
XX  
DR WPI; 2003-328338/31.  
DR P-PSDB; AB071625.  
XX  
PT Isolated nucleic acid useful for e.g., treating pathological disorders  
PT encodes a secreted or transmembrane protein.  
XX  
XX  
PS Claim 2; Fig 73; 473pp; English.  
XX  
CC The invention relates to human PRO polypeptides (secreted or  
CC transmembrane polypeptides) and the polynucleotides encoding them. The  
CC PRO polypeptides and polynucleotides can be used in treating pathological  
CC disorders and tumours, in therapeutic treatment of cardiac insufficiency  
CC disorders and in therapeutic treatment of disorders involving protein  
CC secretion by the pancreas, including diabetes. They can also be used in  
CC treating disorders associated with the preservation and maintenance of  
CC gastrointestinal mucosa and the repair of acute and chronic mucosal  
CC lesions, and skin diseases associated with abnormal keratinocyte  
CC differentiation (e.g., psoriasis, epithelial cancers such as lung

Isolated nucleic acid useful for e.g., treating pathological disorders encodes a secreted or transmembrane protein.

Claim 2; Fig 73; 473pp; English.

The invention relates to human PRO polypeptides (secreted or transmembrane polypeptides) and the polynucleotides encoding them. The PRO polypeptides and polynucleotides can be used in treating pathological disorders and tumours, in therapeutic treatment of cardiac insufficiency disorders and in therapeutic treatment of disorders involving protein secretion by the pancreas, including diabetes. They can also be used in treating disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions, and skin diseases associated with abnormal keratinocyte differentiation (e.g., psoriasis, epithelial cancers such as lung



CC squamous cell carcinoma, epidermoid carcinoma of the vulva and gliomas).  
CC The sequences can be used as molecular markers for protein  
CC electrophoresis purposes and can be utilised in protein-protein binding  
CC assays, biochemical screening assays, immunoassays and cell-based assays.  
XX This sequence represents a human PRO polynucleotide of the invention  
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Query Match 98.3%; Score 1994; DB 7; Length 2372;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY	24	AGCAGGAAATCGGATGCTCGGTATATCAAGTCGAGCAGTCAGTCGAGCCCTCAACATA	83
DB	1	AGCAGGAAATCGGATGCTCGGTATATCAAGTCGAGCAGTCAGTCGAGCCCTCAACATA	60
QY	84	GTTCAGAACTCTCCATCCGACTAGTATATGAGCATCTGCCCTCATATCACCAGTGGC	143
DB	61	GTTCAGAACTCTCCATCCGACTAGTATATGAGCATCTGCCCTCATATCACCAGTGGC	120
QY	144	CATCTGAGGTGTTCCCTGGCTCTGAAGGGTAGGACGATGGCCAGGTGCTTCAGCCTG	203
DB	121	CATCTGAGGTGTTCCCTGGCTCTGAAGGGTAGGACGATGGCCAGGTGCTTCAGCCTG	180
QY	204	GTGTTGCTTCTCACTTCCATCTGGACACGAGGCTCTGGTCCCAAGGCTCTTTGGTGCA	263
DB	181	GTGTTGCTTCTCACTTCCATCTGGACACGAGGCTCTGGTCCCAAGGCTCTTTGGTGCA	240
QY	264	GAAGAGCTTTCCATCCAGGTGTATGAGCAATATGGGGATCACCCCTGTGAGCAAAAAG	323
DB	241	GAAGAGCTTTCCATCCAGGTGTATGAGCAATATGGGGATCACCCCTGTGAGCAAAAAG	300
QY	324	GGAAACAGCAGCTGAATTTACAGAGCTAAGAGGCTGTAGGCTGTGGAGCTAAGT	383
DB	301	GGAAACAGCAGCTGAATTTACAGAGCTAAGAGGCTGTAGGCTGTGGAGCTAAGT	360
QY	384	TTGGCCGCGAAGCAAGCTGAAACAGCCTTGAAGCTAGCTTTCAAACTTGCAGCTAT	443
DB	361	TTGGCCGCGAAGCAAGCTGAAACAGCCTTGAAGCTAGCTTTGAAACTTGCAGCTAT	420
QY	444	GGCTGGGTTGGAGTGGATTCGTGGTCACTCTAGGATTAAGCCCAACCCCAAGTGGG	503
DB	421	GGCTGGGTTGGAGTGGATTCGTGGTCACTCTAGGATTAAGCCCAACCCCAAGTGGG	480
QY	504	AAAATGGGGTGGGTGCTGATTTGGAAAGTTCCAGTGAGCGGACAGTTTGCAGCCTAT	563
DB	481	AAAATGGGGTGGGTGCTGATTTGGAAAGTTCCAGTGAGCGGACAGTTTGCAGCCTAT	540
QY	564	TGTTACAACTCATCTGATATCTGGACTAACTCGTGCAATCCAGAAATTAACACCAAA	623
DB	541	TGTTACAACTCATCTGATATCTGGACTAACTCGTGCAATCCAGAAATTAACACCAAA	600
QY	624	GATCCCATATCAACACTCAAACTGCAACACAAACACAGAAATTTATGTCAGTGACAGT	683
DB	601	GATCCCATATCAACACTCAAACTGCAACACAAACACAGAAATTTATGTCAGTGACAGT	660
QY	684	ACTACTCGGTGGATCCCTTACTCTCAATACCTGCCCCCTACTACTCTCTCTCTCT	743
DB	661	ACTACTCGGTGGATCCCTTACTCTCAATACCTGCCCCCTACTACTCTCTCTCTCT	720
QY	744	CCAGCTTCCACTTCTATTCACGAGAAAAAATGATTTGTGTACAGAAATTTTATG	803
DB	721	CCAGCTTCCACTTCTATTCACGAGAAAAAATGATTTGTGTACAGAAATTTTATG	780
QY	804	GAACTAGACCATGTCACAGAACTGAACCATTTGTTGAAATTAAGCAGCATTAAG	863
DB	781	GAACTAGACCATGTCACAGAACTGAACCATTTGTTGAAATTAAGCAGCATTAAG	840
QY	864	AATGAAGCTGCTGGGTTGGAGGTGCCCCACGGCTCTGCTAGTGTCTCTCTCTCT	923
DB	841	AATGAAGCTGCTGGGTTGGAGGTGCCCCACGGCTCTGCTAGTGTCTCTCTCTCT	900
QY	924	TTTGGTGTGCTGCTGCTTGGATTTTGCTATGTCAAAAAGGTATGTGAAGGCTTCCCT	983

DB	901	TTTGTGTGTCAGCTGGTCTTGGAATTTTGTATGTCAAAAGTATGTGAAGCCCTTCCCT	960
QY	984	TTTCAAAACAAGATCAGCAGAGGAATGATCGAAACCAAAAGTAGTAAAGGAGAGAAG	1043
DB	961	TTTCAAAACAAGATCAGCAGAGGAATGATCGAAACCAAAAGTAGTAAAGGAGAGAAG	1020
QY	1044	GCCATGATAGCAACCTTAATGAGGAATCAAGAAACTGTATAAAACCCCAAGAGTCC	1103
DB	1021	GCCATGATAGCAACCTTAATGAGGAATCAAGAAACTGTATAAAACCCCAAGAGTCC	1080
QY	1104	AAAGAGTCCAAAGCAAACTACCGTGGATGCTCGGAAGCTGGAAGTTTATAGTAGAGACA	1163
DB	1081	AAAGAGTCCAAAGCAAACTACCGTGGATGCTCGGAAGCTGGAAGTTTATAGTAGAGACA	1140
QY	1164	TGAGAGACACACTGAGGCTGTTCTTTCAATGCTCTTACCTGCCCGCAGCTGGGAA	1223
DB	1141	TGAGAGACACACTGAGGCTGTTCTTTCAATGCTCTTACCTGCCCGCAGCTGGGAA	1200
QY	1224	ATCAAAAGGGCCAAAGAACCAAGAAAGTCCACCTTGTCTCTAACTGGAATCAGC	1283
DB	1201	ATCAAAAGGGCCAAAGAACCAAGAAAGTCCACCTTGTCTCTAACTGGAATCAGC	1260
QY	1284	TCAGGACTGCCATTTGCACTATGAGTGCACCAAGAGATGCCCTTCTCTTTATTGTAAAC	1343
DB	1261	TCAGGACTGCCATTTGCACTATGAGTGCACCAAGAGATGCCCTTCTCTTTATTGTAAC	1320
QY	1344	CTGTCTGGATCTATCTCTCTACCTCCAAAGCTTCCACGGCTTCTAGCTGGCTAT	1403
DB	1321	CTGTCTGGATCTATCTCTCTACCTCCAAAGCTTCCACGGCTTCTAGCTGGCTAT	1380
QY	1404	GTCTTAATAATATCCACTGGGAGAAAGGAGTTTTCGAAAGTGAAGGACCTTAAACATC	1463
DB	1381	GTCTTAATAATATCCACTGGGAGAAAGGAGTTTTCGAAAGTGAAGGACCTTAAACATC	1440
QY	1464	TCATCAGTATCCAGTGGTAAAGGCTCTCTGGCTGTCTGAGGCTAGTGGGTGAAAGC	1523
DB	1441	TCATCAGTATCCAGTGGTAAAGGCTCTCTGGCTGTCTGAGGCTAGTGGGTGAAAGC	1500
QY	1524	CAAGAGTCACTGAGACCAAGGCTTCTACTGATTCGCGAGCTCAGACCTTCTTCA	1583
DB	1501	CAAGAGTCACTGAGACCAAGGCTTCTACTGATTCGCGAGCTCAGACCTTCTTCA	1560
QY	1584	GTCTGAAAGAGAAACACGATATCCACCTGACATGCTTCTGAGCCCGGTGAAGACAA	1643
DB	1561	GTCTGAAAGAGAAACACGATATCCACCTGACATGCTTCTGAGCCCGGTGAAGACAA	1620
QY	1644	AGAATGGCAGAAAGTTTAGCCCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA	1703
DB	1621	AGAATGGCAGAAAGTTTAGCCCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAA	1680
QY	1704	TCTCTGTAAGCTATAATTAAGAAATAGAAACAGGCTGAGGATACGACAGTACACTGTCA	1763
DB	1681	TCTCTGTAAGCTATAATTAAGAAATAGAAACAGGCTGAGGATACGACAGTACACTGTCA	1740
QY	1764	GCAGGACTGTAAACACACAGACAGGGTCAAAGTGTCTCTGAAACATTTGAGTGGAAAT	1823
DB	1741	GCAGGACTGTAAACACACAGACAGGGTCAAAGTGTCTCTGAAACATTTGAGTGGAAAT	1800
QY	1824	CAGTGTGTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTCTCT	1883
DB	1801	CAGTGTGTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTCTCT	1860
QY	1884	AGGAATATATCTTTTCAAGTAAACAAATTAATAAACTCTTATAAAATTTCTATTTATCT	1943
DB	1861	AGGAATATATCTTTTCAAGTAAACAAATTAATAAACTCTTATAAAATTTCTATTTATCT	1920
QY	1944	GAGTTACAGAAATGATTACTTAAGAGGATTAAGGAGTAACTTGTGTTAAAGGTAATAAAA	2003
DB	1921	GAGTTACAGAAATGATTACTTAAGAGGATTAAGGAGTAACTTGTGTTAAAGGTAATAAAA	1980
QY	2004	TTCAACAAACATTTAAAAAAA 2025	





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QY 84 GTTCAGAACTCTCCATCCGACTAGTTATTAGACATCTGCCTCTCATATCACCAGTGGC 143
DB 51 GTTCCAGAACTCTCCATCCGACTAGTTATTAGACATCTGCCTCTCATATCACCAGTGGC 120
QY 144 CATCTGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 203
DB 121 CATCTGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTG 180
QY 204 GTGTGCTTCTCACTTCCATCTGGACACGAGGCTCTGGTCCAGGCTCTTTGGGTGCA 263
DB 181 GTGTGCTTCTCACTTCCATCTGGACACGAGGCTCTGGTCCAGGCTCTTTGGGTGCA 240
QY 264 GAAAGACTTTCATCCAGGTGTCATGCAGAAATTATGGGATCACCTCTGTGAGCAAAAG 323
DB 241 GAAAGACTTTCATCCAGGTGTCATGCAGAAATTATGGGATCACCTCTGTGAGCAAAAG 300
QY 324 GCGAACCCAGCAGCTGAATTTCAAGAACTTAAGGAGGCTGTAGGCTGTGGGACTAAGT 383
DB 301 GCGAACCCAGCAGCTGAATTTCAAGAACTTAAGGAGGCTGTAGGCTGTGGGACTAAGT 360
QY 384 TTGGCCGGCAGGACCAAGTTGAAACAGCCTTGAAGCTAGCTTTGAAACTTGCAGCTAT 443
DB 361 TTGGCCGGCAGGACCAAGTTGAAACAGCCTTGAAGCTAGCTTTGAAACTTGCAGCTAT 420
QY 444 GGCTGGGTGGAGATGGATTCTGTGTCTCTAGGATTAGCCCAAAACCCCAAGTGTGG 503
DB 421 GGCTGGGTGGAGATGGATTCTGTGTCTCTAGGATTAGCCCAAAACCCCAAGTGTGG 480
QY 504 AAAAAATGGGTGGGTGCTCTGATTTGGAAGTTCCAGTGAGCCGACAGTTTCAGCCTAT 563
DB 481 AAAAAATGGGTGGGTGCTCTGATTTGGAAGTTCCAGTGAGCCGACAGTTTCAGCCTAT 540
QY 564 TGTTCAACTCATCTGATCTTGGACTAATCGTGCAATTCAGAAATATCAACCACAA 623
DB 541 TGTTCAACTCATCTGATCTTGGACTAATCGTGCAATTCAGAAATATCAACCACAA 600
QY 624 GATCCCATATTCACACTCAAACTGCAACACAAACAAAGAAATTTATGTGAGTGACAGT 683
DB 601 GATCCCATATTCACACTCAAACTGCAACACAAACAAAGAAATTTATGTGAGTGACAGT 660
QY 684 ACCTACTCGTGGGATCCCTTACTCTACAATACCTGCCCCCTACTACTCTCCTGCT 743
DB 661 ACCTACTCGTGGGATCCCTTACTCTACAATACCTGCCCCCTACTACTCTCCTGCT 720
QY 744 CCAGCTTCCACTTCTATTCACGAGAAAAAATTTGATTTGTCACAGAGTTTATTG 803
DB 721 CCAGCTTCCACTTCTATTCACGAGAAAAAATTTGATTTGTCACAGAGTTTATTG 780
QY 804 GAACTAGCACCATGCTACAGAACTGAACCATTTGTTGAAAAATAAAGCAGCATTCAG 863
DB 781 GAACTAGCACCATGCTACAGAACTGAACCATTTGTTGAAAAATAAAGCAGCATTCAG 840
QY 864 AATGAAGCTGTGGGTGGAGGTGTCACAGGCTCTGCTAGTGTGCTCTCCTCTTC 923
DB 841 AATGAAGCTGTGGGTGGAGGTGTCACAGGCTCTGCTAGTGTGCTCTCCTCTTC 900
QY 924 TTTGTGTCTGAGCTGTGCTTGGATTTGCTATGTCAGAAAGTATGTGAGGCTTCCCT 983
DB 901 TTTGTGTCTGAGCTGTGCTTGGATTTGCTATGTCAGAAAGTATGTGAGGCTTCCCT 960
QY 984 TTTCAAAACAAGAAATCAGCAGAGAAATGATCGAAAACCAAGTAGTAAAGGAGGAG 1043
DB 961 TTTCAAAACAAGAAATCAGCAGAGAAATGATCGAAAACCAAGTAGTAAAGGAGGAG 1020
QY 1044 GCCATGATAGCAACCTTAATGAGGAATCAAGAAAACTGATAAAAAACCCAGAGAGTCC 1103
DB 1021 GCCATGATAGCAACCTTAATGAGGAATCAAGAAAACTGATAAAAAACCCAGAGAGTCC 1080
QY 1104 AAGAGTCCAAAGCAAACTACCCTGCGATGCCCTGGAGGCTGAAAGTTTATAGATGAGCAGAAA 1163
DB 1081 AAGAGTCCAAAGCAAACTACCCTGCGATGCCCTGGAGGCTGAAAGTTTATAGATGAGCAGAAA 1140
QY 1164 TGAGGAGACACACTGAGGCTGGTTTCTTTCTATGCTCTTACCCTGCCCCAGCTGGGAA 1223
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DB 1141 TGAGGAGACACACTGAGGCTGGTTTCTTTCAATGCTCTTACCCTGCCCCAGCTGGGAA 1200
QY 1224 ATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCCCTTGTTCTTAACTGGAATCAGC 1283
DB 1201 ATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCCCTTGTTCTTAACTGGAATCAGC 1260
QY 1284 TCAGGACTGCCANTTGGACTATGGAGTGCACCAAGAGAAATGCCCTCTCTTATTGTAAAC 1343
DB 1261 TCAGGACTGCCANTTGGACTATGGAGTGCACCAAGAGAAATGCCCTCTCTTATTGTAAAC 1320
QY 1344 CCTGTCTGATCCTATCCTCTACCTCCAAAGCTTCCACGCGCTTTCTTAGCTCGCTAT 1403
DB 1321 CCTGTCTGATCCTATCCTCTACCTCCAAAGCTTCCACGCGCTTTCTTAGCTCGCTAT 1380
QY 1404 GTCTTAATAATATCCACTGGGAGAAAGAGTGTTCGAAAGTCAAGGACCTTAAACAATC 1463
DB 1381 GTCTTAATAATATCCACTGGGAGAAAGAGTGTTCGAAAGTCAAGGACCTTAAACAATC 1440
QY 1464 TCATCAGTATCCAGTGTATAAAGGCTCCTGGCTGTCTGAGGCTAGGTGGCTTGAAGC 1523
DB 1441 TCATCAGTATCCAGTGTATAAAGGCTCCTGGCTGTCTGAGGCTAGGTGGCTTGAAGC 1500
QY 1524 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCAAGCTCAGACCCCTTCTTCA 1583
DB 1501 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCAAGCTCAGACCCCTTCTTCA 1560
QY 1584 GCTCTGAAGAGAAACACGTATCCACCTGACATGCTCTCTGAGCCCGGTGAAGCAAA 1643
DB 1561 GCTCTGAAGAGAAACACGTATCCACCTGACATGCTCTCTGAGCCCGGTGAAGCAAA 1620
QY 1644 AGAATGGCAGAAAAGTGTAGCCCTGAAAGCCATGAGATTCCTATACTTGAACCTTAA 1703
DB 1621 AGAATGGCAGAAAAGTGTAGCCCTGAAAGCCATGAGATTCCTATACTTGAACCTTAA 1680
QY 1704 TCTCTGTAAGCTAAATAAAGAAATAGAAACAAGGCTGAGGATACGACAGTACACTGTCA 1763
DB 1681 TCTCTGTAAGCTAAATAAAGAAATAGAAACAAGGCTGAGGATACGACAGTACACTGTCA 1740
QY 1764 CGAGGACTGTAAACACACAGAGGTCAAAGTGTTCCTCTGAAACATATGAGTGGAAAT 1823
DB 1741 CGAGGACTGTAAACACACAGAGGTCAAAGTGTTCCTCTGAAACATATGAGTGGAAAT 1800
QY 1824 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT 1883
DB 1801 CACTGTTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT 1860
QY 1884 AGGAATATACCTTTTACAAGTAAACAAAATAAAAACTCTTATAAAATTTCTATTTTATCT 1943
DB 1861 AGGAATATACCTTTTACAAGTAAACAAAATAAAAACTCTTATAAAATTTCTATTTTATCT 1920
QY 1944 GAGTTACAGAAATGATTAAGGAGATTAAGGAGATTAAGTAAATTTGTTTAAAGTAAATAA 2003
DB 1921 GAGTTACAGAAATGATTAAGGAGATTAAGGAGATTAAGTAAATTTGTTTAAAGTAAATAA 1980
QY 2004 TTCAACAACAATTTTAAABAAA 2025
DB 1981 TTCAACAACAATTTGCTGAATA 2002
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## RESULT 13

ACA60164

ID ACA60164 standard; cDNA; 2372 BP.

XX ACA60164;

AC ACA60164;

XX

DT 12-JUN-2003 (first entry)

XX

DE Human cDNA for secreted/transmembrane protein PRO263.

XX

KW Human; ss; gene; secreted protein; transmembrane protein; PRO;

XX

KW gene therapy; chromosome identification; chromosome marker.

OS	Homo sapiens.	PR	20-DEC-1999;	99WO-US030911.	20-DEC-1999;	99WO-US030911.
XX		PR	20-DEC-1999;	99WO-US030999.	20-DEC-1999;	99WO-US030999.
PN	US20030035330-A1.	PR	05-JAN-2000;	2000WO-US000219.	05-JAN-2000;	2000WO-US000219.
XX		PR	11-FEB-2000;	2000WO-US003565.	11-FEB-2000;	2000WO-US003565.
PD	02-JAN-2003.	PR	22-FEB-2000;	2000WO-US004414.	22-FEB-2000;	2000WO-US004414.
XX		PR	24-FEB-2000;	2000WO-US005004.	24-FEB-2000;	2000WO-US005004.
PF		PR	02-MAR-2000;	2000WO-US005841.	02-MAR-2000;	2000WO-US005841.
XX		PR	30-MAR-2000;	2000WO-US007377.	30-MAR-2000;	2000WO-US007377.
XX		PR	30-MAR-2000;	2000WO-US008439.	30-MAR-2000;	2000WO-US008439.
PR		PR	22-MAY-2000;	2000WO-US014042.	22-MAY-2000;	2000WO-US014042.
PR		PR	02-JUN-2000;	2000WO-US015264.	02-JUN-2000;	2000WO-US015264.
PR		PR	28-JUL-2000;	2000WO-US020710.	28-JUL-2000;	2000WO-US020710.
PR		PR	24-AUG-2000;	2000WO-US023328.	24-AUG-2000;	2000WO-US023328.
PR		PR	18-SEP-2000;	2000US-00665350.	18-SEP-2000;	2000US-00665350.
XX		XX				
PA	(GETH ) GENENTECH INC.	PA				
XX		XX				
XX		XX				
PI	Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;	PI				
PI	Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;	PI				
PI	Godowski PU, Grimaldi JC, Gurney AL, Hillan KJ, Kijavini D;	PI				
PI	Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;	PI				
PI	Williams PM, Wood WI;	PI				
XX		XX				
DR	WPI; 2003-329602/31.	DR				
DR	P-PSDB; ABU71926.	DR				
XX		XX				
PT	New transmembrane polypeptides and nucleic acids encoding the	PT				
PT	polypeptides, useful in gene therapy, in chromosome identification, as	PT				
PT	chromosome markers, in generating probes and in tissue typing.	PT				
XX		XX				
PS	Claim 2; Fig 73; 484pp; English.	PS				
XX		XX				
CC	The invention relates to an isolated nucleic acid with at least 80%	CC				
CC	nucleic acid sequence identity to a nucleotide sequence encoding one of	CC				
CC	61 secreted/transmembrane polypeptides, or PRO polypeptides or encoding a	CC				
CC	PRO protein extracellular domain. Also included are a vector comprising	CC				
CC	the PRO nucleic acid, a host cell comprising the vector, producing a PRO	CC				
CC	polypeptide (by culturing the host cell for the expression of the PRO	CC				
CC	polypeptide, and recovering the PRO polypeptide from the cell culture),	CC				
CC	an isolated PRO polypeptide (having at least 80% sequence identity to: (	CC				
CC	a) an amino acid sequence selected from the 61 PRO proteins; (b) an amino	CC				
CC	acid sequence encoded by a nucleic acid molecule deposited with an ATCC	CC				
CC	number (detailed in the specification); or (c) an extracellular domain of	CC				
CC	a PRO polypeptide or to a PRO polypeptide lacking its associated signal	CC				
CC	peptide), a chimeric molecule comprising a PRO polypeptide of fused to a	CC				
CC	heterologous amino acid sequence, an anti-PRO antibody, detecting a	CC				
CC	linking a bioactive molecule to a cell expressing a PRO245 or PRO1868 and	CC				
CC	modulating at least one biological activity of a cell expressing a PRO245	CC				
CC	or PRO1868. Nucleic acids which encode PRO can be used to generate either	CC				
CC	transgenic animals or knock-out animals which may be used in the	CC				
CC	development and screening of therapeutically useful reagents. The nucleic	CC				
CC	acids may also be used in gene therapy, in chromosome identification, as	CC				
CC	chromosome markers, or in generating probes. The PRO polypeptides are	CC				
CC	useful as molecular markers for protein electrophoresis, and the isolated	CC				
CC	nucleic acids may be used for recombinantly expressing those markers. The	CC				
CC	PRO polypeptides and nucleic acids may also be used in tissue typing.	CC				
CC	Anti-PRO antibodies are useful in diagnostic assays for PRO, and in	CC				
CC	affinity purification of PRO from recombinant cell culture or natural	CC				
CC	sources. The present sequence encodes a PRO protein	CC				
XX		XX				
SQ	Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;	SQ				
			Query Match	98.3%;	Score 1994;	DB 7; Length 2372;
			Best Local Similarity	99.8%;	Pred. NO. 0;	
			Matches 1997;	Conservative	0;	Mismatches 5; Indels 0; Gaps 0;
QY		24	AGCAGGGAATCCGGATGTCCTCGGTATGAGTGGAGCAGTGGTGGAGCTCAACATA	83		
DB		1	AGCAGGGAATCCGGATGTCCTCGGTATGAGTGGAGCAGTGGTGGAGCTCAACATA	60		
QY		84	GTTCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCTCTCATATCACCAGTGGC	143		

Db 61 GTTCAGAACTCTCCATCCGAGCTAGTATTATTGAGCATCTGCCTCTCATATCACCAGTGGC 120  
QY 144 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAAGCTTG 203  
Db 121 CATCTGAGGTGTTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAAGCTTG 180  
QY 204 GTGTGCTTCTCAGTCTCCATCTGGACCAAGAGCTCTGGTCCAGGCTCTTGGGTGCA 263  
Db 181 GTGTGCTTCTCAGTCTCCATCTGGACCAAGAGCTCTGGTCCAGGCTCTTGGGTGCA 240  
QY 264 GAAGAGCTTTCATCCAGGTGTCATGAGAAATATGGGGATCAACCTCTGAGCAAAAAG 323  
Db 241 GAAGAGCTTTCATCCAGGTGTCATGAGAAATATGGGGATCAACCTCTGAGCAAAAAG 300  
QY 324 GCGAACAGAGCTGAAATTTTCAGAGCTAAGAGGCTGTAGGCTGTGGGACTAAGT 383  
Db 301 GCGAACAGAGCTGAAATTTTCAGAGCTAAGAGGCTGTAGGCTGTGGGACTAAGT 360  
QY 384 TTGGCCGGCAAGGACCAAGTTGAAACAGCTTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 443  
Db 361 TTGGCCGGCAAGGACCAAGTTGAAACAGCTTTGAAAGCTAGCTTTGAAACTTGCAGCTAT 420  
QY 444 GCGTGGTGGAGATGATTCGTGGTCACTCTAGGATTAGCCCAAAACCCCAAGTGGG 503  
Db 421 GCGTGGTGGAGATGATTCGTGGTCACTCTAGGATTAGCCCAAAACCCCAAGTGGG 480  
QY 504 AAAATGGGGTGGGTGCTGATTTGGAAGGTTCCAGTGAGCGGACAGTTGGAGCCTAT 563  
Db 481 AAAATGGGGTGGGTGCTGATTTGGAAGGTTCCAGTGAGCGGACAGTTGGAGCCTAT 540  
QY 564 TGTTCAACTCATCTGATCTTGGACTAACTCGTGATTCAGAAATATACACCAAAA 623  
Db 541 TGTTCAACTCATCTGATCTTGGACTAACTCGTGATTCAGAAATATACACCAAAA 600  
QY 624 GATCCATATTCAACACTCAAACTGCAACCAAAACAGAAATTTATGTGAGTCAAGT 683  
Db 601 GATCCATATTCAACACTCAAACTGCAACCAAAACAGAAATTTATGTGAGTCAAGT 660  
QY 684 ACCTACTGGTGGATCCCTTACTCTACAATACCTGCCCTCTACTACTCTCTCTGCT 743  
Db 661 ACCTACTGGTGGATCCCTTACTCTACAATACCTGCCCTCTACTACTCTCTCTGCT 720  
QY 744 CCAGCTTCCACTTCTATTCCAGGAGAAAAAATGATTTGTGTCACAGAATTTTATG 803  
Db 721 CCAGCTTCCACTTCTATTCCAGGAGAAAAAATGATTTGTGTCACAGAATTTTATG 780  
QY 804 GAAACTAGCACCATGCTACAGAAACTGAACCATTTGTTGAAAAATAAGCAGCATTCAG 863  
Db 781 GAAACTAGCACCATGCTACAGAAACTGAACCATTTGTTGAAAAATAAGCAGCATTCAG 840  
QY 864 AATGAGCTGCTGGGTTTGGAGGTGTCACGCTCTCTAGTGTGCTCTCTCTCTTC 923  
Db 841 AATGAGCTGCTGGGTTTGGAGGTGTCACGCTCTCTAGTGTGCTCTCTCTCTTC 900  
QY 924 TTTGCTGCTGACGTGGTCTTGATTTTGTATGTCAAAAGGTATGTGAAGGCTTCCCT 983  
Db 901 TTTGCTGCTGACGTGGTCTTGATTTTGTATGTCAAAAGGTATGTGAAGGCTTCCCT 960  
QY 984 TTTCAAAACAGAAATCAGCAGAGGAATGATCGAAACCAAAAGTAGTAAAGGAGAGAG 1043  
Db 961 TTTCAAAACAGAAATCAGCAGAGGAATGATCGAAACCAAAAGTAGTAAAGGAGAGAG 1020  
QY 1044 GCCAATGATAGCAACCTTAATCAGAAATCAAGAGAACTGATAAAACCCAGAGAGTCC 1103  
Db 1021 GCCAATGATAGCAACCTTAATCAGAAATCAAGAGAACTGATAAAACCCAGAGAGTCC 1080  
QY 1104 AAGAGTCCAGCAAACTACCGTGGATGCTGGAAGCTGGAAGTTTAGATGAGACAGAAA 1163  
Db 1081 AAGAGTCCAGCAAACTACCGTGGATGCTGGAAGCTGGAAGTTTAGATGAGACAGAAA 1140  
QY 1164 TGAGAGACACAGCTGAGCTGTTCTTCTATGCTCTTACCTGCCCCAGCTGGGAA 1223  
Db 1141 TGAGAGACACAGCTGAGCTGTTCTTCTATGCTCTTACCTGCCCCAGCTGGGAA 1200

QY 1224 ATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCTTGGTTCCTAACTGGAATCAGC 1283  
Db 1201 ATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCTTGGTTCCTAACTGGAATCAGC 1260  
QY 1284 TCAGAGCTGCCAATTCGAGCTATGAGTGCACCAAGAGAAATGCCCTTCTCTTATTCGTAAC 1343  
Db 1261 TCAGAGCTGCCAATTCGAGCTATGAGTGCACCAAGAGAAATGCCCTTCTCTTATTCGTAAC 1320  
QY 1344 CCGTGTGGATCCTATCCTTACCTCCAAAGCTTCCACGGCTTCTTAGCTGGCTAT 1403  
Db 1321 CCGTGTGGATCCTATCCTTACCTCCAAAGCTTCCACGGCTTCTTAGCTGGCTAT 1380  
QY 1404 GTCTTAATTAATCCCATCGGAGAAAGAGTGTTCGAAAGTGAAGACCTTAAACATC 1463  
Db 1381 GTCTTAATTAATCCCATCGGAGAAAGAGTGTTCGAAAGTGAAGACCTTAAACATC 1440  
QY 1464 TCATCAGTATCCAGTGGTAAAAAGGCTCTCGGCTGTCTGAGGCTAGGTGGGTGAAAGC 1523  
Db 1441 TCATCAGTATCCAGTGGTAAAAAGGCTCTCGGCTGTCTGAGGCTAGGTGGGTGAAAGC 1500  
QY 1524 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCTTCTTCA 1583  
Db 1501 CAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCTTCTTCA 1560  
QY 1584 GCTCTGAAAGAGAAACAGTATCCACCTGACATGCTCTCTGAGCCCGGTGAAGCAAA 1643  
Db 1561 GCTCTGAAAGAGAAACAGTATCCACCTGACATGCTCTCTGAGCCCGGTGAAGCAAA 1620  
QY 1644 AGAATGGCAGAAAGTTTAGCCCTGAAAGCCATGGAGATTCCTATACTTGAGACCTAA 1703  
Db 1621 AGAATGGCAGAAAGTTTAGCCCTGAAAGCCATGGAGATTCCTATACTTGAGACCTAA 1680  
QY 1704 TCTCTGTAAGCTAAAAATAAGAAATAGAAAGCTGAGGATACGACAGTACATGTC 1763  
Db 1681 TCTCTGTAAGCTAAAAATAAGAAATAGAAAGCTGAGGATACGACAGTACATGTC 1740  
QY 1764 CGAGGAGCTGTAACACACAGAGGCTCAAGGTGTTTCTCTGAAACACATTTGAGTTGGAAT 1823  
Db 1741 CGAGGAGCTGTAACACACAGAGGCTCAAGGTGTTTCTCTGAAACACATTTGAGTTGGAAT 1800  
QY 1824 CACTGTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT 1883  
Db 1801 CACTGTTAGAACACACACACTTACTTTTCTGGTCTCTACCACTGCTGATATTTCTCT 1860  
QY 1884 AGGAATATATCTTTTACAGTAAACAAAAATAAAAACTCTTAFAAATTTCTATTTATCT 1943  
Db 1861 AGGAATATATCTTTTACAGTAAACAAAAATAAAAACTCTTAFAAATTTCTATTTATCT 1920  
QY 1944 GAGTTACAGAAATGATTACTAAGGAGATTTACTCAGTAAATTTGTTTAAAGTAATAAA 2003  
Db 1921 GAGTTACAGAAATGATTACTAAGGAGATTTACTCAGTAAATTTGTTTAAAGTAATAAA 1980  
QY 2004 TTCAACAAACATTTAAAAAAA 2025  
Db 1981 TTCAACAAACATTTCTGAATA 2002

RESULT 14  
ACD07564

ID ACD07564 standard; cdna; 2372 BP.

XX ACD07564;

XX AC

XX DT 07-AUG-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO263 cdna.

XX Human; secreted and transmembrane protein; PRO; pharmaceutical;

XX diagnostic; biosensor; bioindicator; Parkinson's disease;

XX Alzheimer's disease; inflammation; nephritis; wound healing;

XX nerve repair; collateral blood vessel formation; cancer;

XX colorectal cancer; haemorrhage; rheumatoid arthritis; diabetes;

ciirrhosis; fibrosis; restenosis; dermal fibrotic condition; keloid;  
scarring; ischaemia; stroke; hypertension; heart attack; atherosclerosis;  
infertility; gene therapy; gene; ss.

Homo sapiens.

US2002197671-A1.

26-DEC-2002.

17-JUL-2001; 2001US-00907824.

17-SEP-1997; 97US-0059113P.  
17-SEP-1997; 97US-0059115P.  
17-SEP-1997; 97US-0059117P.  
17-SEP-1997; 97US-0059119P.  
17-SEP-1997; 97US-0059121P.  
17-SEP-1997; 97US-0059122P.  
17-SEP-1997; 97US-0059184P.  
17-SEP-1997; 97US-0059263P.  
18-SEP-1997; 97US-0059266P.  
18-SEP-1997; 97US-0062125P.  
15-OCT-1997; 97US-0062285P.  
17-OCT-1997; 97US-0062287P.  
21-OCT-1997; 97US-0063486P.  
24-OCT-1997; 97US-0062814P.  
24-OCT-1997; 97US-0062816P.  
24-OCT-1997; 97US-0063045P.  
24-OCT-1997; 97US-0063120P.  
24-OCT-1997; 97US-0063121P.  
24-OCT-1997; 97US-0063127P.  
24-OCT-1997; 97US-0063128P.  
27-OCT-1997; 97US-0063322P.  
27-OCT-1997; 97US-0063329P.  
28-OCT-1997; 97US-0063541P.  
28-OCT-1997; 97US-0063542P.  
28-OCT-1997; 97US-0063544P.  
28-OCT-1997; 97US-0063549P.  
28-OCT-1997; 97US-0063550P.  
28-OCT-1997; 97US-0063564P.  
29-OCT-1997; 97US-0063435P.  
29-OCT-1997; 97US-0063704P.  
29-OCT-1997; 97US-0063732P.  
29-OCT-1997; 97US-0063734P.  
29-OCT-1997; 97US-0063735P.  
29-OCT-1997; 97US-0063738P.  
29-OCT-1997; 97US-0064215P.  
31-OCT-1997; 97US-0063870P.  
31-OCT-1997; 97US-0064103P.  
03-NOV-1997; 97US-0064248P.  
07-NOV-1997; 97US-0064809P.  
12-NOV-1997; 97US-0065186P.  
17-NOV-1997; 97US-0065846P.  
18-NOV-1997; 97US-0065693P.  
21-NOV-1997; 97US-0066120P.  
21-NOV-1997; 97US-0066364P.  
24-NOV-1997; 97US-0068453P.  
24-NOV-1997; 97US-0066466P.  
24-NOV-1997; 97US-0066511P.  
24-NOV-1997; 97US-0066770P.  
24-NOV-1997; 97US-0066772P.  
10-SEP-1998; 98WO-US018824.  
14-SEP-1998; 98WO-US019177.  
16-SEP-1998; 98WO-US019330.  
17-SEP-1998; 98WO-US019437.  
01-DEC-1998; 98WO-US025108.  
08-SEP-1999; 99WO-US020594.  
13-SEP-1999; 99WO-US020944.  
15-SEP-1999; 99WO-US021090.  
15-SEP-1999; 99WO-US021547.  
05-OCT-1999; 99WO-US023089.  
29-NOV-1999; 99WO-US028214.  
30-NOV-1999; 99WO-US028313.

PR 01-DEC-1999; 99WO-US028301.  
PR 02-DEC-1999; 99WO-US028564.  
PR 02-DEC-1999; 99WO-US028565.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 20-DEC-1999; 99WO-US030999.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 30-MAR-2000; 2000WO-US007377.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 18-SEP-2000; 2000US-00665350.

XX (GETH ) GENENTECH INC.

XX

PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;

PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;

PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kijavini IJ;

PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;

PI Williams PM, Wood WI;

XX

XX WPI; 2003-370793/35.

DR P-PSDB; ABO01809.

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Query Match 98.3%; Score 1994; DB 7; Length 2372;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 24 AGCAGGAAATCCGATGTCCTCGGTATGAGTGAGCAGTGAGTGAGCTCAACATA 83  
DB 1 AGCAGGAAATCCGATGTCCTCGGTATGAGTGAGCAGTGAGTGAGCTCAACATA 60  
QY 84 GTTCCAGAACTCTCCATCCGAGCTAGTTATTGAGCATCTGCTCTCATATCACCAGTCGC 143

Db 61 GTTCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGC 120  
QY 144 CATCTGAGTGTTTTCCCTGGCTCTGAAGGGGTAGGCA CGATGGCCAGGTGCTTCAGCCTG 203  
Db 121 CATCTGAGTGTTTTCCCTGGCTCTGAAGGGGTAGGCA CGATGGCCAGGTGCTTCAGCCTG 180  
QY 204 GTGTTGCTTCTCAGTTCCTCATCTGGACCA GAGGCTCCTGGTCCAAGGCTCTTTGGTGCA 263  
Db 181 GTGTTGCTTCTCAGTTCCTCATCTGGACCA GAGGCTCCTGGTCCAAGGCTCTTTGGTGCA 240  
QY 264 GAAGAGCTTTCCATCCAGGTGTCAATGCAGAA TATGGGATCACCCCTGTGGACAAAAG 323  
Db 241 GAAGAGCTTTCCATCCAGGTGTCAATGCAGAA TATGGGATCACCCCTGTGGACAAAAG 300  
QY 324 GCGAACGACAGTGAATTTACAGAACTAGAGG CCGCTGAGGCTGTGGGACTAAGT 383  
Db 301 GCGAACGACAGTGAATTTACAGAACTAGAGG CCGCTGAGGCTGTGGGACTAAGT 360  
QY 384 TTGGCCGGCAAGACCAAGTTGAAACAGCCTT GAAAGCTAGCTTTGAAACTTGCAGCTAT 443  
Db 361 TTGGCCGGCAAGACCAAGTTGAAACAGCCTT GAAAGCTAGCTTTGAAACTTGCAGCTAT 420  
QY 444 GCGTGGTTGGAGATGGATTCGTGGTCACTCTC TAGGATTAGCCCAACCCCAAGTGTGG 503  
Db 421 GCGTGGTTGGAGATGGATTCGTGGTCACTCTC TAGGATTAGCCCAACCCCAAGTGTGG 480  
QY 504 AAAATGGGGTGGGTGCTGATTTGGAAAGGTT CAGTGAGCGGACAGTTTGCAGCCTAT 563  
Db 481 AAAATGGGGTGGGTGCTGATTTGGAAAGGTT CAGTGAGCGGACAGTTTGCAGCCTAT 540  
QY 564 TGTACAACTCATCTGATCTTGGACTTAATCGT GCATTCCAGAAATATACACCACAAA 623  
Db 541 TGTACAACTCATCTGATCTTGGACTTAATCGT GCATTCCAGAAATATACACCACAAA 600  
QY 624 GATCCCATATTCAACTCAAACTCAAACTGCAAC AACAACAAGATTTATTGTGACAGT 683  
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QY 684 ACTACTCGGTGGCTCCCTTACTCTAATACTGC TCCCTTACTACTCTCTCTGCT 743  
Db 661 ACTACTCGGTGGCTCCCTTACTCTAATACTGC TCCCTTACTACTCTCTCTGCT 720  
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QY 804 GAACTAGCACCATGCTACAGAACTGAACCAT TTGTTGAAAAATAAAGCAGCATTCAG 863  
Db 781 GAACTAGCACCATGCTACAGAACTGAACCAT TTGTTGAAAAATAAAGCAGCATTCAG 840  
QY 864 AATGAGCTGCTGGGTTGGAGGTGTCGCCAGG CTCTGCTAGTGTGCTCTCTCTTC 923  
Db 841 AATGAGCTGCTGGGTTGGAGGTGTCGCCAGG CTCTGCTAGTGTGCTCTCTCTTC 900  
QY 924 TTTGTGCTGCACTGCTGCTTGGATTTTGTCTA TGTCAAAAGTATGTGAAGCCTTCCCT 983  
Db 901 TTTGTGCTGCACTGCTGCTTGGATTTTGTCTA TGTCAAAAGTATGTGAAGCCTTCCCT 960  
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QY 1044 GCCAATGATAGCAACCTCAATCAGGAATCAAGA AACTGATAAAACCCAGAAGTCC 1103  
Db 1021 GCCAATGATAGCAACCTCAATCAGGAATCAAGA AACTGATAAAACCCAGAAGTCC 1080  
QY 1104 AAGAGTCCAAGCAAAACTACCGTGGATCGCTG GAAGCTGAAGTTTAGATGAGACAGAA 1163  
Db 1081 AAGAGTCCAAGCAAAACTACCGTGGATCGCTG GAAGCTGAAGTTTAGATGAGACAGAA 1140  
QY 1164 TGAGGAGACACACTGAGGCTGTTCTTTATGCTC CTACCTTACCTGCCCCAGCTGGGA 1223  
Db 1141 TGAGGAGACACACTGAGGCTGTTCTTTTATGCTC CTACCTTACCTGCCCCAGCTGGGA 1200

QY 1224 ATCAAAAGGGCCAAAGAACCAAAAGAAAGTCC ACCCTTGGTTCTTAACGTGAATCAGC 1283  
Db 1201 ATCAAAAGGGCCAAAGAACCAAAAGAAAGTCC ACCCTTGGTTCTTAACGTGAATCAGC 1260  
QY 1284 TCAGGACTGCCATTCGACTATCGAGTGACCAAA GAGAGTCCCTTCTCTTATTGTAAC 1343  
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QY 1344 CTTGTCTGATCCTATCCTCTTACCTCCAAAGCT TCCACGGCTTTCTAGCGTGGCTAT 1403  
Db 1321 CTTGTCTGATCCTATCCTCTTACCTCCAAAGCT TCCACGGCTTTCTAGCGTGGCTAT 1380  
QY 1404 GTTCTAAATAATATCCCATCTGGGAGAAAGGAG TTTTGCAAAAGTGCAGGACCTAAACATC 1463  
Db 1381 GTTCTAAATAATATCCCATCTGGGAGAAAGGAG TTTTGCAAAAGTGCAGGACCTAAACATC 1440  
QY 1464 TCATCAGTATCCAGTGGTAAAGAGCCTCTCGCT GTCTGAGGCTAGGTGGTGAAGC 1523  
Db 1441 TCATCAGTATCCAGTGGTAAAGAGCCTCTCGCT GTCTGAGGCTAGGTGGTGAAGC 1500  
QY 1524 CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTG ATTCGCGAGCTCAGACCCCTTTCTTCA 1583  
Db 1501 CAAGGAGTCACTGAGACCAAGGCTTTCTCTACTG ATTCGCGAGCTCAGACCCCTTTCTTCA 1560  
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Db 1801 CACTGTTTGAACACACACACTTACTTTTTCTGGT GCTCTACCACTGCTCATATTTCTCT 1860  
QY 1884 AGGAAATATACCTTTTACAGTAACAAAAATAAAA AACTCTTATAAAATTTCTATTTTATCT 1943  
Db 1861 AGGAAATATACCTTTTACAGTAACAAAAATAAAA AACTCTTATAAAATTTCTATTTTATCT 1920  
QY 1944 GAGTTACAGAATGATTACTAAGGAAGATTACTC AGTAATTTGTTTAAAGTAATAAAA 2003  
Db 1921 GAGTTACAGAATGATTACTAAGGAAGATTACTC AGTAATTTGTTTAAAGTAATAAAA 1980  
QY 2004 TTCAACAAACATTTTAAAAAAA 2025  
Db 1981 TTCAACAAACATTTGCTGATA 2002

RESULT 15

ACA91166

ID ACA91166 standard; cdna; 2372 BP.

XX ACA91166;

XX AC ACA91166;

XX DT 11-JUL-2003 (first entry)

XX DE Novel human secreted and transmembrane protein PRO263 cdna.

XX KW Human; secreted and transmembrane protein; PRO; antibody therapy;

XX KW Pharmaceutical; diagnostic; biosensor; bioreactor; gene; ss.

XX OS Homo sapiens.

XX

PN US2003018173-A1.  
XX 23-JAN-2003.  
XX 01-MAY-2002; 2002US-00063515.  
XX 06-DEC-2001; 2001US-00006867.  
XX (GETH ) GENENTECH INC.  
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;  
XX P-PSDB; ABU90878.  
XX WPI; 2003-401702/38.  
XX DR P-PSDB; ABU90878.  
XX PT New antibody useful for identifying PRO polypeptides, for affinity  
PT purification of PRO polypeptides, and for preparing a medicament for  
PT diagnosing or treating conditions responsive to the antibody or PRO  
PT polypeptide.  
XX PS Disclosure; Fig 5; 345pp; English.  
XX CC The invention describes an antibody that specifically binds to a PRO  
CC polypeptide having a fully defined amino acid sequence given in the  
CC specification. The antibody is useful in identifying PRO polypeptides  
CC useful for various industrial applications, including pharmaceuticals,  
CC diagnostics, biosensors and bioreactors. The antibody is also used for  
CC affinity purification of PRO polypeptides from recombinant cell culture  
CC or natural sources. The antibody, PRO polypeptide, or its agonists or  
CC antagonists, may be used for preparing a medicament for diagnosing or  
CC treating a condition responsive to the antibody, PRO polypeptide, or its  
CC agonists or antagonists. This sequence encodes a novel human secreted and  
CC transmembrane PRO polypeptide  
XX  
SQ Sequence 2372 BP; 721 A; 524 C; 489 G; 638 T; 0 U; 0 Other;

Query Match 98.3%; Score 1994; DB 7; Length 2372;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1997; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 24 AGCAGGGAATCCGGATGTCGCTGTTATGAAGTGGAGCAGTGAAGTGGAGCCTCAACATA 83  
DB |||||  
1 AGCAGGGAATCCGGATGTCGCTGTTATGAAGTGGAGCAGTGAAGTGGAGCCTCAACATA 60  
QY 84 GTTCAGAACTCTCCATCCGACTAGTATTGAGCAATCTGCTCTCATATCAACAGTGGC 143  
DB |||||  
61 GTTCAGAACTCTCCATCCGACTAGTATTGAGCAATCTGCTCTCATATCAACAGTGGC 120  
QY 144 CATCTGAGTGTTCCCTGGCTCTGAAGGGTAGGACGATGGCCAGTGGCTTCAGCCTG 203  
DB |||||  
121 CATCTGAGTGTTCCCTGGCTCTGAAGGGTAGGACGATGGCCAGTGGCTTCAGCCTG 180  
QY 204 GTGTTGCTTCTCACTTCCATCTGGACACGAGGCTCTGCTCCAAAGGCTCTTTGGGTGCA 263  
DB |||||  
181 GTGTTGCTTCTCACTTCCATCTGGACACGAGGCTCTGCTCCAAAGGCTCTTTGGGTGCA 240  
QY 264 GAAGAGCTTTCATCCAGTGTGTCAGCAATATGGGGATCACCTTGTGAGCAAAAAG 323  
DB |||||  
241 GAAGAGCTTTCATCCAGTGTGTCAGCAATATGGGGATCACCTTGTGAGCAAAAAG 300  
QY 324 GCGAACCCAGCAGTGAATTTACAGAAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGT 383  
DB |||||  
301 GCGAACCCAGCAGTGAATTTACAGAAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGT 360  
QY 384 TTGGCCGGCAAGACCAAGTTGAAACAGCCTTTGAAAGCTAGCTTTGAAACTTTGCAGCTAT 443  
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361 TTGGCCGGCAAGACCAAGTTGAAACAGCCTTTGAAAGCTAGCTTTGAAACTTTGCAGCTAT 420  
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DB |||||  
421 GGCTGGTTGGAGATGGATTCGTGTCATCTAGGATTTAGCCAAACCCCAAGTGTGGG 480

QY 504 ABAATGGGGTGGGTCTCTGATTTGGAAAGTTTCCAGTGAGCCGACAGTTTGAGCCTAT 563  
DB |||||  
481 ABAATGGGGTGGGTCTCTGATTTGGAAAGTTTCCAGTGAGCCGACAGTTTGAGCCTAT 540  
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DB |||||  
541 TGTTCACAACTCATCTGATACCTTGGACTAATCGTGCAATTCAGAAATTTATCACCACAAA 600  
QY 624 GATCCCATATTCACAACTCAAACTGCAACACAAACAGAAATTTATTTGTCAGTGACAGT 683  
DB |||||  
601 GATCCCATATTCACAACTCAAACTGCAACACAAACAGAAATTTATTTGTCAGTGACAGT 660  
QY 684 ACTTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTACTACTACTCTCTCTGCT 743  
DB |||||  
661 ACTTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTACTACTACTCTCTCTGCT 720  
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DB |||||  
781 GAACTAGCACCATGTCTACAGAACTGAACCATTTGTTGAAAAATAAAGCAGCATTCAG 840  
QY 864 AATGAGCTGCTGGGTGGAGGTGTCGCCAGGCTCTGCTAGTGTCTCTCTCTCTC 923  
DB |||||  
841 AATGAGCTGCTGGGTGGAGGTGTCGCCAGGCTCTGCTAGTGTCTCTCTCTCTC 900  
QY 924 TTTGTGCTGTCAGCTGCTTGGATTTTGTCTATGTCAAAAGGTATGTGAAGGCTTCCCT 983  
DB |||||  
901 TTTGTGCTGTCAGCTGCTTGGATTTTGTCTATGTCAAAAGGTATGTGAAGGCTTCCCT 960  
QY 984 TTTACAAACAGAAATCAGCAGAAAGAAATGATCGAAACCAAAAGTAGTAGAAGAGGAGAG 1043  
DB |||||  
961 TTTACAAACAGAAATCAGCAGAAAGAAATGATCGAAACCAAAAGTAGTAGAAGAGGAGAG 1020  
QY 1044 GCCAATGATAGCAACCTTAATCAGGAATCAAGAAAACTGATAAAAAACCAGAGAGTCC 1103  
DB |||||  
1021 GCCAATGATAGCAACCTTAATCAGGAATCAAGAAAACTGATAAAAAACCAGAGAGTCC 1080  
QY 1104 AAGAGTCCAAGCAAACTACCGTGGATGCGCTGGAGCTGAAGTTTAGATGAGACAGAAA 1163  
DB |||||  
1081 AAGAGTCCAAGCAAACTACCGTGGATGCGCTGGAGCTGAAGTTTAGATGAGACAGAAA 1140  
QY 1164 TGAGGAGACACACTGAGGCTGTTTCTTATGCTCTCTTACCTGCCCCAGCTGGGAA 1223  
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1141 TGAGGAGACACACTGAGGCTGTTTCTTATGCTCTCTTACCTGCCCCAGCTGGGAA 1200  
QY 1224 ATCAAAAGGGCCAAAGAACCAAGAAAGTCCACCTTGGTTCTTAATCTGGAATCAGC 1283  
DB |||||  
1201 ATCAAAAGGGCCAAAGAACCAAGAAAGTCCACCTTGGTTCTTAATCTGGAATCAGC 1260  
QY 1284 TCAGGACTGCCATTCGACTATGGAGTGCAACAAAGAGAAATGCCCTTCTCTTATTGTAAC 1343  
DB |||||  
1261 TCAGGACTGCCATTCGACTATGGAGTGCAACAAAGAGAAATGCCCTTCTCTTATTGTAAC 1320  
QY 1344 CTTGCTCGGATCTTATCTCTTACCTCAAAAGCTTCCACGGCCTTTCTAGCCTGGCTAT 1403  
DB |||||  
1321 CTTGCTCGGATCTTATCTCTTACCTCAAAAGCTTCCACGGCCTTTCTAGCCTGGCTAT 1380  
QY 1404 GTCCCTAAATATATCCACTGGGAGAAAGAGTTTGGAAAGTGGAGGCTTAAACATC 1463  
DB |||||  
1381 GTCCCTAAATATATCCACTGGGAGAAAGAGTTTGGAAAGTGGAGGCTTAAACATC 1440  
QY 1464 TCATCAGTATCCAGTGGTAAAAAGGCTCTCTGGCTGTCTGAGGCTAGGTGGGTTGAAAGC 1523  
DB |||||  
1441 TCATCAGTATCCAGTGGTAAAAAGGCTCTCTGGCTGTCTGAGGCTAGGTGGGTTGAAAGC 1500  
QY 1524 CAAGGAGTCACTGAGACCAAGGCTTTCTTACTACTGATTCGGAGCTCAGACCCCTTTCTTCA 1583  
DB |||||  
1501 CAAGGAGTCACTGAGACCAAGGCTTTCTTACTACTGATTCGGAGCTCAGACCCCTTTCTTCA 1560  
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1561	GCTCTGAAGAGAGAAACACGTATCCCACTGACATGTCCTTCTGAGCCGGTAAGAGCAAA	1620
1644	AGAAATGCACGAAAGATTTAGCCCTGAAAGCCATGGAGATTCCTCATAACTTGAGACCTAA	1703
1621	AGAAATGCACGAAAGATTTAGCCCTGAAAGCCATGGAGATTCCTCATAACTTGAGACCTAA	1680
1704	TCTCTGTAAAGCTAAAAATAAAGAAATAGAAACAAGGCTGAGGATACGACAGTACACATGTCA	1763
1681	TCTCTGTAAAGCTAAAAATAAAGAAATAGAAACAAGGCTGAGGATACGACAGTACACATGTCA	1740
1764	GCAGGGACTGTAAACACAGACAGGGTCAAAAGTGTTTTCTCTGAACAACATTTGAGTTGGAAT	1823
1741	GCAGGGACTGTAAACACAGACAGGGTCAAAAGTGTTTTCTCTGAACAACATTTGAGTTGGAAT	1800
1824	CACCTGTTTTAGNACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTCTCT	1883
1801	CACCTGTTTTAGNACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTCTCT	1860
1884	AGGAAATATACTTTTTACAAGTAAACAAAAATAAAAACTCTTATAAAATTTCTATTTTATCT	1943
1861	AGGAAATATACTTTTTACAAGTAAACAAAAATAAAAACTCTTATAAAATTTCTATTTTATCT	1920
1944	GAGTTACAGAAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTTAAAAAGTAATAAAA	2003
1921	GAGTTACAGAAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTTAAAAAGTAATAAAA	1980
2004	TTCAACAAACATTTAAAAAAA	2025
1981	TTCAACAAACATTTGCTGAATA	2002

Search completed: September 15, 2004, 07:40:48  
Job time : 835 secs



GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 13, 2004, 09:54:56 ; Search time 217 Seconds  
(without alignments)  
5283.769 Million cell updates/sec

Title: US-10-079-111-2

Perfect score: 3604

Sequence: 1 ccttgacaagtcagaagcgtt.....aaacatttaaaaaaaaaa 2029

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 3172214

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/uspto.spool\_p/us10079111/runat\_13092004\_102125\_1809/app.query.fasta\_1.2183  
-DB=A Geneseq 29Jan04 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEARSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10079111@cgn\_1\_1\_308@runat\_13092004\_102125\_1809 -NCPU=6 -ICPU=3  
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A Geneseq 29Jan04: \*  
1: Geneseqp1980s: \*  
2: Geneseqp1990s: \*  
3: Geneseqp2000s: \*  
4: Geneseqp2001s: \*  
5: Geneseqp2002s: \*  
6: Geneseqp2003as: \*  
7: Geneseqp2003bs: \*  
8: Geneseqp2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1772	49.2	344	4	AB11979 Human PRO
2	1657	46.0	322	2	AA13379 Amino aci
3	1657	46.0	322	3	AA13379 Human sig
4	1657	46.0	322	3	ADCT78521 Human PRO
5	1657	46.0	322	4	AA880247 Human PRO
6	1657	46.0	322	4	AA887528 Human PRO
7	1657	46.0	322	4	AA888391 Human mem
8	1657	46.0	322	5	ABG95853 Human sec
9	1657	46.0	322	5	AB84832 Human PRO
10	1657	46.0	322	5	AB895438 Human ang

11	1657	46.0	322	6	ABU71625 Human PRO
12	1657	46.0	322	6	ABU71480 Human PRO
13	1657	46.0	322	6	ABU71926 Human sec
14	1657	46.0	322	6	ABO01809 Novel hum
15	1657	46.0	322	6	ABU90878 Novel hum
16	1657	46.0	322	6	ABO33937 Human sec
17	1657	46.0	322	6	ABU71954 Novel hum
18	1657	46.0	322	6	ABU54382 Human sec
19	1657	46.0	322	6	ABO47397 Human sec
20	1657	46.0	322	6	ABU71508 Human sec
21	1657	46.0	322	6	ABU72289 Human PRO
22	1657	46.0	322	6	ABU90962 Human PRO
23	1657	46.0	322	6	ABO27283 Human sec
24	1657	46.0	322	6	ABU64534 Human sec
25	1657	46.0	322	6	ABU67380 Human sec
26	1657	46.0	322	6	ABU92478 Human sec
27	1657	46.0	322	6	ABO14900 Human sec
28	1657	46.0	322	6	ABU81148 Human sec
29	1657	46.0	322	6	ABO53263 Novel hum
30	1657	46.0	322	6	ABU98265 Novel hum
31	1657	46.0	322	6	ABU89270 Novel hum
32	1657	46.0	322	6	ABU82477 Novel hum
33	1657	46.0	322	6	ABU96441 Human PRO
34	1657	46.0	322	6	ABU72111 Human PRO
35	1657	46.0	322	6	ABO14839 Human sec
36	1657	46.0	322	6	AD829406 Human sec
37	1657	46.0	322	6	ADB17063 Human tra
38	1657	46.0	322	6	ABO44241 Human sec
39	1657	46.0	322	6	ADA18262 Human sec
40	1657	46.0	322	6	ABO32791 Human sec
41	1657	46.0	322	6	ADA19868 Novel hum
42	1657	46.0	322	6	ADB17251 Human tra
43	1657	46.0	322	6	ABO34851 Human PRO
44	1657	46.0	322	6	ADA16237 Human sec
45	1657	46.0	322	6	ADA16237 Human sec

#### ALIGNMENTS

RESULT 1

AB11979

ID AB11979 standard; peptide; 344 AA.

XX AB11979;

AC AB11979;

DT 11-JAN-2002 (first entry)

XX Human PRO263 homologue, SEQ ID NO:2349.

Human; cytokine; cell proliferation; cell differentiation; growth factor;  
haematopoiesis regulation; tissue growth; immunomodulator; activin;  
inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;  
proliferation; metastasis; cancer; tumour; haematopoietic disorder;  
myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;  
chronic inflammatory condition; proliferative retinopathy;  
atherosclerosis; coronary heart disease; arterial ischaemia;  
bone disorder; osteoporosis; vascular growth disorder;  
tissue regeneration; wound healing; infection; immune disorder;  
cell culture; drug screening; gene therapy; antiinflammatory;  
antithrombotic; antiarthritic; haemostatic; antiarteriosclerotic;  
cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;  
antifungal; vulnery; antiulcer.

XX Homo sapiens.

XX WO200157188-A2.

XX 09-AUG-2001.

PD 05-FEB-2001; 2001WO-US003800.

XX 03-FEB-2000; 2000US-00496914.

PF 27-APR-2000; 2000US-00560875.

PR

XX (HYSE-) HYSEQ INC.  
XX PA  
XX PI  
XX Tang YT, Liu C, Drmanac RT;  
XX DR  
XX WPI; 2001-457740/49.  
XX DR N-PSDB; ABA09223.  
XX Human proteins and DNA encoding sequences useful for preventing, treating  
PT or ameliorating a medical condition in a mammalian subject e.g. arthritis  
PT and cancer.  
XX  
XX Claim 20; Page 291; 1963pp; English.  
XX  
XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and  
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The  
CC invention also relates to vectors and recombinant host cells comprising a  
CC nucleotide of the invention, methods of producing the novel polypeptides,  
CC antibodies against the polypeptides, methods of detecting the nucleotides  
CC or polypeptides in a sample, and methods of identifying compounds which  
CC bind to polypeptides of the invention. Although novel, many of the  
CC polypeptides of the invention have homology to known proteins, thereby  
CC giving an insight into their probable biological activities, and hence  
CC potential therapeutic applications. The polypeptides of the invention may  
CC have various activities, including cytokine, cell proliferation or cell  
CC differentiation activities; stem cell growth factor activity;  
CC haematopoietic regulatory activity; tissue growth activity;  
CC immunomodulatory activity; activin- or inhibin-related activities;  
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or  
CC thrombolytic activities; receptor or ligand activities; or may be  
CC involved in oncogenesis, cancer cell proliferation or metastasis.  
CC Depending on their biological activities, polypeptides and nucleotides of  
CC the invention are useful for preventing, treating or ameliorating medical  
CC conditions, e.g., by protein or gene therapy. Such conditions include  
CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell  
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),  
CC proliferative retinopathy, atherosclerosis, coronary heart disease,  
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal  
CC vascular growth. Polypeptides involved with tissue regeneration and  
CC repair (or nucleic acids encoding them) may be used to promote wound  
CC healing (e.g., of burns, incisions and ulcers), while those with  
CC immunomodulatory activities may be used in the treatment of viral,  
CC bacterial and fungal infections in addition to immune disorders.  
CC Polypeptides with growth factor activity may be used in cell cultures to  
CC promote cell growth. For example, such polypeptides may be used to  
CC manipulate stem cells in culture to give rise to neuroepithelial cells  
CC that can be used to augment or replace cells damaged by illness,  
CC autoimmune disease or accidental damage. The polypeptides and nucleotides  
CC may also be used in the diagnosis of the above conditions, and in drug  
CC screening techniques. The present sequence represents a novel human  
CC polypeptide of the invention

XX Sequence 344 AA;

Alignment Scores:  
Pred. No.: 3,95e-175 Length: 344  
Score: 1772.00 Matches: 343  
Percent Similarity: 100.00% Conservatives: 1  
Best Local Similarity: 99.71% Mismatches: 0  
Query Match: 49.17% Indels: 0  
DB: 4 Gaps: 0

US-10-079-111-2 (1-2029) x ABB11979 (1-344)

QY 117 GCATCGCTCTCATATACAGTGGCCATCTGAGGTGTTTCCCTGGCTGAGGGGTA 176  
Db 1 AlaSerAlaSerHisIleThrSerGlyHisLeuArgCysPheProGlySerGluGlyVal 20  
QY 177 GGCACCATGGCCAGGTGCTTACGCTGGTGTCTCTCCTCCTTCCATCTGGACACGAG 236  
Db 21 GlyThrMetAlaArgCysPheSerLeuValLeuLeuThrSerIleIlePThrThrA 40  
QY 237 CTCCTGGTCCAGGCTCTTTGGCTGCGAGAAGAGCTTTCCATCCAGGTGTCATGCAGAATT 296

Db 41 LeuLeuValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIle 60  
QY 297 ATGGGGATCACCTCTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTTTCAGAGCTAAG 356  
Db 61 MetGlyIleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPhetThrGluAlaLys 80  
QY 357 GAGGCTGTAGGCTGTGGGACTAAGTTTGGCGGCAAGACCAAGTTCAGAGCTTGG 416  
Db 81 GluAlaCysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeu 100  
QY 417 AAAGCTAGCTTTCAAACTTGCAGCTATGCTGGTTGGAGATGATGATTCGTGGTCACTCT 476  
Db 101 LysAlaSerPheGluThrCysSerIleGlyIleValGlyAspGlyPheValIleSer 120  
QY 477 AGGATTAGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGTCTCTGATTTGGAGGTT 536  
Db 121 ArgIleSerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleIleTpyLysVal 140  
QY 537 CCAGTGCAGCGCAGTTCAGGCTATTGTTCAACTCATCTGATATCTGGACTTAAGTCG 596  
Db 141 ProValSerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSer 160  
QY 597 TGCATTCCAGAAATATATCAACCAAGATCCCATATTCACACTCAAACTGCAACACAA 656  
Db 161 CysIleProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGln 180  
QY 657 ACAACAGAAATTTATTGTCTAGTGACAGTACTACTCGGTGGCATCCCTTACTCTACAATA 716  
Db 181 ThrThrGluPheIleValSerAspSerThrTyrSerValAlaSerProIleProArgLysLys 200  
QY 717 CTGCGCCCTACTACTAT 776  
Db 201 ProAlaProThrThrThrProProAlaProAlaSerThrSerIleProArgLysLys 220  
QY 777 TTGATTGTGTGCAGAACTTTTATGGAACTTAGCACCATGTCTACAGAACTGACAACTGAACCA 836  
Db 221 LeulleCysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluPro 240  
QY 837 TTTGTTGAAAAATAAGACAGCATTCAGAAATGAAGTCTGGGTTCGAGGTGTCCCCACG 896  
Db 241 PheValGluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThr 260  
QY 897 GCTCTGCTAGTCTGCTAT 956  
Db 261 AlaLeuLeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyr 280  
QY 957 GTCAAAAGGTATGTGAAGGCTTTCCTTTTACAAACAAGAAATCAGCAGAGGAATAATGATC 1016  
Db 281 ValLysArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIle 300  
QY 1017 GAAACCAAGTAGTAAAGGAGGAGGAGGCAATAGTACCAACCTTAATGAGGAATCAAG 1076  
Db 301 GluThrLysValValLysGluLysAlaAsnAspSerAsnProAsnGluGluSerLys 320  
QY 1077 AAAACTGATAAAACCCCAAGAGTCCAGAGTCCCAAGCAAACTACCTCGGATCGCTG 1136  
Db 321 LysThrAspLysAsnProGluSerLysSerProSerLysThrThrMetArgCysLeu 340  
QY 1137 GAAGCTGAGATT 1148  
Db 341 GluAlaGluVal 344

RESULT 2

AA113379  
ID AAY13379 standard; protein; 322 AA.  
XX  
AC AAY13379;  
XX  
DT 25-JUN-1999 (first entry)  
XX Amino acid sequence of protein PRO263.  
XX

KW Secreted protein; transmembrane protein; human; enterocolitis;  
 KW Zollinger-Ellison syndrome; gastrointestinal ulceration;  
 KW congenital microvillus atrophy; skin disease; cell growth;  
 KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;  
 KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin;  
 KW dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic;  
 KW wound healing; tissue repair.  
 XX  
 OS Homo sapiens.  
 PN WO9914328-A2.  
 XX  
 XX 25-MAR-1999.  
 XX  
 PF 16-SEP-1998; 98WO-US019330.  
 XX  
 PR 17-SEP-1997; 97US-00591113P.  
 PR 17-SEP-1997; 97US-00591115P.  
 PR 17-SEP-1997; 97US-00591117P.  
 PR 17-SEP-1997; 97US-00591119P.  
 PR 17-SEP-1997; 97US-00591211P.  
 PR 17-SEP-1997; 97US-00591222P.  
 PR 17-SEP-1997; 97US-0059184P.  
 PR 18-SEP-1997; 97US-0059263P.  
 PR 18-SEP-1997; 97US-0059266P.  
 PR 15-OCT-1997; 97US-0062123P.  
 PR 17-OCT-1997; 97US-0062285P.  
 PR 17-OCT-1997; 97US-0062287P.  
 PR 21-OCT-1997; 97US-0063486P.  
 PR 24-OCT-1997; 97US-0062814P.  
 PR 24-OCT-1997; 97US-0062816P.  
 PR 24-OCT-1997; 97US-0063043P.  
 PR 24-OCT-1997; 97US-0063120P.  
 PR 24-OCT-1997; 97US-0063121P.  
 PR 24-OCT-1997; 97US-0063127P.  
 PR 24-OCT-1997; 97US-0063128P.  
 PR 27-OCT-1997; 97US-0063327P.  
 PR 27-OCT-1997; 97US-0063329P.  
 PR 28-OCT-1997; 97US-0063541P.  
 PR 28-OCT-1997; 97US-0063542P.  
 PR 28-OCT-1997; 97US-0063544P.  
 PR 28-OCT-1997; 97US-0063549P.  
 PR 28-OCT-1997; 97US-0063550P.  
 PR 28-OCT-1997; 97US-0063564P.  
 PR 29-OCT-1997; 97US-0063435P.  
 PR 29-OCT-1997; 97US-0063704P.  
 PR 29-OCT-1997; 97US-0063732P.  
 PR 29-OCT-1997; 97US-0063733P.  
 PR 29-OCT-1997; 97US-0063735P.  
 PR 29-OCT-1997; 97US-0063738P.  
 PR 29-OCT-1997; 97US-0064215P.  
 PR 31-OCT-1997; 97US-0063870P.  
 PR 31-OCT-1997; 97US-0064103P.  
 PR 03-NOV-1997; 97US-0064248P.  
 PR 07-NOV-1997; 97US-0064809P.  
 PR 12-NOV-1997; 97US-0065186P.  
 PR 17-NOV-1997; 97US-0065846P.  
 PR 18-NOV-1997; 97US-0065693P.  
 PR 21-NOV-1997; 97US-0066120P.  
 PR 21-NOV-1997; 97US-0066364P.  
 PR 24-NOV-1997; 97US-0066453P.  
 PR 24-NOV-1997; 97US-0066466P.  
 PR 24-NOV-1997; 97US-0066511P.  
 PR 24-NOV-1997; 97US-0066770P.  
 PR 24-NOV-1997; 97US-0066772P.  
 PR 25-NOV-1997; 97US-0066840P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 XX Wood WI, Gurney AL, Goddard A, Pennica D, Chen J, Yuan J;  
 XX  
 DR WPI: 1999-229533/19.  
 DR N-PSDB; AAX52250.

XX  
 PT New isolated human genes and polypeptides used in, e.g. treatment of  
 PT gastrointestinal ulceration.  
 XX  
 PS Claim 12; Fig 74; 320pp; English.  
 XX  
 CC AAY13344-403 represent secreted and transmembrane human proteins. The  
 CC cDNA sequences are obtained from cDNA libraries, prepared from fetal  
 CC lung, fetal kidney, fetal brain, and fetal retina. The  
 CC encoded polypeptides have specific uses based on their homology to known  
 CC polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated  
 CC with the preservation and maintenance of gastrointestinal mucosa and the  
 CC repair of acute and chronic mucosal lesions (e.g. enterocolitis,  
 CC Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital  
 CC microvillus atrophy), skin diseases associated with abnormal keratinocyte  
 CC differentiation (e.g. psoriasis, epithelial cancers such as lung squamous  
 CC cell carcinoma of the vulva and gliomas), potent effects on cell growth  
 CC and development, diseases related to growth or survival of nerve cells  
 CC including Parkinson's disease, Alzheimer's disease, ALS, neuropathies or  
 CC cancer. PRO265 can be used as for fibromodulin, e.g. for reducing dermal  
 CC scarring. PRO264 can be used as a target for anti-tumor drugs. PRO533 may  
 CC be used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can  
 CC be used as an anti-thrombotic agent; PRO287 polypeptides and portions may  
 CC have therapeutic applications in wound healing and tissue repair; PRO317  
 CC can be used for treating problems of the kidney, uterus, endometrium,  
 CC blood vessels, or related tissue, e.g. in the heart of genital tract  
 XX  
 SQ Sequence 322 AA;  
 Alignment Scores:  
 Pred. No.: 3,74e-163 Length: 322  
 Score: 1657.00 Matches: 322  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 45.98% Indels: 0  
 DB: 2 Gaps: 0  
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 QY 183 ATGCCAGGTGCTTCAGCTGGTGTGTCTTCTCACTCCATCGCACACAGGCTCTGT 242  
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 Db 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20  
 QY 243 GTCGAAGGCTCTTCGCTGCAGAGAGCTTCCATCCAGGTGTCATGAGATTATGGGG 302  
 |||||  
 Db 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40  
 QY 303 ATCACCTTGTGAGCAAAAGCGAACACGACGAGCTGAATTTCCACAGAGCTAAGCAGGCC 362  
 |||||  
 Db 41 IleThrLeuValSerLysLysAlaAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
 QY 363 TGTAGGCTGCTGGGACTAAGTTTGGCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 422  
 |||||  
 Db 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
 QY 423 AGCTTTGAAACTTGACGTATGCGTGGGTGGGTGGAGATGAGATTCGTCGTCTCTAGGATT 482  
 |||||  
 Db 81 SerPheGluThrCysSerTyrglyTrpValGlyAspGlyPheValIleSerArgIle 100  
 QY 483 AGCCCAAAACCCCAAGTGGGAAATAATGGGTGGGTGGTCTGATTGGGAAGGTTCCAGTG 542  
 |||||  
 Db 101 SerProAsnProLysCysGlyAsnGlyValGlyValLeuIleTrpLysValProVal 120  
 QY 543 AGCCGACAGTTTGCAGCCTATTGTTTACAACTCATCTGATCTACTTGGACTACTCGTCGATT 602  
 |||||  
 Db 121 SerArgGlnPheAlaAlaTyrcystyrAsnSerSerAspThrTrpThrAsnSerCysile 140  
 QY 603 CCAGAAATATCACCCAAAGATCCCATATTTCAACACTCAAACTCAAACTGCAACAAACAACA 662  
 |||||  
 Db 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
 QY 663 GAATTTATTGTCAGTGACGTACCTACTCGGTGGGATCCCTTACTCTACTACATACCTGCC 722  
 |||||







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QY 603 CCAGAAATTATCCACCACCAAGATCCCATATTACACACTCAAACTGCACACACAAACA 662
Db 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
QY 663 GAAATTATTGTCAGTGACAGTACTACTCGGTGGCATCCCTTACTCTACATACTGCC 722
Db 161 GluPheIleValSerAspSerThrThrValAlaSerProTyrSerThrIleProAla 180
QY 723 CCTACTACTCTCTCTGCTCCAGCTTCCATCTTATTCACGGAGAAAAAATGATT 782
Db 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgLysLysLeuIle 200
QY 783 TGTGTACAGAGTTTATGAACTAGCACCATGCTCTACAGAACTGAACATTGTT 842
Db 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
QY 843 GAAATAAAGCAGCATTTCAAGATCAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 902
Db 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
QY 903 CTAGTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 962
Db 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysThrValLys 260
QY 963 AGGTATGTGAAGGCTCTCCCTTTTACAAACAAGATCAGCAGAGGAATGATCGAAAC 1022
Db 261 ArgThrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280
QY 1023 AAAGTAGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1082
Db 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
QY 1083 GATAAAACCCAGAGAGTCCAAAGAGTCCAAAGAGTCCAAAGAGTCCAAAGAGTCC 1142
Db 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
QY 1143 GAAGTT 1148
Db 321 GluVal 322

RESULT 6
ID AAB87528 standard; protein; 322 AA.
XX AC AAB87528;
XX DT 15-MAY-2001 (first entry)
XX DE Human PRO263.
XX KW Human; PRO protein; mapping.
XX OS Homo sapiens.
XX PN WO2001163118-A2.
XX PD 08-MAR-2001.
XX PF 24-AUG-2000; 2000WO-US023328.
XX PR 01-SEP-1999; 99WO-US020111.
XX PR 15-SEP-1999; 99WO-US021090.
XX PR 07-DEC-1999; 99US-0169495P.
XX PR 11-JAN-2000; 2000US-0170262P.
XX PR 18-FEB-2000; 2000WO-US004341.
XX PR 22-FEB-2000; 2000WO-US004342.
XX PR 01-MAR-2000; 2000WO-US004414.
XX PR 03-MAR-2000; 2000WO-US005601.
XX PR 21-MAR-2000; 2000US-0187202P.
XX PR 30-MAR-2000; 2000WO-US008439.
XX PR 25-APR-2000; 2000US-0199397P.

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PR 22-MAY-2000; 2000WO-US014042.
PR 05-JUN-2000; 2000US-0209832P.
XX PA (GETH ) GENENTECH INC.
XX Eton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WL;
XX WPI; 2001-183260/18.
DR N-PSDB; AAF92060.
XX Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
PT biology, including use as hybridization probes, and in chromosome and
PT gene mapping.
XX Claim 12; Fig 6; 278pp; English.
XX The present sequence is a human PRO polypeptide (secreted and
CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
CC anti-PRO antibodies are useful for preparation of a medicament useful in
CC the treatment of a condition which is responsive to the PRO protein,
CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
CC employed as molecular weight markers for protein electrophoresis. The PRO
CC coding sequence has applications in molecular biology, including use as
CC hybridisation probes, and in chromosome and gene mapping
XX Sequence 322 AA;
SQ

Alignment Scores:
Pred. No.: 3,74e-163 Length: 322
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.98% Indels: 0
DB: 4 Gaps: 0

US-10-079-111-2 (1-2029) x AAB87528 (1-322)
QY 183 ATGGCCAGGTCTTCAGCCTGGTGTGTTGCTTCTCATTCTGCACACGAGGCTCTG 242
Db 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleThrThrArgLeuLeu 20
QY 243 GTCCAGGCTCTTTCGTCGACAGAGCTTTCATCCAGGTGTCATCGAGAATTATGGG 302
Db 21 ValGlnGlySerLeuArgAlaGluGluSerIleGlnValSerCysArgIleMetGly 40
QY 303 ATCACCTTGTGAGCAAAAGCGCAACACGACAGCTGAATTTCCACAGAGCTAAGGAGCC 362
Db 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuLeuAsnPheThrGluAlaLysGluAla 60
QY 363 TGTAGCTGCTGGGACTAAGTTTGGCGGACAGGACCAAGTTGAAACAGCCTTGAAGCT 422
Db 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
QY 423 AGCTTTGAAACTTGACAGCTATCGCTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 482
Db 81 SerPheGluThrCysSerThrGlyThrValGlyAspGlyPheValIleSerArgIle 100
QY 483 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 542
Db 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleThrLysValProVal 120
QY 543 AGCCGACAGTTTGGAGCCTATTGTTACAACTCATCTGATCTGACTTGGACTTAACCTGTCG 602
Db 121 SerArgGlnPheAlaAlaTyrCysThrAsnSerSerAspThrThrThrAsnSerCysIle 140
QY 603 CCAGAAATTATCCACCACCAAGATCCCATATTACAACTCAAACTGCACACACAAACA 662
Db 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
QY 663 GAATTTATTGTCAGTGACAGTACTACTCGGTGGCATCCCTTACTCTACATACTGCC 722
Db 161 GluPheIleValSerAspSerThrThrValAlaSerProTyrSerThrIleProAla 180

```

QY 723 CCTACTACTCTCTCTCAGCTTCCACTTCTATTCCAGCGAAGAAAATGATT 782  
 Db 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200  
 QY 783 TGTGTCACAGAAGTTTTTATGAAACTAGCACCATGCTACAGAAACTGAACCATTTGTT 842  
 Db 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
 QY 843 GAAATAAGCAGCATTCAGAAATGAAGTGTGGGTGGAGGTGCCCGCGCTCTG 902  
 Db 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240  
 QY 903 CTAGTCTCTCTCTCTCTCTTTTGTGCTGCAGCTGGTCTTGGAATTTGCTATGTCAAA 962  
 Db 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
 QY 963 AGGTATGTGAAGCCTTCCTCTTTTACAAACAAGAAATCAGCAGAAGAAATGATCGAAACC 1022  
 Db 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
 QY 1023 AAAGTAGTAAAGGAGAGAGGCCAATGATAGCAACCTTAATGAGGAATCAAGAAAAT 1082  
 Db 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
 QY 1083 GATAAAACCCAGACAGTCCAGAGTCCCAAGCAAAACTACCGTGCATGCCCTGGAGCT 1142  
 Db 301 AspLysAsnProGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
 QY 1143 GAAGTT 1148  
 Db 321 GluVal 322

## RESULT 7

AAB88391  
 ID AAB88391 standard; protein; 322 AA.

AC AAB88391;

DT 23-MAY-2001 (first entry)

XX Human membrane or secretory protein clone P8EC0135.

KW Human; secretory protein; membrane protein; vaccine; gene therapy;  
 KW rheumatoid arthritis; diabetes.

XX Homo sapiens.

XX EP1067182-A2.

XX 10-JAN-2001.

XX 07-JUL-2000; 2000EP-00114090.

XX 08-JUL-1999; 99JP-00194179.

PR 11-JAN-2000; 2000JP-00118775.

XX 02-MAY-2000; 2000JP-00183766.

XX (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;

DR WPI; 2001-093989/11.

DR N-PSDB; AAF93818.

XX Nucleic acids encoding secretory proteins/membrane proteins, useful in  
 PT gene therapy or as candidate target molecules in drug development.

XX Claim 1; SEQ ID NO 150; 609pp + Sequence Listing; English.

XX This invention relates to nucleic acid sequences AAF93744 - AAF93916  
 CC which encode human secretory or membrane proteins represented by AAB88317  
 CC - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and

CC AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the  
 CC invention. The invention also includes methods for the production of  
 CC antibodies directed against the proteins, and cDNA sequences, which can  
 CC be used in vaccines. The polynucleotide sequences can be used in gene  
 CC therapy. The polynucleotide sequences and the proteins they encode may be  
 CC used in the prevention, treatment and diagnosis of diseases associated  
 CC with inappropriate secretory protein/membrane protein expression. The  
 CC nucleic acids and complementary sequences may also be used as DNA probes  
 CC in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect  
 CC and quantitate the presence of similar nucleic acid sequences in samples.  
 CC They may also be used to study the expression and function of secretory  
 CC proteins/membrane polypeptides and their role in metabolism. The  
 CC polypeptides may be used as antigens in the production of antibodies  
 CC against them and in assays to identify modulators (agonists and  
 CC antagonists) of expression and activity. The antibodies and antagonists  
 CC may also be used as therapeutic agents to down regulate expression and  
 CC activity. The antibodies may also be used as diagnostic agents for  
 CC detecting the presence of the polypeptides in samples (e.g. by enzyme  
 CC linked immunosorbent assay (ELISA)). Examples of diseases which may be  
 CC treated include rheumatoid arthritis and diabetes

XX Sequence 322 AA;

## Alignment Scores:

Pred. No.: 3 74e-163 Length: 322  
 Score: 1657.00 Matches: 322  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 45.98% Indels: 0  
 DB: 4 Gaps: 0

US-10-079-111-2 (1-2029) x AAB88391 (1-322)

QY 183 ATGCCAGGTGCTTCAGCTGTGTGCTTCTCACTTCATCGACACGAGGTCTCTG 242  
 Db 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTyrThrArgLeuLeu 20  
 QY 243 GTCCAAGGCTCTTTCGGTGCAGAGAGCTTTTCATCCAGGTGTCATGAGATTATGGGG 302  
 Db 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40  
 QY 303 ATCACCTTGTGACAAAAAGCGAACACAGACAGCTGAATTTCCACAGAACTAAGAGGCC 362  
 Db 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
 QY 363 TGTAGGTCTGGGACTAAGTTTGGCCGCAAGACCAAGTTGAAACAGCCTTGAAGCT 422  
 Db 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
 QY 423 AGCTTTGAAACTTCAGCTATGGCTGGCTGGAGATGGATTCTGCTCATCTCTAGGATT 482  
 Db 81 SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle 100  
 QY 483 AGCCCAAAACCCCAAGTGTGGAAAAATGGGGTGGTCTCTGATTGGAAGTTCAGTG 542  
 Db 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTyrLysValProVal 120  
 QY 543 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTACTGTCGTAACCTCGTCG 602  
 Db 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerSerAspThrTyrThrAsnSerCysIle 140  
 QY 603 CCAGAAATATCACCACCAAGATCCCATATTTCACACTCAAACTGCAACACACAAACACA 662  
 Db 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
 QY 663 GAATTTATGTGACGACAGTACTACTCGGTGGCATCCCTTACTTACTACATACCTGCC 722  
 Db 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
 QY 723 CCTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTTCACGGAGAAAAAATTTGATT 782  
 Db 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200



```

QY 783 TGTGTCACAGAGCTTTTATGGAACTAGCACCATGCTACAGAACTGAACCATTTGTT 842
Db |||||ThruValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
QY 843 GAAAAATAAGCAGCATTCAGAAATGAAGCTGTCTGGGTTTGGAGGTGTCCCCACGGCTCTG 902
Db |||||GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
QY 903 CTAGTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 962
Db |||||LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyPheCysTyrValLys 260
QY 963 AGGTATGTGAAGCCCTTCCCTTTTCAAAACAAGAAATCAGCAGAGGAATGATCGAAACC 1022
Db |||||ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
QY 1023 AAAGTAGTAAAGGAGGAGGAGGCAATGATAGCAACCTAATGAGGAATCAAGAAACT 1082
Db |||||LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
QY 1083 GATAAAACCCAGAGAGTCCAGAGTCCAGAGTCCAGCAAACTACCGTGGATGCTTGAAGCT 1142
Db |||||AspLysAsnProGluGluSerLysSerProSerLysThrValArgCysLeuGluAla 320
QY 1143 GAAGTT 1148
Db |||||
321 GluVal 322

RESULT 8
ABG95853
ID ABG95853 standard; protein; 322 AA.
AC ABG95853;
XX
XX
DT 10-DEC-2002 (first entry)
DE
DE Human secreted/transmembrane protein PRO263.
KW Human; secreted protein; transmembrane protein; antirheumatic;
KW antirheumatic; osteopathic; sports-related joint problem;
KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.
XX
XX Homo sapiens.
OS
PN US2002119130-A1.
XX
PD 29-AUG-2002.
XX
PF 06-DEC-2001; 2001US-0006867.
XX
XX 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0064215P.
PR 22-APR-1998; 98US-0082797P.
PR 29-APR-1998; 98US-0083495P.
PR 15-MAY-1998; 98US-0085579P.
PR 02-JUN-1998; 98US-0087759P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 11-JUN-1998; 98US-0088863P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089653P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 24-JUN-1998; 98US-0090444P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090696P.

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PR 26-JUN-1998; 98US-0090862P.
PR 02-JUL-1998; 98US-0091628P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097979P.
PR 01-SEP-1998; 98US-0098749P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100662P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100930P.
PR 23-SEP-1998; 98US-0101279P.
PR 24-SEP-1998; 98US-0101475P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101743P.
PR 30-SEP-1998; 98US-0101916P.
PR 06-OCT-1998; 98US-0102570P.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 22-DEC-1999; 99WO-US021194.
PR 18-FEB-2000; 99WO-US030720.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004342.
PR 01-MAR-2000; 2000WO-US005601.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032378.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUL-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX
XX (GETH ) GENENTECH INC.
PA
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
XX WPI: 2002-731348/79.
XX N-PSDB; ABS74380.
XX
XX New isolated secreted and transmembrane PRO polypeptide useful for
PT modulating biological activity of a cell, or for treating sports-related
PT joint problems, osteoarthritis or rheumatoid arthritis.
XX
XX Claim 20; Fig 6; 399pp; English.
XX
XX The invention relates to an isolated secreted and transmembrane PRO
CC polypeptide having 80 % sequence identity to a sequence appearing as
CC ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
CC extracellular domain of the proteins with their associated signal peptide

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CC or lacking its associated signal peptide. Also included are the nucleic  
CC acids encoding the proteins, vectors, host cells, fusion proteins and  
CC antibodies which specifically bind to the proteins. The proteins are  
CC useful for detecting a polypeptide designated as A, B, C or D in a sample  
CC suspected of containing A, B, C or D polypeptide, by contacting the  
CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)  
CC and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide  
CC conjugate in the sample, where the formation of the conjugate is  
CC indicative of the presence of an A, B, C or D polypeptide in the sample,  
CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a  
CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801  
CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a  
CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises  
CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,  
CC H or I polypeptide is labeled with a detectable label or is attached to a  
CC solid support. The proteins are useful for linking a bioactive molecule  
CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,  
CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.  
CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,  
CC or I, or antibodies against them are useful for modulating a biological  
CC activity of a cell expressing a polypeptide designated as A, B, C or D or  
CC E, F, G, H, or I. The cell is killed. The proteins are useful for  
CC identifying agonists or antagonists, for the preparation of a medicament  
CC useful in the treatment of a condition which is responsive to the  
CC proteins, as molecular weight markers for protein electrophoresis  
CC purposes, and as therapeutic agents for treating sports-related joint  
CC problems, articular cartilage defects, osteoarthritis or rheumatoid  
CC arthritis. Nucleic acids encoding the proteins are useful as  
CC hybridisation probes, in chromosome and gene mapping, in the generation  
CC of anti-sense RNA and DNA, for the preparation of the proteins, to  
CC generate transgenic or knockout animals which are useful in the  
CC development and screening of therapeutic useful reagents, for chromosome  
CC identification, and in gene therapy. The antibody is useful as a  
CC therapeutic agent, in a diagnostic assay and for affinity purification of  
CC the protein from recombinant cell culture natural sources. The present  
CC sequence represents a novel secreted or transmembrane protein of the  
CC invention

XX Sequence 322 AA;

## Alignment Scores:

Pred. No.:	3,74e-163	Length:	322
Score:	1657.00	Matches:	322
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	45.98%	Indels:	0
DB:	5	Gaps:	0

US-10-079-111-2 (1-2029) x ABG95853 (1-322)

QY	183	ATGCCAGGTGCTTCAGCTGGTGTGCTTCTCACTTCATCTGGACCGAGGCTCCTG	242
DB	1	MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeu	20
QY	243	GTCCAGAGGCTCTTGCGTGCAGAAAGCTTTCATCCAGGTGTCATGCAGAAATTATGGGG	302
DB	21	ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly	40
QY	303	ATCACCTCTGTGAGCAAAAGCGCAACACGACGTGAATTTTCAGAGCTAAGAGGCC	362
DB	41	IleThrLeuValSerIlyLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
QY	363	TGTAGGCTCGTGGACTAGTTTGGCGCGCAAGCAACAGTTCGAACAGCTTGAAGCT	422
DB	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
QY	423	AGCTTTTGAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCGTGCTCATCTCTAGATT	482
DB	81	SerPheGluThrCysSerTyrglyTrpValGlyAspGlyPheValValIleSerArgIle	100
QY	483	AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCTGATTTGGAAAGGTTCCAGTG	542
DB	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120

QY	543	AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATACTTGGACTTAACCTGTCGATT	602
DB	121	SerArgGlnPheAlaAlaTyrcysTyraenSerSerAspThrTrpThrAsnSerCysIle	140
QY	603	CCAGAAATATCACCAACAAAGATCCCATATTCAACACTCAAACTCAACACAAACAACA	662
DB	141	ProGluIleIleThrThrLysaspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
QY	663	GAATTTATTGTCAGTGACAGTACCTACTCGTGGGATCCCTTACTCTCAATACCTGCC	722
DB	161	GluPheIleValSerAspSerThrTyraenValAlaSerProTyraenThrIleProAla	180
QY	723	CCTACTACTACTCTCTCTCTCCAGCTTCCACTTCTATTCCAGGAGAAAAAATTGATT	782
DB	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgargLysLysLeuIle	200
QY	783	TGTGTCCACAGAAGTTTTTATGGAACTAGCACCATGTCTACAGAAACTGAACCATTTGT	842
DB	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
QY	843	GAATAAAGCAGCATTCAGATGAAGCTGCTGGGTTTGGAGGTGTCCCGCGCTCTG	902
DB	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
QY	903	CTAGTCTTGTCT	962
DB	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyraenLys	260
QY	963	AGTATGTGAAGCCCTTCCCTTTTACAAACAAGATCAGCAGAGGAAATGATCGAAACC	1022
DB	261	ArgTyraenValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr	280
QY	1023	AAAGTAGTAAAGAGAGAGAGGCGCCATGATAGCAACCTTAATGAGAGAAATCAAGAAACT	1082
DB	281	LysValValLysGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
QY	1083	GATAAAACCCAGAGAGTCCAGAGTCCCAAGAGTCCCAAGCAAAACTACCGTGGGATCGCTGGAAGCT	1142
DB	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
QY	1143	GAAGTT 1148	
DB	321	GluVal 322	
RESULT 9			
ABB84832			
ID	ABB84832		
XX	standard; protein; 322 AA.		
AC	ABB84832;		
XX			
DT	16-MAY-2002 (first entry)		
DE	Human PRO263 protein sequence SEQ ID NO:32.		
XX	Human; angiogenesis; cardiac; cytostatic; antiangiogenic; hypotensive;		
KW	vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;		
KW	gene therapy; cardiovascular disorder; endothelial disorder; cancer;		
KW	angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;		
KW	age-related macular degeneration; arterial restenosis; angina;		
KW	rheumatoid arthritis; myocardial infarction; thrombophlebitis;		
KW	lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;		
XX	wound healing; chromosome mapping; gene mapping.		
OS	Homo sapiens.		
XX			
PN	WO200200690-A2.		
XX			
PD	03-JAN-2002.		
XX			
PF	20-JUN-2001; 2001WO-US019692.		
XX			
PR	23-JUN-2000; 2000US-0213637P.		

PR 20-JUL-2000; 2000US-0219556P.  
 PR 25-JUL-2000; 2000US-0220624P.  
 PR 25-JUL-2000; 2000US-0220664P.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 02-AUG-2000; 2000US-0222695P.  
 PR 17-AUG-2000; 2000US-00643657.  
 PR 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 07-SEP-2000; 2000US-0230978P.  
 PR 18-SEP-2000; 2000US-00664610.  
 PR 18-SEP-2000; 2000US-00665350.  
 PR 24-OCT-2000; 2000US-0242922P.  
 PR 08-NOV-2000; 2000US-00709238.  
 PR 10-NOV-2000; 2000WO-US030952.  
 PR 01-DEC-2000; 2000WO-US030873.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 20-DEC-2000; 2000US-00747259.  
 PR 20-DEC-2000; 2000WO-US034956.  
 PR 22-JAN-2001; 2001US-00767609.  
 PR 28-FEB-2001; 2001US-00796498.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-MAR-2001; 2001WO-US006666.  
 PR 09-MAR-2001; 2001US-00802706.  
 PR 14-MAR-2001; 2001US-00808689.  
 PR 22-MAR-2001; 2001US-00816744.  
 PR 05-APR-2001; 2001US-00828366.  
 PR 10-MAY-2001; 2001US-00854208.  
 PR 10-MAY-2001; 2001US-00854280.  
 PR 25-MAY-2001; 2001US-00866034.  
 PR 25-MAY-2001; 2001US-00866034.  
 PR 25-MAY-2001; 2001WO-US017092.  
 PR 30-MAY-2001; 2001US-00870574.  
 PR 30-MAY-2001; 2001WO-US017443.  
 PR 01-JUN-2001; 2001WO-US017800.  
 XX (GETH ) GENENTECH INC.  
 XX  
 XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
 PI Stephan JF, Watanabe CK, Williams PM, Wood WL, Ye W;  
 XX  
 DR WPI; 2002-090516/12.  
 DR N-PSDB; ABL88087.  
 XX  
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal.  
 XX  
 PS Claim 11; Fig 32; 565pp; English.  
 XX  
 CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,  
 CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic  
 CC activities, and can be used in gene therapy. The PRO polynucleotides,  
 CC proteins, agonists and antagonists are useful for treating or diagnosing  
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.  
 CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,  
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
 CC healing. The PRO polynucleotides have applications in molecular biology,  
 CC including use as hybridisation probes, and in chromosome and gene  
 CC mapping. ABL88259 to ABL88267 represent primers and probes used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 322 AA;

Alignment Scores:  
 Pred. No.: 3,74e-163 Length: 322  
 Score: 1657.00 Matches: 322  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 45.98% Indels: 0

DB: 5 Gaps: 0  
 US-10-079-111-2 (1-2029) x ABB84832 (1-322)  
 QY 183 ATGGCCAGGTGCTTCAGGCTGTGTGCTTCTCACTTCCATCTGACACGAGGCTCTG 242  
 |||||  
 Db 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrrThrThrArgLeuLeu 20  
 |||||  
 QY 243 GTCCAAAGGCTCTTTCGCTGCAGAGAGCTTTCATCCAGGTGTCATGCAGAAATATGGGG 302  
 |||||  
 Db 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
 |||||  
 QY 303 ATCACCCCTTGTGAGCAAAAGCGCAACGACGAGCTGAATTCACAGAACTAAGGAGGCC 362  
 |||||  
 Db 41 IleThrLeuValSerLysLysAlaAsnGlnLeuAsnPheThrGluAlaLysGluAla 60  
 |||||  
 QY 363 TGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 422  
 |||||  
 Db 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
 |||||  
 QY 423 AGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGGTCACTCTAGGATT 482  
 |||||  
 Db 81 SerPheGluThrCysSerTyrGlyTrrValGlyAspGlyPheValValIleSerArgIle 100  
 |||||  
 QY 483 AGCCCAAAACCCCAAGTGTGGGAAAATGGGTGGGTGCTGATTTGGAAGCTTCCAGTG 542  
 |||||  
 Db 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrrLysValProVal 120  
 |||||  
 QY 543 AGCCGACAGTTTGCAGCCTATTGTTTACAACCTCATCTGATCTTGGACTAATCTGTCGATT 602  
 |||||  
 Db 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrrThrAsnSerCysIle 140  
 |||||  
 QY 603 CCAGAAATATCACCAACCAAGATCCCATATTCACACTCAACTCAACACTGCAACACAACA 662  
 |||||  
 Db 141 ProGluIleIleThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
 |||||  
 QY 663 GAATTTATTGTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 722  
 |||||  
 Db 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
 |||||  
 QY 723 CCTACTACT 782  
 |||||  
 Db 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200  
 |||||  
 QY 783 TGTGTACAGAAAGTTTTTATGGAACCTAGCACCATGTCTACAGAACTGAACCATTTGTT 842  
 |||||  
 Db 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
 |||||  
 QY 843 GAAATAAAGCAGCATTCAAGAATCAAGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTG 902  
 |||||  
 Db 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
 |||||  
 QY 903 CTAGTGCTTGTCT 962  
 |||||  
 Db 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
 |||||  
 QY 963 AGGTATGCAAGGCT 1022  
 |||||  
 Db 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280  
 |||||  
 QY 1023 AAAGTAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1082  
 |||||  
 Db 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluLysLysLysThr 300  
 |||||  
 QY 1083 GATAAAAAACCCAGAGAGTCCAAAGAGTCCAAAGAGTCCAAAGAGTCCAAAGAGTCCAAAG 1142  
 |||||  
 Db 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
 |||||  
 QY 1143 GAAGTT 1148  
 |||||  
 Db 321 GluVal 322  
 |||||  
 RESULT 10

(WOOD//) WOOD W I.

Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF; Stephan JF, Watanabe CK, Williams PW, Wood WI, Ye W; WPI; 2002-171999/22. N-PSDB; ABL95576.

One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.

Claim 11; Fig 32; 567pp; English.

The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial stenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a PRO protein of the invention

XX Sequence 322 AA;

Alignment Scores:

Pred. No.:	3,74e-163	Length:	322
Score:	1657.00	Matches:	322
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	45.98%	Indels:	0
DB:	5	Gaps:	0

US-10-079-111-2 (1-2029) x ABB95438 (1-322)

Qy	183	ATGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACTTCATCTGCACAGAGCTCCTG	242
Db	1	MetAlaArgCysPheSerLeuValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu	20
Qy	243	GTCCAAAGGCTCTTTGGTGCAGAGAGCTTTCCATCCAGGTGTCTATCAGAAATTATCGGG	302
Db	21	ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly	40
Qy	303	ATCACCTCTGTGAGCAAAAGCGACAGAGCTGAATTCACAGAGCTTAGGAGGCC	362
Db	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
Qy	363	TGTAGGCTCTGGGACTAAGTTGTGCCCGCAGACCAAGTGAACAGCCTTGAAAGCT	422
Db	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
Qy	423	AGCTTTGAAACTTGACGATATGGCTGGGTTGGAGATGGATTCGTTGTCATCTCTAGGATT	482
Db	81	SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle	100
Qy	483	AGCCCAAAACCCAGCTGTGGGAAAATGGGTGGGTCTCTGATTCGAGGTTCCAGTG	542
Db	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTyrLysValProVal	120
Qy	543	AGCCACAGCTTTGCAGCCTATTGTTACAACTCATCTGATCTTGCATCTAACTCGTCATT	602
Db	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTyrThrAsnSerCysIle	140
Qy	603	CCAGAAATTATCACCAAGATGCCCATATTCAACTCAAACTGCAACACAAACAACA	662
Db	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Qy	663	GAATTATTGTGTCAGTGACGATCTACTTCGGTGCATCCCTTACTCTCAAACTACCTGCC	722
Db	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Qy	723	CCTACTACTACTCTCCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTTGATT	782

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|||||
181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLeuIle 200
QY TGTGTACAGAGTATTTTATGGAACTAGCACCATGTCTACAGAACTGAACATTTGTT 842
Db |||||||
201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
QY GAAATAAGCAGCATTCAAGAAATCAAGCTGCTGGTGGTGGAGGTGCTCCACGGCTCTG 902
Db |||||||
221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
QY CTAGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 962
Db |||||||
241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysIleValLys 260
QY 963 AGGTATGTGAGGCTCTCCCTTTTCAACAAGATCAGCAGAGAAATGATCGAAACC 1022
Db |||||||
261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
QY 1023 AAAGTAGTAAAGGAGGAGGAGCCATGATGACCACTTATGAGCAATCAAGAAACT 1082
Db |||||||
281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluLysLysThr 300
QY 1083 GATAAAACCCAGAGAGTCCAAAGAGTCCAAAGCAAACTACCGTGGATGCTCGAAGCT 1142
Db |||||||
301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
QY 1143 GAAGTT 1148
Db |||||||
321 GluVal 322

RESULT 11
ABU71625
ID ABU71625 standard; protein; 322 AA.
XX AC ABU71625;
XX DT 16-JUN-2003 (first entry)
XX DE Human PRO polypeptide #36.
KW Human; PRO; secreted polypeptide; transmembrane polypeptide;
KW pathological disorder; cardiac insufficiency disorder; protein secretion;
KW pancreas; diabetes; gastrointestinal mucosa; mucosal lesion; psoriasis;
KW skin disease; keratinocyte differentiation; epithelial cancer; tumour;
KW lung squamous cell carcinoma; epidermoid carcinoma; vulva; glioma;
KW cytostatic; cardiac; endocrine; antidiabetic; gastrointestinal;
KW antiulcer; dermatological; vulnery.
XX OS Homo sapiens.
XX PN US2002146709-A1.
XX PD 10-OCT-2002.
XX PF 18-JUL-2001; 2001US-00909088.
XX PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063122P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 01-DEC-1998; 98WO-US025108.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 20-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX (GETH ) GENENTECH INC.
XX PA Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gerber H, Gerritsen ME, Goddard A;
PI Godowski FJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX WPI; 2003-328338/31.
```



PR 27-OCT-1997; 97US-0063329P.  
 PR 28-OCT-1997; 97US-0063541P.  
 PR 28-OCT-1997; 97US-0063542P.  
 PR 28-OCT-1997; 97US-0063544P.  
 PR 28-OCT-1997; 97US-0063549P.  
 PR 28-OCT-1997; 97US-0063550P.  
 PR 28-OCT-1997; 97US-0063564P.  
 PR 29-OCT-1997; 97US-0063435P.  
 PR 29-OCT-1997; 97US-0063704P.  
 PR 29-OCT-1997; 97US-0063732P.  
 PR 29-OCT-1997; 97US-0063733P.  
 PR 29-OCT-1997; 97US-0063735P.  
 PR 29-OCT-1997; 97US-0064215P.  
 PR 31-OCT-1997; 97US-0063870P.  
 PR 31-OCT-1997; 97US-0064103P.  
 PR 03-NOV-1997; 97US-0064248P.  
 PR 07-NOV-1997; 97US-0064809P.  
 PR 12-NOV-1997; 97US-0065186P.  
 PR 17-NOV-1997; 97US-0065846P.  
 PR 18-NOV-1997; 97US-0065693P.  
 PR 21-NOV-1997; 97US-0066120P.  
 PR 21-NOV-1997; 97US-0066364P.  
 PR 24-NOV-1997; 97US-0066453P.  
 PR 24-NOV-1997; 97US-0066466P.  
 PR 24-NOV-1997; 97US-0066511P.  
 PR 24-NOV-1997; 97US-0066770P.  
 PR 24-NOV-1997; 97US-0066772P.  
 PR 10-SEP-1998; 98WO-US018824.  
 PR 14-SEP-1998; 98WO-US019177.  
 PR 16-SEP-1998; 98WO-US019330.  
 PR 17-SEP-1998; 98WO-US019437.  
 PR 01-DEC-1998; 98WO-US025108.  
 PR 08-SEP-1999; 99WO-US020594.  
 PR 13-SEP-1999; 99WO-US020944.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 15-SEP-1999; 99WO-US021547.  
 PR 05-OCT-1999; 99WO-US023089.  
 PR 30-NOV-1999; 99WO-US028214.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 02-DEC-1999; 99WO-US028564.  
 PR 02-DEC-1999; 99WO-US028565.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 20-DEC-1999; 99WO-US030911.  
 PR 20-DEC-1999; 99WO-US030999.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 11-FEB-2000; 2000WO-US003565.  
 PR 22-FEB-2000; 2000WO-US004414.  
 PR 24-FEB-2000; 2000WO-US005004.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 20-MAR-2000; 2000WO-US007377.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 18-SEP-2000; 2000US-00665350.  
 XX (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;  
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;  
 PI Godowski P, Grimaldi JC, Gurney AL, Hillan KJ, Kijavini LJ;  
 PI Mathier JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;  
 PI Williams PW, Wood WI;  
 XX WPI: 2003-361832/34.  
 DR N-PSDB; ACA58457.  
 DR  
 XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or  
 PT PRO1868, useful in molecular biology, chromosome and gene mapping, in  
 PT generating antisense RNA and DNA, and in gene therapy.

XX  
 PS Claim 12; Fig 74; 474pp; English.  
 XX  
 CC The present invention relates to the isolation of novel human secreted  
 CC and transmembrane proteins (PRO polypeptides), and the polynucleotide  
 CC sequences encoding them. The polynucleotide sequences are useful in  
 CC molecular biology, as hybridisation probes, in chromosome and gene  
 CC mapping, in generating antisense RNA and DNA, and in gene therapy. The  
 CC polynucleotide sequences may also be used in preparing PRO polypeptides  
 CC by recombinant techniques, and in generating either transgenic animals or  
 CC knock-out animals which, in turn, are useful in the development and  
 CC screening of therapeutically useful reagents. The PRO polypeptides or  
 CC their antibodies are useful in preparing a medicament for treating a  
 CC condition responsive to the polypeptide or antibody, such as cancer,  
 CC Alzheimer's disease or ischaemia, and in various diagnostic assays.  
 CC ABU71445-ABU71505 represent human PRO polypeptides of the invention  
 XX  
 SQ Sequence 322 AA;  
 Alignment Scores:  
 Pred. No.: 3,74e-163 Length: 322  
 Score: 1657.00 Matches: 322  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 45.98% Indels: 0  
 DB: Gaps: 0

US-10-079-111-2 (1-2029) x ABU71480 (1-322)  
 QY 183 ATGGCCAGGTCTTCAGCCTGGTGTGCTTCTCCTCCATCTGGACACGAGGCTCCG 242  
 Db 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu 20  
 QY 243 GTCCAAGGCTTTTCGCTGCAGAGAGCTTTCCATCCAGGTGTCATGCAGAAATTATGGGG 302  
 Db 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
 QY 303 ATCACCTTGTGAGCAAAAGCGAACCGAGCTGAATTTACAGAACTAAGAGGCC 362  
 Db 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
 QY 363 TGTAGGCTGTGGGACTAAGTTTGGCGCAGAGACCAAGTTGAACACGCTTGAAGCT 422  
 Db 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
 QY 423 AGCTTTGAAACTTGACGCTATGGCTGGTGGATGGATTCGTCGTCATCTCTAGGATT 482  
 Db 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100  
 QY 483 AGCCCAAAACCAAGTGGGAAAATGGGTGGGTGCTCGATTTGGAGGTTCCAGTG 542  
 Db 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
 QY 543 AGCCGACAGATTGACGCTATTGTTACAACTCATCTGATCTTGGACTTAACCTCGTCATT 602  
 Db 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
 QY 603 CCAGAAATTATCACCAACCAAGATCCCATATTTCACACTCAAACTCAACACAAACAACA 662  
 Db 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
 QY 663 GAATTTATGTGTCAGTGACAGTACCTACTCGGTGGGATCCCTTACTCTACATACCTGCC 722  
 Db 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
 QY 723 CCTACTACT 782  
 Db 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLeuLeu 200  
 QY 783 TGTGTACAGAGATTTTATGAAACTAGACCACTGCTCTACAGAACTCAACCACTTTGTT 842  
 Db 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220





the PRO nucleic acid, a host cell comprising the vector, producing a PRO polypeptide (by culturing the host cell for the expression of the PRO polypeptide, and recovering the PRO polypeptide from the cell culture), an isolated PRO polypeptide (having at least 80% sequence identity to: (a) an amino acid sequence selected from the 61 PRO proteins; (b) an amino acid sequence encoded by a nucleic acid molecule deposited with an ATCC number [detailed in the specification]; or (c) an extracellular domain of a PRO polypeptide or to a PRO polypeptide lacking its associated signal peptide), a chimeric molecule comprising a PRO polypeptide of fused to a heterologous amino acid sequence, an anti-PRO antibody, detecting a PRO245 or PRO1868 in a sample suspected of containing the polypeptide, linking a bioactive molecule to a cell expressing a PRO245 or PRO1868 and modulating at least one biological activity of a cell expressing a PRO245 or PRO1868. Nucleic acids which encode PRO can be used to generate either transgenic animals or knock-out animals which may be used in the development and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy, in chromosome identification, as chromosome markers, or in generating probes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and the isolated nucleic acids may be used for recombinantly expressing those markers. The PRO polypeptides and nucleic acids may also be used in tissue typing. CC Anti-PRO antibodies are useful in diagnostic assays for PRO, and in CC affinity purification of PRO from recombinant cell culture or natural CC sources. The present sequence represents a PRO protein XX SQ Sequence 322 AA;

Alignment Scores:  
Pred. No.: 3,74e-163 Length: 322  
Score: 1657.00 Matches: 322  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 45.98% Indels: 0  
DB: 6 Gaps: 0

US-10-079-111-2 (1-2029) x ABU71926 (1-322)

QY	183	ATGGCCAGGTCTTCAGCTGGTGGTCTTCACCTCCATCCATCGACCGAGGCTCCTG	242
Db	1	MetAlaArgCysPheSerLeuValLeuLeuLeuLeuSerIleTrpThrArgLeuLeu	20
QY	243	GTCCAAGGCTCTTTCGGTCGACAGAGCTTTCCATCCAGGTGTCACGAGATTATGGG	302
Db	21	ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly	40
QY	303	ATCACCTTGTGAGCAAAAGCGAACCGAGCTGAATTCACAGAACTAAGGAGGCC	362
Db	41	IleThrLeuValSerIleLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60
QY	363	TCTAGGCTCTGGACTAAGTTGGCCGCAAGGACCAAGTTGMAACAGCCTTGAAGCT	422
Db	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80
QY	423	AGCTTTGAAACTTGACGCTATGCTGGTGGAGATGGATTCGTGCTCATCTCTAGGATT	482
Db	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle	100
QY	483	AGCCCAAAACCCCAAGTGTGGGAAAATGGGTGGGTGCTCTGATTGGAAAGTTCCAGTG	542
Db	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
QY	543	AGCCGACAGTTTGCAGCTATTGTTACACTCATCTGATACCTTGGACTTAACCTGTCATT	602
Db	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
QY	603	CCAGAAATATCACCAACCAAGATCCCATTTCAACACTCAAACTGCAACACAAACAACA	662
Db	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
QY	663	GAATTATTGTGAGTGACAGTACTTCTCGGTGGGATCCCTTACTCTACAATACCTGCC	722
Db	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180

QY	723	CCTACTACTACTCTCTCTCTCAGCTTCACCTTCTATTCACGAGAGAAAAAATTCATT	782
Db	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
QY	783	TGTGTGCACAGAGCTTTTATGGAACTAGCACCATCTCTACAGAACTGAACCATTTGTT	842
Db	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
QY	843	GAAATAAAGCAGCATTCAGATGAAGTGTGGGTTCGAGGTGTCCTCCACGGCTCTG	902
Db	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu	240
QY	903	CTAGTCT	962
Db	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
QY	963	AGTATGTGAAGGCTTCCT	1022
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QY	1023	AAAGTAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1082
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ABO01809  
ID ABO01809 standard; protein; 322 AA.  
XX  
AC ABO01809;  
DT 07-AUG-2003 (first entry)  
XX  
DE Novel human secreted and transmembrane protein PRO263.  
XX  
KW Human; secreted and transmembrane protein; PRO; pharmaceutical;  
KW diagnostic; biosensor; bioindicator; Parkinson's disease;  
KW Alzheimer's disease; inflammation; nephritis; wound healing;  
KW nerve repair; collateral blood vessel formation; cancer;  
KW colorectal cancer; haemorrhage; rheumatoid arthritis; diabetes;  
KW cirrhosis; fibrosis; restenosis; dermal fibrotic condition; keloid;  
KW scarring; ischaemia; stroke; hypertension; heart attack; atherosclerosis;  
XX infertility; gene therapy.  
XX Homo sapiens.  
XX OS  
XX US2002197671-A1.  
XX  
XX PD 26-DEC-2002.  
XX  
XX PF 17-JUL-2001; 2001US-00907824.  
XX  
XX PR 17-SEP-1997; 97US-0059113P.  
XX PR 17-SEP-1997; 97US-0059113P.  
XX PR 17-SEP-1997; 97US-0059117P.  
XX PR 17-SEP-1997; 97US-0059119P.  
XX PR 17-SEP-1997; 97US-0059121P.  
XX PR 17-SEP-1997; 97US-0059122P.  
XX PR 17-SEP-1997; 97US-0059184P.  
XX PR 18-SEP-1997; 97US-0059263P.  
XX PR 18-SEP-1997; 97US-0059266P.  
XX PR 15-OCT-1997; 97US-0062125P.  
XX PR 17-OCT-1997; 97US-0062285P.  
XX PR 17-OCT-1997; 97US-0062287P.  
XX PR 21-OCT-1997; 97US-0063486P.  
XX PR 24-OCT-1997; 97US-0062814P.

PR 24-OCT-1997; 97US-0062816P.  
 PR 24-OCT-1997; 97US-0063045P.  
 PR 24-OCT-1997; 97US-0063120P.  
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 PR 28-OCT-1997; 97US-0063541P.  
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 PR 28-OCT-1997; 97US-0063550P.  
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 PR 29-OCT-1997; 97US-0063435P.  
 PR 29-OCT-1997; 97US-0063704P.  
 PR 29-OCT-1997; 97US-0063732P.  
 PR 29-OCT-1997; 97US-0063734P.  
 PR 29-OCT-1997; 97US-0063735P.  
 PR 29-OCT-1997; 97US-0063738P.  
 PR 29-OCT-1997; 97US-0064215P.  
 PR 31-OCT-1997; 97US-0063870P.  
 PR 31-OCT-1997; 97US-0064103P.  
 PR 03-NOV-1997; 97US-0064248P.  
 PR 07-NOV-1997; 97US-0064809P.  
 PR 12-NOV-1997; 97US-0065186P.  
 PR 18-NOV-1997; 97US-0065846P.  
 PR 18-NOV-1997; 97US-0065693P.  
 PR 21-NOV-1997; 97US-0066120P.  
 PR 21-NOV-1997; 97US-0066364P.  
 PR 24-NOV-1997; 97US-0066453P.  
 PR 24-NOV-1997; 97US-0066466P.  
 PR 24-NOV-1997; 97US-0066511P.  
 PR 24-NOV-1997; 97US-0066770P.  
 PR 24-NOV-1997; 97US-0066772P.  
 PR 10-SEP-1998; 98WO-US018824.  
 PR 14-SEP-1998; 98WO-US019177.  
 PR 16-SEP-1998; 98WO-US019330.  
 PR 17-SEP-1998; 98WO-US019437.  
 PR 01-DEC-1998; 98WO-US020108.  
 PR 08-SEP-1999; 99WO-US020594.  
 PR 13-SEP-1999; 99WO-US020944.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 15-SEP-1999; 99WO-US021547.  
 PR 05-OCT-1999; 99WO-US023089.  
 PR 29-NOV-1999; 99WO-US028214.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 02-DEC-1999; 99WO-US028564.  
 PR 02-DEC-1999; 99WO-US028565.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 20-DEC-1999; 99WO-US030911.  
 PR 20-DEC-1999; 99WO-US030999.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 11-FEB-2000; 2000WO-US000356.  
 PR 22-FEB-2000; 2000WO-US000414.  
 PR 24-FEB-2000; 2000WO-US005004.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 20-MAR-2000; 2000WO-US007377.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 18-SEP-2000; 2000US-00665350.  
 XX  
 (GETH ) GENENTECH INC.  
 PA  
 XX Ashkenazi A, Botstein D, Desnovers L, Eaton DL, Ferrara N;  
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;  
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kijavini IJ;  
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;  
 PI Williams PM, Wood WI;

XX WPI; 2003-370793/35.  
 DR N-PSDB; ACD07564.  
 XX  
 PT New genes and secreted and transmembrane polypeptides (e.g. PRO245 or  
 PT PRO335), useful for treating or diagnosing e.g. Alzheimer's disease,  
 PT cancers, hemorrhage, rheumatoid arthritis, diabetes, cirrhosis, ischemia  
 PT or strokes.  
 XX Claim 12; Fig 74; 482pp; English.  
 XX  
 CC The invention describes a new isolated nucleic acid molecule comprising  
 CC the full length coding sequence of the DNA deposited with the American  
 CC Type Culture Collection (e.g. ATCC Deposit No. 209258) or a sequence  
 CC with at least 80% identity to a DNA encoding a PRO polypeptide comprising  
 CC any of 61 sequences having 164-1119 amino acids fully defined in the  
 CC specification. The PRO polypeptides or polynucleotides are useful as  
 CC pharmaceuticals, diagnostics, biosensors or bioreactors. These are  
 CC particularly useful for detecting or treating e.g. Parkinson's disease,  
 CC Alzheimer's disease, inflammations, nephritis, wound healing, nerve  
 CC repair, collateral blood vessel formation, cancers (e.g. colorectal  
 CC cancer), haemorrhage (or reduce risk for haemorrhage), rheumatoid  
 CC arthritis, diabetes, cirrhosis of the liver, fibrosis of the lungs,  
 CC restenosis, dermal fibrotic conditions (e.g. keloids or scarring),  
 CC ischaemia, strokes, hypertension, heart attacks, atherosclerosis, or  
 CC infertility in mammals (e.g. humans, dogs, cats, cattle, horses, sheep,  
 CC pigs, goats, or rabbits) The PRO polypeptides are useful as targets for  
 CC therapeutic intervention in these diseases, and diagnostic determination  
 CC of the presence of these diseases. The PRO polypeptides are also useful  
 CC as molecular weight markers, or for chromosome identification. The PRO  
 CC genes are useful as hybridisation probes, or for screening libraries of  
 CC human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene  
 CC therapy, particularly for replacing a defective gene. This is the amino  
 CC acid sequence of a novel human secreted and transmembrane PRO polypeptide  
 XX  
 SQ Sequence 322 AA;  
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 Pred. No.: 3,74e-163 Length: 322  
 Score: 1657.00 Matches: 322  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 45.98% Indels: 0  
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 QY 243 GTCCAAAGGCTCTTGGTGCAGAGAGACTTCCATCCAGGTGTCATGCAGAAATATGGG 302  
 Db 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
 QY 303 ATCACCTTGTGAGCAAAAGGCAACACGACCTGAATTTACAGAAGTAAGGAGGCC 362  
 Db 41 IleThrLeuValSerIlyslsAlaAsnGlnGlnLeuAsnPhetrGluAlaLysGluAla 60  
 QY 363 TGTAGGCTGCTGGACTAAAGTTTGGCCGGCAAGACCAAGTTCAGAGCTTGAAGCT 422  
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 QY 423 AGCTTTGAACTTGCAGCTATGCTGGTGGAGATGGATTCGTGCTCATCTCTAGGATT 482  
 Db 81 SerPheGluThrCysSerTyrglytrpValGlyAspGlyPheValValIleSerArgIle 100  
 QY 483 AGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTCTGATTTGGAAAGTTCCAGTG 542  
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 QY 543 AGCCGACAGTTTGCAGCCTATTGTTTACAACCTCATCTGATCTTGGACTACTCTGCGATT 602





GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 13, 2004, 10:06:01 ; Search time 201.5 Seconds

(without alignments)  
6459.355 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1335176 seqs, 320689617 residues

Total number of hits satisfying chosen parameters: 2670352

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	1772	49.2	344	12	US-10-276-774-2349	Sequence 2349, Ap
2	1657	46.0	322	9	US-09-909-320-201	Sequence 201, App
3	1657	46.0	322	9	US-09-909-088B-201	Sequence 201, App
4	1657	46.0	322	9	US-09-905-291A-201	Sequence 201, App
5	1657	46.0	322	9	US-09-902-853-201	Sequence 201, App
6	1657	46.0	322	9	US-09-907-824-201	Sequence 201, App
7	1657	46.0	322	9	US-09-907-841-201	Sequence 201, App
8	1657	46.0	322	10	US-09-904-011-201	Sequence 201, App
9	1657	46.0	322	10	US-09-906-742-201	Sequence 201, App
10	1657	46.0	322	10	US-09-906-838-201	Sequence 201, App
11	1657	46.0	322	10	US-09-907-613-201	Sequence 201, App
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17	1657	46.0	322	10	US-09-906-646-201	Sequence 201, App
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34	1657	46.0	322	10	US-09-905-381-201	Sequence 201, App
35	1657	46.0	322	10	US-09-905-088-201	Sequence 201, App
36	1657	46.0	322	10	US-09-907-575-201	Sequence 201, App
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39	1657	46.0	322	10	US-09-902-634-201	Sequence 201, App
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45	1657	46.0	322	10	US-09-903-823-201	Sequence 201, App

## ALIGNMENTS

### RESULT 1

US-10-276-774-2349  
; Sequence 2349, Application US/10276774  
; Publication No. US20040053245A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; APPLICANT: Tang, Y, Tom et al  
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides  
; FILE REFERENCE: 21272-030  
; CURRENT APPLICATION NUMBER: US/10/276,774  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 09/560,875  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: 09/496,914  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 2700  
; SOFTWARE: Custom  
; SEQ ID NO 2349  
; LENGTH: 344  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-276-774-2349

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Query Match:	49,17%	Indels:	0
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QY	237	CTCCTGGTCCAGGCTCTTTGGTGCAGAGAGCTTTCATCCAGGTGTCATGCAGATT	296
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QY	357	GAGGCTGTAGGTGCTGGGACTAAGTTTGGCCGGCAAGCAAGTGAACAGCCTTG	416
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QY	537	CGAGTGGCGGACAGTTGGAGCTATTGTTTCAACTCATCTGATCTGGACTACTCG	596
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QY	1017	GAACCAAGTAGTAAGAGGAGGAGGCAAGCCCAATGATAGCAACCTTATGAGGAATCAAAG	1076
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RESULT 2		
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; Sequence 201, Application US/09909320		
; Patent No. US20020132240A1		
; GENERAL INFORMATION:		
; APPLICANT: Genentech, Inc.		
; APPLICANT: Ashkenazi, Avi		
; APPLICANT: Botstein, David		
; APPLICANT: Desnoyers, Luc		
; APPLICANT: Eaton, Dan L.		
; APPLICANT: Ferrara, Napoleone		
; APPLICANT: Filvaroff, Ellen		
; APPLICANT: Fong, Sherman		
; APPLICANT: Gao, Wei-Qiang		
; APPLICANT: Gerber, Hanspeter		
; APPLICANT: Gerritsen, Mary E.		
; APPLICANT: Goddard, A.		
; APPLICANT: Godowski, Paul J.		
; APPLICANT: Grimaldi, Christopher J.		
; APPLICANT: Gurney, Austin L.		
; APPLICANT: Hillan, Kenneth, J.		
; APPLICANT: Kljavin, Ivar J.		
; APPLICANT: Mather, Jennie P.		
; APPLICANT: Pan, James		
; APPLICANT: Paoni, Nicholas F.		
; APPLICANT: Roy, Margaret Ann		
; APPLICANT: Stewart, Timothy A.		
; APPLICANT: Tumas, Daniel		
; APPLICANT: Williams, P. Mickey		
; APPLICANT: Wood, William, I.		
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic		
; FILE REFERENCE: 10466-14		
; CURRENT APPLICATION NUMBER: US/09/909,320		
; CURRENT FILING DATE: 2002-01-04		
; PRIOR APPLICATION NUMBER: PCT/US00/04414		
; PRIOR FILING DATE: 2000-02-22		
; PRIOR APPLICATION NUMBER: US 60/143,048		
; PRIOR FILING DATE: 1999-07-07		
; PRIOR APPLICATION NUMBER: US 60/145,698		
; PRIOR FILING DATE: 1999-07-26		
; PRIOR APPLICATION NUMBER: US 60/146,222		
; PRIOR FILING DATE: 1999-07-28		
; PRIOR APPLICATION NUMBER: PCT/US99/20594		
; PRIOR FILING DATE: 1999-09-08		
; PRIOR APPLICATION NUMBER: PCT/US99/20944		
; PRIOR FILING DATE: 1999-09-13		
; PRIOR APPLICATION NUMBER: PCT/US99/21090		
; PRIOR FILING DATE: 1999-09-15		
; PRIOR APPLICATION NUMBER: PCT/US99/21547		
; PRIOR FILING DATE: 1999-09-15		
; PRIOR APPLICATION NUMBER: PCT/US99/23089		
; PRIOR FILING DATE: 1999-10-05		
; PRIOR APPLICATION NUMBER: PCT/US99/28214		
; PRIOR FILING DATE: 1999-11-29		
; PRIOR APPLICATION NUMBER: PCT/US99/28313		
; PRIOR FILING DATE: 1999-11-30		
; PRIOR APPLICATION NUMBER: PCT/US99/28564		
; PRIOR FILING DATE: 1999-12-02		
; PRIOR APPLICATION NUMBER: PCT/US99/28565		
; PRIOR FILING DATE: 1999-12-02		
; PRIOR APPLICATION NUMBER: PCT/US99/30095		
; PRIOR FILING DATE: 1999-12-16		
; PRIOR APPLICATION NUMBER: PCT/US99/30911		
; PRIOR FILING DATE: 1999-12-20		

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; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein
US-09-909-320-201

Alignment Scores:
Pred. No.:      4,44e-148      Length:      322
Score:          1657.00      Matches:      322
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      45.98%      Indels:      0
DB:              9          Gaps:      0

US-10-079-111-2 (1-2029) x US-09-909-320-201 (1-322)
QY 183 ATGGCCAGGTGCTCAGCCTGGTGTGCTTCTCACTTCCATCTGGACACGAGGCTCTG 242
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QY 243 GTCCAAAGCTCTTTCGGTCGACAGAGCTTTCATCCAGGTGTCATGCAAGATTATGGGG 302
Db 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgileMetGly 40
QY 303 ATCACCCCTGTGAGCAAAAGCGACACGACGAGCTGAATTCACACAGCTTAAGAGGCC 362
Db 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
QY 363 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAAGCT 422
Db 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
QY 423 AGCTTTGAAACTTGACGATATGGCTGGTGGTGGATGGATGGATTCGTGTCATCTAGGATT 482
Db 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgile 100
QY 483 AGCCCAAAACCCCAAGTGGGAAATGGGTGGGTGGTCCCTGATTTGGAGGTTCCAGTG 542
Db 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
QY 543 AGCCGACACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTTGGACTAACTCGTGCAAT 602
Db 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
QY 603 CCAGAAATATCACACCAAGATCCCATATTCAACACTCAAACTGCAACAAACAACA 662
Db 141 ProGluIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
QY 663 GAATTTATTGTGAGTACAGTACCTACTCGGTGGATCCCTTACTCTACATACTGCG 722
Db 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
QY 723 CCTACTACTACTCTCTCTCAGCTTCCAGCTTCCACTTCTATTCCAGGAGAAAAAATGATT 782
Db 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeu 200
QY 783 TGTGTACAGAGATTTTATGAAACTAGCACATGCTTACAGAACTGAAACCAATTTGTT 842
Db 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
QY 843 GAAATTAAGACGACATTCAGATGAGCTGCTGGTTGGAGGTGTCCTCCACGCTCTG 902
Db 221 GluAsnLysAlaAlaPheLysAsnGluAlaGlyPheGlyGlyValProThrAlaLeu 240
QY 903 CTAGTGCTTGCTCTCTCTTCTTGGTGTGCTGAGCTGGTCTTGGATTTTGGCTATGTCAAA 962
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QY 963 AGGTATGTGAAGGCTTCCCTTTTCAAAACAAGATCAGCAGAGAAATGATCGAAACC 1022
Db 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
QY 1023 AAAGTAGTAAAGGAGGAGCCCAATGATAGCAACCCCTTAATGAGGAATCAAGAAACT 1082
Db 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysThr 300
QY 1083 GATAAAAAACCCAGAGAGTCCAAAGAGTCCAAACAAACTTACCGTCGATGCTCGAAGCT 1142
Db 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
QY 1143 GAAGTT 1148
Db 321 GluVal 322

RESULT 3
US-09-909-088B-201
; Sequence 201, Application US/09909088B
; Patent No. US20020146709A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,088B
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
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; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein
;
US-09-909-088B-201

Alignment Scores:
Pred. No.: 4,44e-148 Length: 322
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.98% Indels: 0
DB: Gaps: 0

US-10-079-111-2 (1-2029) x US-09-909-088B-201 (1-322)

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QY 243 GTCCAGGCTCTTGGTCGACAGAGCTTCCATCCAGGTGTCATGCAGAAATTAGGG 302
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QY 303 ATCACCCCTTGTGAGCAAAAGCGCAACAGCAGCTGAATTTCCACAGAAGCTAAGGAGGCC 362
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QY 363 TGTAGCTCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 422
Db 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
QY 423 AGCTTTGAACTTGACGCTATCGCTGGTGGAGATGGATTCTGGTCACTCTAGGATT 482
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QY 483 AGCCCAAAACCCCAAGTTGGGAAAATGGGGTGTCTCTGATTTGGAAGGTTCAGTG 542
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QY 603 CCAGAAATATCACCAACCAAGATCCCATATTTCAACACTCAACTGCAACACAAACA 662
Db 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
QY 663 GAATTTATTTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAAATACGTC 722
Db 161 GluPheIleValSerAspSerThrTrpSerValAlaSerProTrpSerThrIleProAla 180
QY 723 CCTACTACTACTCTCTCTCCAGTTCACCTTCTATTCCAGGAGAAAAAATGATT 782
Db 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200

US-09-905-291A-201
; Sequence 201, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,291A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
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; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
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; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein
US-09-905-291A-201

Alignment Scores:
Pred. No.:          4,44e-148      Length:          322
Score:              1657.00        Matches:          322
Percent Similarity: 100.00%        Conservative:      0
Best Local Similarity: 100.00%      Mismatches:       0
Query Match:        45.98%         Indels:           0
DB:                 9              Gaps:             0

US-10-079-111-2 (1-2029) x US-09-905-291A-201 (1-322)
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Db 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
QY 303 ATCACCCTTGTGAGCAAAAGCGCAACGAGCTGAATTCACAGAACTAAGAGGCC 362
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QY 363 TGTAGCTGCTGGAGTAAAGTTGGCCGCAAGGACCAAGTTCAACACGCTTGAAGCT 422
Db 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
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QY 483 AGCCCAACCCCAAGTGTGGGAAAATGGGTGGGTGCTCTGATTTGGAGGTTCCAGTG 542
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QY 543 AGCCGACAGTTTGCAGCTATTGTTACAACTCATCTGATCTTGGACTGAACCTCGTCATT 602
Db 121 SerArgGlnPheAlaAlaIleCysIleAsnSerSerAspThrTrpThrAsnSerCysIle 140
QY 603 CCAGAAATATTACCAACCAAGATCCCATTTCAACACTCAAACTGCAACACAAACA 662

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Db 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
QY 663 GAATTATTGTTCAGTGACAGTACTACTCGGTGGCATCCCTTACTCTCAATACCTGCC 722
Db 161 GluPheIleValSerAspSerThrIleValAlaSerProIleProIleProAla 180
QY 723 CCTACTACTACTCCTCTGCTCCAGTCTCCACTTCTTATTCACGGAGAAAAATGATT 782
Db 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgGlyLysLeuIle 200
QY 783 TGTGTGCACAGAAAGTTTATGAAACTAGCACCATGTCTACAGAAACTCAACCATTTGTT 842
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QY 843 GAAATATAAGCAGCATTTCAAGAAATGAAGCTGTGGGTGTTGGAGGTGTCCTCCACGGCTCTG 902
Db 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240
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Db 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysIleValLys 260
QY 963 AGGTATGTGAAGGCTTCCCTTTTACAAACAAGAATCAGCAGAAAGAAATGATCGAAACC 1022
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QY 1023 AAAGTAGTAAAGGAGAGAGAGCCCAATGATACAAACCCCTTAATGAGGAATCAAGAAAACT 1082
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QY 1083 GATATAAACCCAGAGAGTCCAGAGTCCAGAGTCCAGCAAACTACCGTGGATGCTGGAGCT 1142
Db 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320
QY 1143 GAAAGTT 1148
Db 321 GluVal 322

RESULT 5
US-09-902-853-201
; Sequence 201, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853
; CURRENT FILING DATE: 2001-07-10

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; PRIOR APPLICATION NUMBER: US/09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
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; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-902-853-201

Alignment Scores:
Pred. No.: 4,44e-148 Length: 322
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.98% Indels: 0
DB: Gaps: 0

US-10-079-111-2 (1-2029) x US-09-902-853-201 (1-322)

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QY 243 GTCCAGGCTCTTGGTGCAGAAAGCTTCATCCAGGTGCATGSCAGAAATTATGGG 302
Db 21 ValGInGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
QY 303 ATCACCCCTTGTGAGCAAAAGCGCAACCGAGCTGAATTTACAGAAGCTAAGGAGGCC 362
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QY 363 TGTAGGCTGCTGGACTAAGTTTGGCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 422
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Db 81 SerPheGluThrCysSerTrpGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
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Db 101 SerProAsnProLysCysGlyLysAenGlyValGlyValLeuIleTrpLysValProVal 120
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Db 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
QY 603 CCAGAAATTTATCACCAACCAAGATCCCATATTCAACACTCAAACTGCACACACAAACA 662
Db 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
QY 663 GAATTTATTGTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTCAATACACTGCC 722
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QY 903 CTAGTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 962
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Db 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
QY 1083 GATAAAACCCAGAGAGTCCAGAGTCCAGAGTCCAGCAAAACTACCGTGGATGCTCGGAGCT 1142
Db 301 AspLysAsnProGluGluSerLysSerProSerLysThrValArgCysLeuGluAla 320
QY 1143 GAAGTT 1148
Db 321 GluVal 322

RESULT 6
US-09-907-824-201
; Sequence 201, Application US/09907824
; Publication No. US20020197671A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Faoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.

```

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; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907, 824
; CURRENT FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-824-201

Alignment Scores:
Pred. No.: 4,448-148 Length: 322
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.98% Indels: 0
Dbs: 9 Gaps: 0

US-10-079-111-2 (1-2029) x US-09-907-824-201 (1-322)

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QY 243 GTCCAGGCTCTTCGGTGCAGAGAGCTTTCCATCCAGGTGTCATGCAGAATTATGGG 302
Db 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40

QY 303 ATCCACCTTGTGAGCAAAAGCGAACCGAGCTGAATTCACAGAGCTGAAGGAGGCC 362
Db 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
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QY 363 TGAGGCTGCTGGGACTAAGTTTGGCCGCGCAGGACCAAGTTGAAACACGCTTGAAGCT 422
Db 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80

QY 423 AGCTTTGAAACTTGACGCTATGGCTGGGTGGAGATGGATTCTGGTCTCATCTCTAGGATT 482
Db 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100

QY 483 AGCCCAAAACCCCAAGCTGGGGAATAATGGGTGGGTGCTCCTGATTTGGAAGGTTCCAGTG 542
Db 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120

QY 543 AGCCGACAGTTTGCAGCCTATTGTTACAACATCATCTGATCTACTTGACTAACTCCTGCATT 602
Db 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140

QY 603 CCAGAAATTTATCACCAACCAAGATCCCATATTTCACACTCAAACTGCAACACAAACAACA 662
Db 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160

QY 663 GAATTTATGTCAGTGACAGTACTCTCGGTGGGATCCCTTACTCTACAATACCTGCTGCC 722
Db 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180

QY 723 CCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGAGAGAAAATTTGATT 782
Db 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgLysLysLeuIle 200

QY 783 TGTGTACAGAAAGTTTATGGAAACTAGCACCATGTCTCACAGAAACTGAACCATTTGTT 842
Db 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220

QY 843 GAAATAAAGCAGCATTCAGAAATGAAAGTCTCGGTGGTGGAGGTGTCCTCCACGCTCTG 902
Db 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240

QY 903 CTAGTGTCTGCTCTCCTCTCTCTTTGGTGTGTCAGCTGCTTGGATTTTGTCTATGTCAA 962
Db 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260

QY 963 AGGTATGTGAAGGCTTCCCTTTTACAAACAGAAATCAGCAGAGAAATGATCGAAACC 1022
Db 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280

QY 1023 AAAGTAGTAAAGGAGGAGGAGGCAATGATAGCAACCCCTAATGAGGAATCAAGAAACT 1082
Db 281 LysValValLysGluGluLysAlaAlaAsnAspSerAsnProAsnGluSerLysLysThr 300

QY 1083 GATAAAACCCAGAGAGCTCCAAAGAGTCCAAAGAACTACCGTCGATGCTGGAAGCT 1142
Db 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320

QY 1143 GAAATT 1148
Db 321 GluVal 322

RESULT 7
US-09-907-841-201
; Sequence 201, Application US/09907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Astkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
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Qy	423	AGCTTTGAAACTTTGCAGCTATGGCTGGGTTGGAGATGGATTCTGTGGTCATCTCTAGGATT	482
Db	81	SerPheGluThrCysSerTyrGlyTyrValGlyAspGlyPheValValIleSerArgIle	100
Qy	483	AGCCCAACCCCAAGTGTGGGAAANAATGGGGTGGTCTCGATTGGGAAGGTTCCAGTG	542
Db	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120
Qy	543	AGCCGACAGTTTGCAGCCTATTGCTTACAACTCATCTGATACTTGGACTAACTCGTGCATT	602
Db	121	SerArgGlnPheAlaIleTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140
Qy	603	CGAGAAATTATACCACCAAGATCCCATANTCAACACTCAAACTGCAACACAAAACAACA	662
Db	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160
Qy	663	GAATTATTCTCAGTGACAGTACTCTACTCGTGGCATCCCTTACTCTCAATACACTGCC	722
Db	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180
Qy	723	CCTACTACTCTCTCTCTCCAGTCTCCAGTCTCCACTTCTATTCCACGGAGAAAAAATGATT	782
Db	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle	200
Qy	783	TGTGTCACAGAAGTTTTATGGAACTAGCACCATCTCTACAGAAATGNAACATTGTT	842
Db	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220
Qy	843	GAATAATAAGCAGCATTCAAGATGAAGTCGTGGGTTTGGAGGTGTCCCCACGGCTCTG	902
Db	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240
Qy	903	CTAGTGTCT	962
Db	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260
Qy	963	AGCTATGTGAAGCCCTTCCCTTTTACAAAACAAGAAATCAGCAGAAGGAAATGATCGAAACC	1022
Db	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr	280
Qy	1023	AAAGTGTAGTAAGGAGGAGGAAGGCCAATGATAGCAACCCCTAATGAGGAATCAAGAAA	1082
Db	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
Qy	1083	GATAAAAACCCAGACAGTCCAGAGTCCCAAGCAGAAATACCGTGCAGTCCCTCGGAAGCT	1142
Db	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
Qy	1143	GAAGTT 1148	
Db	321	GluVal 322	
RESULT 8			
US-09-904-011-201			
; Sequence 201, Application US/09904011			
; Publication No. US20030003530A1			
; GENERAL INFORMATION:			
; APPLICANT: Genentech, Inc.			
; APPLICANT: Ashkenazi, Avi			
; APPLICANT: Botstein, David			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Eaton, Dan L.			
; APPLICANT: Ferrara, Napoleone			
; APPLICANT: Filvaroff, Ellen			
; APPLICANT: Fong, Sherman			
; APPLICANT: Gao, Wei-Qiang			
; APPLICANT: Gerber, Hanspeter			
; APPLICANT: Gerrietsen, Mary E.			
; APPLICANT: Goddard, A.			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Grimaldi, Christopher J.			
; APPLICANT: Gurnev, Austin L.			

APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/904,011  
CURRENT FILING DATE: 2001-07-11  
PRIOR APPLICATION NUMBER: 09/665,350  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 201  
LENGTH: 322  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-09-904-011-201

Alignment Scores:  
Pred. No.: 322  
Score: 1657.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 45.98%  
DB: 10  
Gaps: 0

US-10-079-111-2 (1-2029) x US-09-904-011-201 (1-322)

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QY 243 GTCCAAGGCTCTTTGGCTGCAGAGAGCTTTCCATCCAGGTCTCATGCAGAAATTATGGGG 302

Db 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
QY 303 ATCACCCCTTTGTGAGCAAAAAGCGAACACGACGCTGAATTTCAAGAAAGTAAGGAGGCC 362  
Db 41 IleThrLeuValSerLysLysAlaAsnGlnLeuAsnPheThrGluAlaLysGluAla 60  
QY 363 TGTAGGCTCTGGGACTAAGTTTGGCCGCAAGACCAAGTTGAAACAGCCTTGAAGCT 422  
Db 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
QY 423 AGCTTTGAACCTTGACGCTATGCTGGTTGGAGATGGATTCGTGCTCATCTAGGATT 482  
Db 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100  
QY 483 AGCCCAACCCCAAGTGTGGGAAAATGGGTGGTCTCTGATTTGGAGGTTCCAGTG 542  
Db 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
QY 543 AGCCGACAGTTTGCAGCCTTATTTTACAACCTCATCTGATCTTGGACTAATCGTGCATT 602  
Db 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
QY 603 CCAGAAATTTATCACACCAAGATCCATATTTCAACACTCAAACTGCAACACAAACA 662  
Db 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
QY 663 GAATTTATTTGTCAGTGACAGTACCTACCTCGGTGGCATCCCTTACTCTACAATACCTGCC 722  
Db 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
QY 723 CCTACTACT 782  
Db 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200  
QY 783 TGTGTCCACAGAAAGTTTATGAAACTAGCACCATGTCTACAGAACTGAACCATTTGTT 842  
Db 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
QY 843 GAAATAAAGCAGCATTCAAGAAATGAAGCTGTGGGTTTGGAGGTGTCCCGCAGGCTCTG 902  
Db 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
QY 903 CTAGTGTCT 962  
Db 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
QY 963 AGGTATGTGAAGGCT 1022  
Db 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280  
QY 1023 AAAGTAGTAAAGGAG 1082  
Db 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysThr 300  
QY 1083 GATAAAACCCAGAGAGTCCAGAGTCCAGCAAAACTACCGTCGATGCTCGAGCT 1142  
Db 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
QY 1143 GAAATT 1148  
Db 321 GluVal 322  
RESULT 9  
US-09-906-742-201  
; Sequence 201, Application US/0906742  
; Publication No. US20030023054A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US 09/906,742  
CURRENT FILING DATE: 2001-07-16  
PRIOR APPLICATION NUMBER: 09/665,350  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
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PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 201  
LENGTH: 322  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-09-906-742-201

Alignment Scores: 4,44e-148 Length: 322  
Pred. No.: 1657.00 Matches: 322  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00%

Query Match: 45.98% Indels: 0  
DB: 10 Gaps: 0  
US-10-079-111-2 (1-2029) x US-09-906-742-201 (1-322)  
QY 183 ATGGCCAGGTGCTTCAGCCTGGTGTCTTCACATTCCTGACACAGAGGCTCCCTG 242  
DB 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20  
QY 243 GTCCAAAGGCTCTTTCGTCGACAGAGCTTTCATCCAGGTGTCAATGAGAATTAATGGGG 302  
DB 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
QY 303 ATCACCTTGTGACAAAAGGCGACACAGAGCTGAATTTACAGAGAGTAAAGAGGCC 362  
DB 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
QY 363 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAGCT 422  
DB 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
QY 423 AGCTTTGAAACTTGACGCTATCGCTGGTGGAGATGGATTCTGTGTCATCTAGATT 482  
DB 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100  
QY 483 AGCCCAACCCCAAGTGTGGGAAAATGGGGTGGTCTCTGATTTGGAGGTTCCAGTG 542  
DB 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
QY 543 AGCGACAGCTTTGCAGCCTATTGTTACAACTCATCTGATCTTGGACTAACTCGTCATT 602  
DB 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
QY 603 CCAGAAATTAACACCAAGATCCCATATTCAACACTCAACACTCAACACCAACAAACA 662  
DB 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
QY 663 GAATTTATTGTCAGTCACAGTACTCTCGTGGGATCCCTTACTCTCAATACCTGCTGC 722  
DB 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
QY 723 CCTACTACTCTCTCTCTCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATGATT 782  
DB 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgGlyLysLeuIle 200  
QY 783 TGTGTCACAGAGTTTATGGAAACTAGCACATGTCTACAGAACTCAACCATTTGTT 842  
DB 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
QY 843 GAAATAAAGCAGCATTCAGAGATGAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 902  
DB 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240  
QY 903 CTAGTGTCTGCTCTCTCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 962  
DB 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
QY 963 AGGTATGTGAAGGCTTCCCTTTTACAAACAGATCAGCAGAGAGAAATGATCGAAACC 1022  
DB 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
QY 1023 AAAGTAGTAAAGGAGAGGAGCCCAATGATAGCAACCTTAATGAGGAATCAAGAAAAACT 1082  
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QY 1083 GATAAAACCCAGAGAGTCCAGAGTCCAAAGAGTCCAAAGCAAAACTACCGTGCATGCTCGAAGCT 1142  
DB 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
QY 1143 GAAGTT 1148  
DB 321 GluVal 322



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Db      281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluCluSerLysLysThr 300
QY      1083 GATMAAACCCAGAGAGTCCAGAGTCCAGCAAAACTACCGTGGGATGCGCTGGAGCT 1142
Db      301 AspLysAsnProGluGluSerLysSerProSerLysThrValArgCysLeuGluAla 320
QY      1143 GAAGTT 1148
Db      321 GluVal 322

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RESULT 11

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US-09-907-613-201
; Sequence 201, Application US/09907613
; Publication No. US20030027145A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Pao, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,613
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16

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; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein
US-09-907-613-201

Alignment Scores:
Pred. No.:      4,44e-148      Length:      322
Score:          1657.00      Matches:    322
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    45.98%      Indels:    0
DB:             10          Gaps:      0

US-10-079-111-2 (1-2029) x US-09-907-613-201 (1-322)

QY      183 ATGGCCAGGTGCTTCAGCCTGGTGTCTCTCCTCCTCCTCCTCCTCCTCCTCCTCCTG 242
Db      1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20
QY      243 GTCCAAAGGCTCTTTCGTGCAGAGAGCTTTCATCCAGGTGTCTATGCAAGATTTATGGG 302
Db      21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
QY      303 ATCACCCCTGTGAGCAAAAGCGAACCCAGAGCTGAATTTCCAGAAAGCTAAGGAGGCC 362
Db      41 IleThrLeuValSerLysLysAlaAsnGlnLeuAsnPheThrGluAlaLysGluAla 60
QY      363 TGTAGGCTGCTGGGACTAAGTTTGGCGCAGAGGACCAAGTTGAACACGCCCTTGAAGCT 422
Db      61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
QY      423 AGCTTTGAAACTTGCAGCTATGCTGGGTGGAGATGGATTCTGTCTCATCTCTAGGATT 482
Db      81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100
QY      483 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGTCTCTGATTGGGAAGGTTCAGTGG 542
Db      101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
QY      543 AGCCGACAGTTTGCAGCGCTATTGTTACAACTCATCTGATCTACTTGGACTTAACCTCGTGCATT 602
Db      121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140
QY      603 CCAGAAATTTATCACCACCAAGATCCCATATTTCAACACTCAAACTGCAACACAAACAA 662
Db      141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
QY      663 GAATTTATTGTCAGTGACAGTACCTACTCGGTGGGATCCCTTACTTACTTACATACTGCTGCC 722
Db      161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
QY      723 CCTACTACTCTCTCTCTCTCCAGCTTCCACTTCTATTCCACGAGAGAAAAAATTTGATT 782
Db      181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeu 200
QY      783 TGTGTGCAGAGATTTTATGGAAACTAGCACCATCTCTACAGAACTGAACTTTGTT 842
Db      201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
QY      843 GNAATAAAGCAGCATTTCAAGATCAAGCTGCTGGGTTTGGAGGTGTCCTCCAGGCTCTG 902
Db      221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240

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QY 603 CCAGAAATATCACCAACCAAGATCCCATATTCAACACTCAACTGCACACCAACACA 662  
Db |||||||  
QY 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
Db |||||||  
QY 663 GAAATTTATTGTGAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 722  
Db |||||||  
QY 161 GluPheIleValSerAspSerThrThrThrValAlaSerProTyrSerThrIleProIle 180  
Db |||||||  
QY 723 CCTACTACT 782  
Db |||||||  
QY 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgIlysLysLeuIle 200  
Db |||||||  
QY 783 TGTGTCCACAGAGTCTTTATGTGAACACTAGCACCATGTCTACAGAACTGAACCATTTGTT 842  
Db |||||||  
QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
Db |||||||  
QY 843 GAAAAATAAGCAGCATCTCAAGAAATGAAGCTGTGGGTGTTGAGAGTGTCCCCACGCTCTG 902  
Db |||||||  
QY 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240  
Db |||||||  
QY 903 CTAGTGTCT 962  
Db |||||||  
QY 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
Db |||||||  
QY 963 AGTATGTGAAGGCTCTCCCTTTTACAAACAGAAATCAGCAGAGAAATGATCGAAACC 1022  
Db |||||||  
QY 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
Db |||||||  
QY 1023 AAAGTAGTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1082  
Db |||||||  
QY 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
Db |||||||  
QY 1083 GATAAAACCCAGAGAGTCCAAGAGTCCAAGAGTCCAAGAGTCCAAGAGTCCAAGAGT 1142  
Db |||||||  
QY 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
Db |||||||  
QY 1143 GAAGTT 1148  
Db |||||||  
QY 321 GluVal 322  
Db |||||||

## RESULT 14

US-09-909-204-201  
; Sequence 201, Application US/09909204  
; Publication No. US20030036061A1  
; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/909,204  
; CURRENT FILING DATE: 2001-07-18  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
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; PRIOR FILING DATE: 1999-09-15  
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; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 201  
; LENGTH: 322  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic protein  
US-09-909-204-201

## Alignment Scores:

Pred. No.:	4,44e-148	Length:	322
Score:	1657.00	Matches:	322
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	45.98%	Indels:	0
DB:	10	Gaps:	0

US-10-079-111-2 (1-2029) x US-09-909-204-201 (1-322)

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QY	243	GTCCAAAGGCTCTTTCGCTGCAGAGAGCTTTCATCCAGGTGTCATGCAGAAATTATGGG	302
Db	21	ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly	40
QY	303	ATCACCTTTGTGAGCAAAAAGCGAACCCAGCAGCTGAAATTTTCACAGAAGCTAAGAGGCC	362
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QY	363	TGTAGCTGTGGGACTAAGTTTGGCCGCGAAGGACCAAGTTGAAACAGCCTTGAAGCT	422
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QY	423	AGCTTTGAACCTTCAGCTATGGCTGGTGTGAGATGATTCGTGCTCATCTCTAGGATT	482



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QY 663 GAATTTATTGTCAGTGACAGTACTACTCGGTGGCATCCCTTACTTACATACCTGCTGCC 722
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Db |||||||
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QY 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
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QY 1083 GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCTGGAGCT 1142
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QY 1143 GAAGTT 1148
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QY 321 GluVal 322
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Search completed: September 13, 2004, 10:32:08  
Job time : 213.5 secs

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Db 66 AspGlnMetLysLeuAlaLeuSerLysGlyPheGluThrCysArgTyrGlyPheIle--- 84  
QY 456 GATGGATTCTGGTCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAATGGGGTG 515  
Db 85 GluGlyAsnValValIleProGlnIleHisProAsnAlaIleCysAlaAlaAsnHisThr 104  
QY 516 GTGTCTCTGATTGGAGGTTCCAGTGAGCGGACAGTTTGTGACGCTATTGTTACAACTCA 575  
Db 105 GlyValTyrIleLeuValThrSerAsnThrSerHisTyrAspThrTyrCysPheAsnAla 124  
QY 576 TGTGATCTTGGACTAATCTGTCATTCAGAAATATCACCACCAAGATCCCATATTC 635  
Db 125 SerAlaProProGluAspCys-----ThrSerValThrAspLeuPro 139  
QY 636 AACACTCAAACTGCAACACACAGAAATTTATGTCAGTGACAGTACC---TACTCG 692  
Db 140 AsnSerPheAspGlyProValThrIleThrIleValAsnArgAspGlyThrArgTyrSer 159  
QY 693 GTGGCATCCCTTACTCTACA-----ATACCTGCCCTACT----- 728  
Db 160 LysLysGlyGluTyrArgThrHisGlnGluAspIleAspAlaSerAsnIleIleAspAsp 179  
QY 729 -----ACTACTCTCTGCT---CCAGCTTCCACT 755  
Db 180 AspValSerSerGlySerThrIleGluLysSerThrProGluGlyTyrIleLeuHisThr 199  
QY 756 TCTATTCCACGGAGAAAAATGATTGTGTCACAGAAAGTTTATGGAACTACACCC 815  
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QY 816 ATGTCTTACA---GAAACTGAACCATTTGTTGAAATAAAGCAGCATTCAG----- 863  
Db 220 LeuAlaThrArgAspArgAspSerSerLysAspSerArgGlySerSerArgThrValThr 239  
QY 864 -----AATGAGCTGCTGGTGGAGGT----- 887  
Db 240 HisGlySerGluLeuAlaGlyHisSerSerAlaAsnGlnAspSerGlyValThrThrThr 259  
QY 888 -----GTCCCCACGGCTCTGCTAGTGTCTGCTCTCCCTTC 923  
Db 260 SerGlyProMetArgArgProGlnIleProGluThrPheIleIleLeuAlaSerLeu--- 278  
QY 924 TTGTGTGTCAGCTGGTCTTGGATTTCATATGTCAAAAGGTATGTGAGGCTTCCCT 983  
Db 279 LeuAlaLeuAlaLeuIleLeuAlaValCys-----IleAlaValAsnSer 293  
QY 984 TTTACAAACAAGAAACAGCAGAGGAAATGATC-----GAAACCAAGTAGTAAAG 1034  
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QY 1035 GAGGAGAGGCGCAATGATAGCAACCCCTAATAGGAATCAAGAAACTATATAAAACCCA 1094  
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Db 333 LeuValAsnLysGluProSerGluThrProAspGlnCysMetThrAlaAsp 349

RESULT 2  
B38745  
cell adhesion molecule CD44 precursor, long form (meta-1) - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 05-Nov-1999  
C:Accession: B38745; A38745  
R:Guenther, U.; Hofmann, M.; Rudy, W.; Reber, S.; Zoeller, M.; Haubmann, I.; Matzku, S.  
Cell 65, 13-24, 1991  
A:Title: A new variant of glycoprotein CD44 confers metastatic potential to rat carcinoma  
A:Reference number: A38745; MUID:91191552; PMID:1707342  
A:Accession: B38745

A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-503 <GUE>  
A:Cross-references: GB:M61874; NID:G576534; PIDN:AAA53534.1; PID:G576535  
A:Accession: A38745  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-223,386-503 <GU2>  
A:Cross-references: GB:M61875  
C:Keywords: cell adhesion

Alignment Scores:  
Pred. No.: 8,92e-12 Length: 503  
Score: 228.50 Matches: 126  
Percent Similarity: 36.19% Conservative: 60  
Best Local Similarity: 24.51% Mismatches: 242  
Query Match: 6.34% Indels: 86  
DB: 21

US-10-079-111-2 (1-2029) x B38745 (1-503)

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Db 10 TrpGlyLeuLeuCysLeuLeuGlnLeuSerLeuAlaGlnGlnIleAspLeuAsnIle 29  
QY 285 TCATGCAGAAATTATGGGATCACCCCTTGTGAGCAAAAAGCGCAACACGAGCAGTGAATTC 344  
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QY 345 ACAGAAGCTAAGGAGCGCTGAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTT 404  
Db 50 ThrGluAlaAlaAspLeuCysGluAlaPheAsnThrThrLeuProThrMetAlaGlnMet 69  
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QY 465 GTGGTCTATCTAGGATTAGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGTGTCTCG 524  
Db 89 ValValIleProArgIleHisProAsnAlaIleCysAlaAlaAsnAsnThrGlyValTyr 108  
QY 525 ATTTGGAAGTTTCCAGTGAGCGCAGCTTTGCAGCCTATTGTTACAACTCATCTGATACT 584  
Db 109 IleLeuLeuAlaSerAsnThrSerHisTyrAspThrTyrCysPheAsnAlaSerAlaPro 128  
QY 585 TGGACTAACTCGTGATTCAGAAATATATCACCAAGATCCCATATTCACACTCAA 644  
Db 129 LeuGluGluAspCys-----ThrSerValThrAspLeuProAsnSerPhe 143  
QY 645 ACTGCAACACCAACACAGAAATTTATTGTCAGTGACAGTACC---TACTCGGTGGCATCC 701  
Db 144 AspGlyProValThrIleThrIleValAsnArgAspGlyThrArgTyrSerLysLysGly 163  
QY 702 CCTTACTCTACA-----ATACCTGCCCTACT----- 728  
Db 164 GluTyrArgThrHisGlnGluAspIleAspAlaSerAsnIleIleAspGluAspValSer 183  
QY 729 -----ACTACTCTCTCTGCT---CCAGCTTCCACTTCTTATTCOA 764  
Db 184 SerGlySerThrIleGluLysSerThrProGluGlyTyrIleLeuHisThrAspLeuPro 203  
QY 765 CGGAGAAAAAATTGATTGTGTACAGAGTTTATGGAACTTAGCACTAGCACTGTCTACA 824  
Db 204 ThrSerGlnProThrGlyAspArgAspAlaPhePheIleGlySerThrLeuAlaThr 223  
QY 825 ---GAAACTGAACCATTTGTTGAAATAAAGCAGCATTCAGAAATGAAGCTGCTGGTTT 881  
Db 224 IleAlaThrThrProThrValSerAlaHisThrLysGlnAsnGlnGluArgThrGlnTrp 243  
QY 882 GGAGGTGC-----CCACGGCTCTGTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 932  
Db 244 AsnProIleHisSerAsnProGluValLeuLeuGlnThrThrThrArgMetThrAspIle 263



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QY 933 GCAGCTGCTCTGGATTTTCTATGTCARAAAGGTATGTGAAG-----GCCTTCCTCTTTT 986
Db 264 AspArgAsnSerThrSerAlaHisGlyGluAsnTrpThrGlnGluProGlnProPhe 283
QY 987 ACAACAAGAATCAGCAGAGGAAA-----ATGATC 1016
Db 284 AsnAsnHisGluTyrGlnAspGluGluThrProHisAlaThrSerThrTrpAla 303
QY 1017 GAACCAAGTAGTAAGAGGAGGAGGCAATGATAGCAACCTTAATGAGGAATCAAG 1076
Db 304 AspProAsnSerThrThrGluGluAlaAlaThrGlnLysGluLysTrpPheGluAsnGlu 323
QY 1077 AAAACTGATAAAACCCA-----GAAGAGTCCAAGAGTCCACGACAAAATACC 1124
Db 324 TrpGlnGlyAsnProThrProSerGluAspSerHisValThrGluGlyThrThr 343
QY 1125 GTGCGAGTCTGGAAGCTGAAGTTTAGATGAGA-----CAGAAATGAGGAGCACACA 1175
Db 344 AlaSerAlaHisAsnAsnHisProSerGlnArgMetThrThrGlnSerGlnGluAspVal 363
QY 1176 CTGAGGCTGTTCTTTCATGCTCTTACCTGCCCGAGCTGGGGAATCAAAAGGCC 1235
Db 364 SerTrpThrAspPheAsp---ProIleSerHisProMetGlyGln-----Gly 379
QY 1236 AAAGAACCAAGAAAGATCCACCTCTGTTCTTAAGTGAATCAGCTCAGGACTGCCA 1295
Db 380 HisGlnThrGluSerLysGlyHis-----SerSerGly---Asn 391
QY 1296 TTGGACTATGGATGACCAAGAGAAATCCCTTCT-----CCTTATTGTAACCTGTGC 1349
Db 392 GlnAspSerGlyValThrThrSerGlyProAlaArgArgProGlnIle---ProGlu 410
QY 1350 TGGATCCTATCTCTACCTACCTCCAAAGCTCCACAGCCCTTTAGCCTGGCTATGCTTA 1409
Db 411 TrpLeu---IleIleLeuAlaSerLeuLeuAlaLeuAlaLeuIleLeuAlaValCys--- 428
QY 1410 ATAATATCCACTGGGAGAAAGAGTTTGTCAAGTGCAAGGACCTAAACATCTCATCA 1469
Db 429 -----IleAlaValAsnSerArgArgCysGlyGlnLysLysLeuVal- 444
QY 1470 GTATCCAGTGGTAAA-----AAGGCC 1490
Db 445 IleAsnSerGlyAsnGlyThrValGluAspArgLysProSerGluLeuAsnGlyGluAla 464
QY 1491 TCCTGGCTCTCGAGCTAGTGGTGAAGCCAGGAGTCACTGAGACC---AAGGCT 1547
Db 465 SerLysSerGlnGluMetValHisLeuValAsnLysGluProThrGluThrProAspGln 484
QY 1548 TTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA 1583
Db 485 PheMetThrAlaAspGluThrArgAsnLeuGlnSer 496

RESULT 3
A30901
Lymphocyte adhesion receptor precursor - baboon
C:Species: Papio sp. (baboon)
C:Date: 18-Apr-1989 #sequence_revision 18-Apr-1989 #text_change 21-Jul-2000
C:Accession: A33935; A30901
R:Ridzenda, R.L.; Carter, W.G.; Nottenburg, C.; Wayner, E.A.; Gallatin, W.M.; St. John, T.
Proc. Natl. Acad. Sci. U.S.A. 86, 4659-4663, 1989
A:Title: Isolation and DNA sequence of a cDNA clone encoding a lymphocyte adhesion recep
A:Reference number: A33935; MUID:89282830; PMID:2471974
A:Accession: A33935
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-362 <IDZ>
C:CROSS-references: GB:M22452; NID:g176576; PID:g176577
C:Comment: This protein was isolated from the herpes papio induced B cell lymphoma.
C:Genetics:
A:Gene: CD44; ECMRIII; Hermes-1 antigen
C:Superfamily: human cell adhesion protein CD44
C:Keywords: cytoskeleton; extracellular matrix; glycoprotein; lipoprotein; surface anti
F:1-20/Domain: signal sequence #status predicted <SIG>

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F:21-362/Product: lymphocyte adhesion receptor #status predicted <MAT>
F:21-270/Domain: extracellular #status predicted <EXT>
F:271-290/Domain: transmembrane #status predicted <TM>
F:291-362/Domain: intracellular #status predicted <CYT>
F:25,57,100,110,120,256/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:296/Binding site: palmitate (Cys) (covalent) #status predicted

```

```

Alignment Scores:
Pred. No.: 2,89e-11 Length: 362
Score: 222.50 Matches: 92
Percent Similarity: 37.40% Conservative: 43
Best Local Similarity: 25.48% Mismatches: 127
Query Match: 6.17% Indels: 99
DB: 2 Gaps: 16

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US-10-079-111-2 (1-2029) x A30901 (1-362)

```

QY 240 CTGGTCCAGGCTCTTTGGTGCAGAGAGCTTTCATCCAGGTGTCATGCAGAAATTATG 299
Db 14 LeuValGlnLeuSerLeu-----AlaGlnIleAspLeuAsnIleThrCysArgPheGlu 31
QY 300 GGGATCACCTTGTGAGCAAAAAGGCGAACACGACGTGAATTTCAAGAAGCTAAGGAG 359
Db 32 GlyIleTyrHisValGluLysAsnGlyArgTyrSerIleSerArgThrGluAlaAsp 51
QY 360 GCCTGTAGCTCTGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACAGCCTTGAAA 419
Db 52 LeuCysLysAlaPheAsnSerThrLeuProThrMetAlaGlnMetGluLysAlaLeuSer 71
QY 420 GCTAGCTTTGAAACTTGACGATCTATGCTGGTGGAGATGATGCTGCTATCTCTAGS 479
Db 72 IleGlyPheGluThrCysArgTyrGlyPheIle---GluGlyHisValIleProArg 90
QY 480 ATTAGCCCAACCCCAAGTGTGGGAAAATGGGTGGTCTCTGATTTGGAAGGTTCCA 539
Db 91 IleHisProAsnSerIleCysAlaAlaAsnAsnThrGlyValTyrIleLeuThrSerAsn 110
QY 540 GTGAGCCGACAGTTTGCAGCCTTATGTTTACAACTCATCTGATACTTGGACTAATCGTGC 599
Db 111 ThrSer---GlnTyrAspThrTyrCysPheAsnAlaSerAlaProGlyGluAspCys 129
QY 600 ATTCCAGAAATTTATCACCACCAAGATCCATATTCAACACTCAAACTCCACACAAACA 659
Db 130 -----ThrSerValThrAspLeuProAsnAlaPheAspGlyProIleThr 144
QY 660 ACAGAATTTATGTCAGTGACAGTACC---TACTCGTGGCATCCCTTACTCTCAATA 716
Db 145 IleThrIleValAsnArgAspGlyThrArgTyrValLysGlyGluTyrArgThrAsn 164
QY 717 CCT-----GCCCTACT----- 728
Db 165 ProGluAspIleAsnProSerSerProThrAspAspValSerSerGlySerSerSer 184
QY 729 -----ACTACTCTCTCT 740
Db 195 GluArgSerSerThrLeuGlyGlyTyrIlePheTyrAsnHisPheSerThrSerProPro 204
QY 741 GCTCCAGCTTCCACTTCTATTCCACGAGAAAAAATGATTGTGTACAGAGAGTTTTT 800
Db 205 IleProAspGluAspGly----- 210
QY 801 ATGGAACATAGCACCATCTCTACAGAAACTGACCATTTGTTGTAATAAAGCAGCATTC 860
Db 211 ---ProTrpIleThrAspSerThrAspArgThrProAlaThrArgAspGlnGlyAlaPhe 229
QY 861 AAG-----AATGAAGCTGCTGGGTTT----- 881
Db 230 AspProSerGlyGlySerHisThrThrHisGlySerGluSerAlaGlyHisSerHisGly 249
QY 882 -----GGAGGT----- 896
Db 250 SerArgGluGlyGlyAlaAsnThrThrSerGlyProLeuArgThrProGlnIleProGlu 269

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Qy	450	GTGGAGATCGATTCTGCTGTCATCTCTAGAAATTAGCCAAACCCCAAGTGTGGAAAAAT	509
Db	86	Ile---GluGlyAsnValIleProArgIleHisProAsnAlaIleCysAlaAlaAsn	104
Qy	510	GGGGTGGGTCTCTGATTGGAAAGGTTCCAGTTCAGTCAGCGCGACAGATTGCGAGCTATTGTTAC	569
Db	105	HisThrGlyValTyrIleLeuValThrSerAsnThrSerHisTyrzAspThrTyrCysPhe	124
Qy	570	AACTCTCATGACTTGGACTAACTCGTCCATTCACGAAATTTATCCACCACCAAGATCCC	629
Db	125	AsnAlaSerAlaProProGluGluAspCys-----ThrSerValThrAsp	139
Qy	630	ATATTCAACTCAAACTGCAACACAAACAGAAATTTATTCAGTCAGTCAGTACC---	686
Db	140	LeuProAsnSerPheAspGlyProValThrIleThrIleValAsnArgAspGlyThrArg	159
Qy	687	TACTCGGTGCATCCCTTACTCTACA-----	713
Db	160	TyrSerLysGlyGluTyrArgThrHisGlnGluAspIleAspAlaSerAsnIleIle	179
Qy	714	-----ATACCTGCCCTTACTTACTTACTCTCTCTCTCCAGCTTCC-----	752
Db	180	AspAspAspValSerSerGlySerThrIleGluLysSerThrProGluSerTyrIleLeu	199
Qy	753	---ACTTCTATTCCACGGAGAAAAATTGATTGTGTACACAGATTTTATGGAAACT	809
Db	200	HisThrTyrLeuProThrGluGlnProThrGlyAspGlnAspSerPhePheIleArg	219
Qy	810	AGCACCATGCTACA--GAACATGAACCATTTGTTGMAAATAAAGCAGCATTCAAAG--	863
Db	220	SerThrLeuAlaThrArgAspArgAspSerSerLysAspSerArgGlySerSerArgThr	239
Qy	864	-----AATGAAGCTCTGGGTTTGGAGGT-----	887
Db	240	ValThrHisGlySerGluLeuAlaGlyHisSerSerAlaAsnGlnAspSerGlyValThr	259
Qy	888	-----GTCCCCACGGCTCTGTAGTGTGTCTCTC	917
Db	260	ThrThrSerGlyProMetArgArgProGlnIleProGluThrIleLeuAlaSer	279
Qy	918	CTCTCTTTTGGTGTGCTGAGTGTCTTGGATTTGTATGTCAAAAGGTATGTGAAGGCC	977
Db	280	Leu---LeuAlaLeuAlaLeuIleLeuAlaValCys-----IleAlaVal	293
Qy	978	TTCCCTTTTCAACAAAGATTCAGCAGAGAAATGATC-----GAAACCAAGTA	1028
Db	294	AsnSerArgArgArgCysGlyGlnLysLysLeuValIleAsnGlyGlyAsnGlyThr	313
Qy	1029	GTAAGGAGGAGAGGCCAATGATAGCAACCCCTAATCAGGAATCAAGAAACTGATAAA	1088
Db	314	ValGluAspArgLysProSerGluLeuAsn--GlyGluAlaSerLysSerGlnGluMet	332
Qy	1089	AAUCCAGAGATCCCAAGAGTCCAAGCAAACTACCTGCGATGCTCTGGAAGCTGAA	1145
Db	333	ValHisLeuValAsnLysGluProSerGluThrProAspGlnCysMetThrAlaAsp	351
RESULT 5			
A35616			
T-cell surface glycoprotein CD44 - hamster			
C:Species: Cricetinae gen. sp. (hamster)			
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 21-Jul-2000			
R:Aruffo, A.; Stamenkovic, I.; Melnick, M.; Underhill, C.B.; Seed, B.			
Cell 61, 1303-1313, 1990			
A:Title: CD44 is the principal cell surface receptor for hyaluronate.			
A:Reference number: A35616; PMID:90304889; PMID:1694723			
A:Accession: A35616			
A:Status: nucleic acid sequence not shown; not compared with conceptual translation			
A:Molecule type: mRNA			
A:Residues: 1-362 <ARU>			
C:Superfamily: human cell adhesion protein			
C:Keywords: cell adhesion; glycoprotein; transmembrane protein			

## Alignment Scores:

```
Pred. No.:      8,01e-11      Length:      362
Score:          217.50      Matches:      88
Percent Similarity: 38.73%      Conservative: 46
Best Local Similarity: 25.43%      Mismatches: 149
Query Match:      6.03%      Indels:      63
DB:              2          Gaps:      12

US-10-079-111-2 (1-2029) x A35616 (1-362)

QY 252 TCTTTGCGTCAGAGAGCTTCCATCCAGGTGTCATGCAGAAATTATGGGGATCACCCCTT 311
Db SerLeuAlaHisGlnIleAspLeuAsnIleThrCysArgTyrAlaGlyValPheHis 37
QY 312 GTGAGCAAAAGCGGACCAAGCAGCTGAATTTCCAGAAAGCTTAAGAGCCCTGTAGGCTG 371
Db ValGluLysAsnGlyArgTyrSerIleSerArgThrGluAlaAlaAspLeuCysGlnAla 57
QY 372 CTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAACAGCCCTTGAAAGCTAGCTTTGAA 431
Db PheAsnSerThrLeuProThrMetAspGlnMetValMetAlaLeuSerLysGlyPheGlu 77
QY 432 ACTTCAGCTATGCGTGGGTGGAGATGATTGCGTCATCTCTAGGATTAGCCCAAC 491
Db ThrCysArgTyrGlyPheIle---GluGlyHisValValIleProArgIleGlnProAsn 96
QY 492 CCCAAGTGTGGGAAAATGGGGTGGGTCTCGATTGGGAAGGTTCCAGTGAGCCGACAG 551
Db AlaIleCysAlaAlaAsnHisThrGlyValTyrIleLeuThrSerAsnThrSer---His 115
QY 552 TTTGCGAGCTATTGTTTACAACTCATCTGATACTTGGACTTAACCTGCGATTCCAGAAAT 611
Db TyrAspThrTyrCysPheAsnAlaSerAlaProLeuGluGluAspCys----- 131
QY 612 ATCACCAACCAAGATCCCATATTCACACTCAACTCAAACTGCAACCAACACAGAAATTTAT 671
Db ---ThrSerValThrAspLeuProAsnSerPheGluGlyProValThrIleThrIleVal 150
QY 672 GTCAGTGACAGTACC---TACTCGGTGGCATCCCTTACTCTACA-----ATA 716
Db AsnArgAspGlyThrArgTyrSerLysLysGlyGluTyrArgThrHisGlnGluAspIle 170
QY 717 CTGCGCCCTACTACTCTCTCTGCTCCAGCTTC----- 752
Db AspAlaSerAsnThrThrAspAspValSerPheGlySerSerGlySerSerGluLysSerThr 190
QY 753 -----ACTTCTATTCACGCGAGAAAAAATGATTGTTGTGCACA 791
Db SerGlyGlyTyrValPheHisThrTyrLeuProThrIleHisSerThrAlaAspGlnAsp 210
QY 792 GAAGTTTTTATGGAACATGACCACTGCTACAGAA----- 827
Db AspProTyrPheIleGlySerThrMetAlaThrArgAspGlnAspSerSerMetAspPro 230
QY 828 -----ACTGAACCACTTCTGTAATAAT 848
Db ArgGlyAsnSerLeuThrValThrAspGlySerLysLeuThrGlyHisSerSerGlyAsn 250
QY 849 AAAGCAGCATCAAGAATGAAGCTGCTGGTTTGA-----GGTGTCCCAAGCGCT 899
Db GlnAspSerGlyAlaAsnThrThrSerArgProGlyArgLysProGlnIleProGluTrp 270
QY 900 CTGCTAGTCTGCTCTCTCTCTTTTGGTGTGCTGAGCTGGTCTGGATTTTGGTATGTC 959
Db LeuIleValLeuAlaSerLeu---LeuAlaLeuAlaLeuIleLeuAlaValCys----- 287
QY 960 AAAAGGTATGAAGGCCCTTCCTTTTACAAACAAGAATCAGCAGAGGAATGATCGAA 1019
Db -----IleAlaValAsnSerArgArgArgCysGlyGlnLysLysLysValIle 304
QY 1020 ACCAAAGTAGTAAGGAGGAGGACCAATGATAGCAACCTTAATCAGAAATCAAGAA 1079
Db 305 AsnSer-----GlyAsnGlyLysValGluAspArgLysProSerGluLeuAsnGlyGlu 322
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```
QY 1080 ACTGATAAAACCCAGAA-----GAGTCCAAAGAGTCCAAAGCAAACTACCGTG 1127
Db 323 AlaSerLysSerGlnGluMetValHisLeuValAsnLysGluProSerGluThrProAsp 342
QY 1128 CGATCGCTGGAAGCTGAA 1145
Db 343 GlnPheMetThrAlaAsp 349

RESULT 6
A47195
Lymphocyte homing receptor isoform CD44 - human
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
C:Accession: A47195
R:Scraton, G.R.; Bell, M.V.; Jackson, D.G.; Cornelis, F.B.; Gerth, U.; Bell, J.I.
Proc. Natl. Acad. Sci. U.S.A. 89, 12160-12164, 1992
A:Title: Genomic structure of DNA encoding the lymphocyte homing receptor CD44 reveals a
A:Reference number: A47195; MUID:93101687; PMID:1465456
A:Accession: A47195
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-742 <SCR>
A>Note: sequence inconsistent with the nucleotide translation
A>Note: sequence extracted from NCBI backbone (NCBIN:120731, NCBIN:120737, NCBIN:120739,
, NCBIN:120764, NCBIN:120766, NCBIN:120770, NCBIN:120772, NCBIN:120774, NCBIN:120776, NC
BIN:120777, NCBIN:120778, NCBIN:120779, NCBIN:120780, NCBIN:120781, NCBIN:120782, NCBIN:120783, NCBIN:120784, NCBIN:120785, NCBIN:120786, NCBIN:120787, NCBIN:120788, NCBIN:120789, NCBIN:120790, NCBIN:120791, NCBIN:120792, NCBIN:120793, NCBIN:120794, NCBIN:120795, NCBIN:120796, NCBIN:120797, NCBIN:120798, NCBIN:120799, NCBIN:120800, NCBIN:120801, NCBIN:120802, NCBIN:120803, NCBIN:120804, NCBIN:120805, NCBIN:120806, NCBIN:120807, NCBIN:120808, NCBIN:120809, NCBIN:120810, NCBIN:120811, NCBIN:120812, NCBIN:120813, NCBIN:120814, NCBIN:120815, NCBIN:120816, NCBIN:120817, NCBIN:120818, NCBIN:120819, NCBIN:120820, NCBIN:120821, NCBIN:120822, NCBIN:120823, NCBIN:120824, NCBIN:120825, NCBIN:120826, NCBIN:120827, NCBIN:120828, NCBIN:120829, NCBIN:120830, NCBIN:120831, NCBIN:120832, NCBIN:120833, NCBIN:120834, NCBIN:120835, NCBIN:120836, NCBIN:120837, NCBIN:120838, NCBIN:120839, NCBIN:120840, NCBIN:120841, NCBIN:120842, NCBIN:120843, NCBIN:120844, NCBIN:120845, NCBIN:120846, NCBIN:120847, 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QY 714 -----ATACCTGCCCTACT-----ACTACTCCTCTCTCCAGCTTCCACT 755
Db 215 SerThrAspArgIleProIleThrLeuMetSerThrSerAlaThrAlaThrGluThr 234
QY 756 TCTATTCCCGAGAGAAAAATTGATTGTGTACAGAGTGTGTTTATG----- 803
Db 235 AlaThrLysArgGlnGluThrTrpAspTrpPheSerTrpLeuPheLeuProSerGluSer 254
QY 804 -----GAACTAGCACCATGTCTACAGAACTGAACCATTT 839
Db 255 LysAsnHisLeuHisThrThrThrSerSerAsnThrIleSerAlaGlyTrpGluProAsn 274
QY 840 GTTGAATAATAA-----GCAGCATTCAGAATCAAGCTCGTGGTTTGAGGT 887
Db 275 GluGluAsnGluAspThrGlnMetAlaGlyGluArgAspArgHisLeuSerPheSerGly 294
QY 888 GTCCCCACGGCTCTGTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 947
Db 295 -----SerGlyIle--- 297
QY 948 TTTTGTCTATGTCAAAAGGTATGTGAAGGCTTCCCTTTTACAAACAAGATCAGCAGAAG 1007
Db 298 -----AspAspAspGlu 301
QY 1008 GAAATGATCGAAACCAAGTAGTAAAGAGGAGGAGGCAATGATAGCAACCTCATGATG 1067
Db 302 AspPheIleSerSerThrIleSerThrThrProArgAlaPheAsp---HisThrLysGln 320
QY 1068 GAATCAAGAAACTGATTAACCCAGAGAGTCCAGAGTCCAGC-----AAA 1118
Db 321 AsnGlnAspTrpThrGlnTrpAsnProSerHisSer---AsnProGluValLeuLeuGln 339
QY 1119 ACTACCGTCGAGTCGCTGAAGCTGAAGTTTAGATGAGACAGAAATGAGGACACACCT 1178
Db 340 ThrThrThrArgMetThrAspValAsp-----ArgAsnGlyThrThrAla 354
QY 1179 GAGGTGTTTCTTCTCATGCTCTCTTACCTGCGCCAGCTGGGGAATCAAAAGGCCAAA 1238
Db 355 TyrGluGlyAsnTrpAsn----- 360
QY 1239 GAACCAAGAGAGAAAGTCCACCTTGTTCCTTAACCTGGAATCAGCTCAGACTGCCATG 1298
Db 361 -----ProGluAlaHisPro-----ProLeu 367
QY 1299 GACTATGGAGTGCAACCAAGAGAAATGCCCTTCTCTCTTATTGTAACCTGTCTGGATCCTA 1358
Db 368 IleHisHisGluHisHisGluGluGluGluThrProHisSer----- 381
QY 1359 TCTCTCTACTCTCAAGCTTCCGACGGCTTCTAGCTGGCTGTATGCTTAATAATATCC 1418
Db 382 ThrSerThrIleGluAlaThrProSer----- 390
QY 1419 CACTGGGAGAAAGGAGTTTGCAGAGTGCAGACCTAAACATCTCATCAGTATCCAGT 1478
Db 391 -----SerThrThrGluGluThrAla 397
QY 1479 GGTAAAGAGGCTCTCTGGCTGTCTGAGGCTAGTGGGTTGAAAGCCAGGATCACTGAG 1538
Db 398 ThrGlnLysGluGlnTrpPheGlyAsn---ArgTrpHisGlu-----GlyTrpArgGln 414
QY 1539 ACCAAGGCTTCTCTACTGATCCGAGCTCAGACCTTCTTTCAGCTCTGAAAGAGAAA 1598
Db 415 Thr-----ProArgGluAspSerHisSerThrThrGlyThrAlaAlaLaSerAla 431
QY 1599 CAGGTATCCAC-----CTGACATGCTCTTCTGAGCCCGGTAAGACAAAGA 1646
Db 432 HisThrSerHisProMetGlnGlyArgThrThrProSerProGluAspSerSer----- 449
QY 1647 ATGGCAGAAAGTTTAGCCCC 1667
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Db 450 TrpThrAspPhePheAsnPro 456
RESULT 7
A53286
cell-surface glycoprotein CD44 precursor - bovine
N:Alternate names: CD44 protein
C:Species: Bos primigenius taurus (cattle)
C>Date: 02-May-1994 #sequence revision 18-Nov-1994 #text_change 21-Jul-2000
C:Accession: A53286; S22123
R:Bosworth, B.T.; St John, T.; Gallatin, W.M.; Harp, J.A.
Mol. Immunol. 28, 1131-1135, 1991
A:Title: Sequence of the bovine CD44 cDNA: comparison with human and mouse sequences.
A:Reference number: A53286; MUID:92017904; PMID:1922105
A:Accession: A53286
A:Molecule type: mRNA
A:Residues: 1-366 <BOS>
A:Cross-references: EMBL:X62881; NID:G186; PIDN:CAA44675.1; PID:G187
A>Note: sequence extracted from NCBI backbone (NCBIN:63418, NCBI:P:63419)
C:Superfamily: human cell adhesion protein CD44
C:Keywords: cell adhesion; glycoprotein; transmembrane protein
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-366/Product: cell-surface glycoprotein CD44 #status predicted <MAT>
F:274-294/Domain: transmembrane #status predicted <TM>
F:25,57,100,110,120,222,260/Binding site: carbohydrate (Asn) (covalent) #status predicted
Alignment Scores:
Pred. No.: 5,04e-10 Length: 366
Score: 208.50 Matches: 81
Percent Similarity: 36.76% Conservative: 44
Best Local Similarity: 23.82% Mismatches: 142
Query Match: 5.79% Indels: 73
DB: 2 Gaps: 11
US-10-079-111-2 (1-2029) x A53286 (1-366)
QY 240 CTGGTCCAAAGCTCTTTGGTGCAGAAAGAGCTTTCATCCAGGTGTGTCAGCAATATG 299
Db 14 LeuValGlnLeuSerLeu-----AlaGlnIleAspLeuAsnIleThrCysArgTyrAla 31
QY 300 GGGATCACCTTGTGTAGCAAAAGCGCAACACGACGCTGAATTTTCAGAGCTAAGGAG 359
Db 32 GlyValPheHisValGluLysAsnGlyArgTyrSerIleSerIleThrGluAlaAlaAsp 51
QY 360 GCCTGTAGCTGCTGGACTAGTTTGGCGGCAAGCAAGTTCACAGCTTCAACAGCTTGAAA 419
Db 52 LeuCysLysAlaPheAsnSerThrLeuProThrMetAlaGlnMetGluAlaAlaArgAsn 71
QY 420 GCTAGCTTTGAACTTGCAGCTATGGCTGGGTGGAGATGGATTCGTGGTCACTCTAGG 479
Db 72 IleGlyPheGluThrCysArgTyrGlyPheIle---GluGlyHisValIleProArg 90
QY 480 ATTAGCCCAACCCCAAGTGTGGGAAAAATGGGGTGGTGTCTGATTTTGAAGGTCCA 539
Db 91 IleHisProAsnSerIleCysAlaAlaAsnThrGlyValTyrIleLeuThrSerAsn 110
QY 540 GTGACCCGACAGTTTCCAGCCTATTGTTACACTCATCTGATCTGGACTACTCGTCC 599
Db 111 ThrSer---GlnTyrAspThrIleCysPheAsnAlaSerAlaProProGlyGluAspCys 129
QY 600 ATTCCAGAAATTATACCAACCAAGATCCCATATTCAACACTCAAACTCAACACACAAACA 659
Db 130 -----ThrSerValThrAspLeuProAsnAlaPheGluGlyProIleThr 144
QY 660 ACAGAAATTATTGTCAGTCAGCAGTACC---TACTGGTGGCATCCCTTACTCTACAATA 716
Db 145 IleThrIleValAsnArgAspGlyThrArgTyrThrLysLysGlyGluTyrArgThrAsn 164
QY 717 CCT-----GCCCTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 752
Db 165 ProGluAspIleAsnProSerValValSerProSerProProAspAspGluMetSer 184
QY 753 ACTTCTATTCCACGGAGAAAAAATTGATTGTGTGCACAGAGTTTTTT----- 800
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R;Stamenkovic, I.; Aruffo, A.; Amiot, M.; Seed, B.  
EMBO J. 10, 343-348, 1991  
A;Title: The hematopoietic and epithelial forms of CD44 are distinct polypeptides with different extracellular domains  
A;Reference number: S13530; MUID:91122041; PMID:1991450  
A;Accession: S13530  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-493 <STA>  
A;Cross-references: EMBL:X55150; NID:g29800; PIDN:CAA38951.1; PID:g29801  
C;Keywords: transmembrane protein

Alignment Scores:  
Pred. No.: 1.32e-09 Length: 493  
Score: 204.00 Matches: 104  
Percent Similarity: 33.20% Conservative: 62  
Best Local Similarity: 20.80% Mismatches: 173  
Query Match: 5.66% Indels: 161  
DB: 2 Gaps: 16

US-10-079-111-2 (1-2029) x S13530 (1-493)

QY	255	TTCTGTCGACAGAGCTTTCCATCCAGGTGTCATGACGAATTTATGGGATCACCTTTGTG	314
Db	17	LeuSerLeuAlaGlnIleAspLeuAsnIleThrCysArgPheAlaGlyValPheHisVal	36
QY	315	AGCAAAAGGCGAACACGACGCTGAATTTCCACAGAGCTAAGGAGCCCTGAGCTGCTG	374
Db	37	GluLysAsnGlyArgTyrSerIleSerArgThrGluAlaAlaSerLeuCysLysAlaPhe	56
QY	375	GGACTAAGTTGGCCGCAAGACCAAGTTGAACAGCCCTTGAAGCTAGCTTTGAAACT	434
Db	57	AsnSerThrLeuProThrMetAlaGlnMetGluLysAlaLeuSerIleGlyPheGluThr	76
QY	435	TCGAGTATGGCTGGGTGGAGATGATCGTGGTCACTCTAGGATAGCCCAACCC	494
Db	77	CysArgTyrGlyPheIle---GluGlyHisValIleProArgIleHisProAsnSer	95
QY	495	AAGTGTGGGAAAAATGGGTGGTCTGATTTGGAAGTTCCAGTGAGCCGACAGTTT	554
Db	96	IleCysAlaAlaAsnAsnThrGlyValTyrIleLeuThrTyrAsnThrSer---GlnTyr	114
QY	555	GCAGCCTATTGTTCACAACTCATCTGATCTTGGACTTAACCTCGTGCAAT	602
Db	115	AspThrTyrCysPheAsnAlaSerAlaProProGluGluAspCysThrSerValThrAsp	134
QY	602	-----	602
Db	135	LeuProAsnAlaPheAspGlyProIleThrIleThrIleValAsnArgAspGlyThrArg	154
QY	603	-----CCAGAAATTATCACCACCAACCAAGATCCCAT	632
Db	155	TyrValGlnLysGlyGluTyrArgThrAsnProGluAspIleTyrProSerAsnProThr	174
QY	633	TTCAACACTCAAACTGCACACAAACACAGAA	671
Db	175	AspAspValSerSerGlySerSerGluArgSerThrSerGlyGlyTyrIle	194
QY	672	-----GTCAGTGAC	680
Db	195	PheTyrThrPheSerThrValHisProIleProAspGluAspSerProTrpIleThrAsp	214
QY	681	AGTACC-----TACTCGTGGCATCCCTTACTCTACATACTGCCCCCT	725
Db	215	SerThrAspArgIleProArgThrAsnMetAspSerSerHisSerThrThrLeuGlnPro	234
QY	726	ACTACTACTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTGT	785
Db	235	ThrAlaAsnProAsnThrGlyLeuValGluAspLeuAspArgThrGlyProLeuSerMet	254
QY	786	GTACAGAGAGTTTATGGAAGTACGACATGCTACAGAACTGAACATTTGTTGAA	845
Db	255	ThrThrGlnGln---SerAsnSerGlnSerPheSerThrSerHisGluGlyLeuGluGlu	273

QY	846	AATAAA-----GCAGCATTCAGAAATGAGTGTGGG	878
Db	274	AspLysAspHisProThrThrSerThrLeuThrSerSerAsnArgAspValThrGly	293
QY	879	TTTGGAGGTGTCCTCC	920
Db	294	GlyArgArgAspProAsnHisSerGluGlySerThrHisLeuLeu	308
QY	921	TTCTTTTGTGCTCAGCTGCTTGGATTTTGTCTCAAAAGGTATGTGAAGGCCTTC	980
Db	309	-----GluGlyTyrThrSerHisTyr	315
QY	981	CTTTTACAAACAGAAATCAGCAGAGGAATGATGAACCAAGTA	1028
Db	316	ProHisThrLysGluSerArgThrPheIleProValThrSerAlaLysThrGlySerPhe	335
QY	1029	---GTAAGGAGGAGGAGGCAATGATGACCACTCAACCTCAATGAGGACATCAAGAAACTGAT	1085
Db	336	GlyValThrAlaValThrValGlyAspSerAsnSerAsn	348
QY	1086	AAAAACCCAGAGAGTCCAGAGTCCAGCAAACTACCGTGGATGCTTGGAGCTGAA	1145
Db	349	ValAsn---ArgSerLeuSerGlyAspGlnAspThrPheHisProSerGlyGlySerHis	368
QY	1146	GTTAGATGAGACAGAAATGAGGAGACACACTGAGGCTGGTTCTTCTCATGCTCCTTAC	1205
Db	368	hrThrHisGlySerGluSerAspGlyHis	377
QY	1206	CTGCCCCAGCTGGGGAATCAAAAGGGCCAAAGAACCAAGAAAGTCCA	1258
Db	378	-----SerHisGlySerGlnGluGlyGlyAlaAsnThrThrSerGlyProIleArgT	395
QY	1259	---CCCTGGTTCTTAATCGAATCACTCAGGACTCCCATTCAGTATGAGTGCACCA	1316
Db	395	hrProGlnIleProGluTrp	401
QY	1317	AGAGATGCCCTTCTCTTATTGTATACCTGTCTGATCTATCTCTCTACCTCCAAAGC	1376
Db	402	-----LeuIleIleLeuAlaSerLeuL	409
QY	1377	TTCCCAACGGCTTTCTAGCTGTGCTATGCTTAATAATATCCACCTGGGAGAAAGGATT	1436
Db	409	euAlaLeuAlaLeuLeuLeuAlaValCys	424
QY	1437	TTGCAAGTGCAGGACCTAAACATCTCATCATGATCCAGTGGTAAAAAGGCC	1490
Db	424	rgArgArgCysGlyGlnLysLysLeuVal-IleAsnSerGlyAsnGlyAla	441

#### RESULT 11

S45305  
CD44 antigen precursor - dog (fragment)  
C:Species: Canis lupus familiaris (dog)  
C>Date: 20-Oct-1994 #sequence\_revision 21-Jul-1995 #text\_change 21-Jul-2000  
C:Accession: S45305  
R:Milde, K.F.; Alejandro, R.; Mintz, D.H.; Pastori, R.L.  
Biochim. Biophys. Acta 1218, 112-114, 1994  
A;Title: Molecular cloning of the canine CD44 antigen cDNA.  
A;Reference number: S45305; MUID:94250687; PMID:7514890  
A;Accession: S45305  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-351 <MIL>  
A;Cross-references: EMBL:Z27115; NID:g473226; PIDN:CAA81630.1; PID:g473227  
C:Superfamily: human cell adhesion protein CD44

Alignment Scores:  
Pred. No.: 1.7e-09 Length: 351  
Score: 202.50 Matches: 84  
Percent Similarity: 37.05% Conservative: 49  
Best Local Similarity: 23.40% Mismatches: 145  
Query Match: 5.62% Indels: 81  
DB: 2 Gaps: 15

US-10-079-111-2 (1-2029) x S45305 (1-351)

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QY 225 TGGACACAGAGCTCTCTGTCACAGGCTTTTGCAGACAGAGCTTTCCATCCAGGTG 284
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Db 3 TrpGlyLeuCysLeuLeu-----ArgLeuSerLeuAlaGlnIleAspLeuAsnIle 19
QY 285 TCATGCAGAAATATGGGGATACCCCTTGTCAGCAAAAGCGGACACAGCAGCTGAATTC 344
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Db 20 ThrCysArgTyrAlaGlyValPheHisValGluLeuLysAsnGlyArgTyrSerIleArg 39
QY 345 ACAGAAAGCTAAGAGAGCCCTGTAGCTGCTGGGACTAAGTTTGGCCGCGAAGACCAAGTT 404
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Db 40 ThrAlaAlaAlaAspLeuLysCysLysAlaPheAsnSerThrLeuProThrMetAlaGlnMet 59
QY 405 GAAACAGCCTTGAAGCTAGCTTTGAACTTCGAGCTATGCTGGTGGTGGAGATGATTC 464
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Db 60 GluArgAlaLeuSerValGlyPheGluThrCysArgTyrGlyPheIle---GluGlyHis 78
QY 465 GTGGTCATCTCTAGGATTAGCCCAACCCCAAGTGGGAAATCGGTGGTGGCTGCTG 524
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Db 79 ValValIleProArgIleGlnProAsnAlaIleCysAlaAlaAsnHisThrGlyValTyr 98
QY 525 ATTTGGAAGGTTCCAGTAGAGCCGACAGCTTATGTCAGCTTATTTACAACTCATCTGATCT 584
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 99 Ile---LeuIleSerAsnThrSerGlnTyrAspThrTyrCysPheAsnAlaSerAlaPro 117
QY 585 TGGACTAATCTGTGCATTCAGAAATATCACCACCAAGATCCCATTTTCAACACTCAA 644
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 118 ProGluGluAspCys-----ThrSerValThrHisLeuProAsnAlaPhe 132
QY 645 ACTGCAACACAAACAGAAATTTATTTGTCAGTGACAGTACC---TACTCGGTGGCATCC 701
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Db 133 AspGlyProIleThrIleValAsnArgAspGlyThrArgTyrSerGlnLysGly 152
QY 702 CCTTACTCTACATACTGCTGCC-----CCTTACTACTCTCTCTGCTCCAGCTTCC 752
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Db 153 GluTyrArgThrAsnProGluAspIleAsnProSerAsnProThrAspAspValSer 172
QY 753 ACTTCTATTCCCGAGAGAAAATTTGATTGTGTGTCACAGAACTTTT-----800
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Db 173 SerGlySerSerSerGluArgSerThrSerAlaGlyTyrAsnIlePheHisThrHisLeu 192
QY 801 -----ATGGAACTAGCACCACCATGCTCAGAAACTGAA---833
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Db 193 ProThrAlaTyrProThrGluAspGlnAspSerSerValHisProSerGluArgSerHisThr 212
QY 834 -----CCATTGTGTGAAATAAAGCAGCA 857
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 213 ThrProIleThrLysAspHisAspSerSerValHisProSerGluArgSerHisThrThr 232
QY 858 TTCAGAATGAAGCTCTGGGTTT-----CGAGGT-----887
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Db 233 HisGlySerGluSerAlaGlyHisSerSerGlySerGlnGluGlyAlaAsnThrThr 252
QY 888 -----GTCCCCACGGCTCTGCTAGTGTGCTGCTGCTCTCTCTCTCTCTCT 923
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Db 253 SerGlyProMetArgLysProGlnIleProGluTrpLeuIleLeuAlaSerLeu---271
QY 924 TTTGGTGTCTGACGTGCTTGTGATTTTGTATGTCAAAAGGTATGTGAAGGCTCTCCCT 983
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 272 LeuAlaLeuAlaLeuIleLeuAlaValCysIleAla-----283
QY 984 TTTTACAAACAGATCAGCAGAGGAATATCATGAAACCAAGTAGTAAAGGAGGAGAAG 1043
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Db 284 -----ValAsnSerArgArgArgCysGlyGlnLysLysLysLeuValIleAsnAsn 300
QY 1044 GCCAAT-----GATAGCAACCTC-----AATGAGGAATCAAGAAACT 1082
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Db 301 GlyAsnGlyAlaValAlaGlyAspArgLysProSerGlyIleAsnGlyGluAlaSerLysSer 320
QY 1083 GATAAA-----AACCCAGAGAGTCCAAAGTCCAAAGCAAACTACC 1124
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Db 321 GlnGluMetValHisLeuValAsnLysGluProSerGluThrProAspGlnTyrThr 339

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RESULT 12

JH0518  
 lymphocyte homing receptor CD44, splice form CD44R1 - human  
 N/Alternate names: cell adhesion molecule core protein CD44E, keratinocyte; cell surface  
 N/Contains: lymphocyte homing receptor CD44, splice form CD44R1; lymphocyte homing recep  
 C/Species: Homo sapiens (man)  
 C/Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 18-Aug-2000  
 C/Accession: JH0518; JH0519; PH0859; A39209; A42402; C42402; A53029; S16147  
 R/Dougherty, G.J.; Lansdorf, P.M.; Cooper, D.L.; Humphries, R.K.  
 J. Exp. Med. 174, 1-5, 1991  
 A/Title: Molecular cloning of CD44R1 and CD44R2, two novel isoforms of the human CD44 ly  
 A/Reference number: JH0518, MUID:91277598; PMID:2056274  
 A/Accession: JH0518  
 A/Molecule type: mRNA  
 A/Residues: 1-426 <DOU>  
 A/Experimental source: lymphocytes, cell line KGLa  
 A/Accession: JH0519  
 A/Molecule type: mRNA  
 A/Residues: 1-223, 288-426 <DO2>  
 A/Experimental source: lymphocyte, cell line KGLa  
 R/Cooper, D.L.; Dougherty, G.; Harn, H.J.; Jackson, S.; Baptist, E.W.; Byers, J.; Datta,  
 Biochem. Biophys. Res. Commun. 182, 569-578, 1992  
 A/Title: The complex CD44 transcriptional unit: alternative splicing of three internal e  
 A/Reference number: PH0859; MUID:92134271; PMID:1734871  
 A/Accession: PH0859  
 A/Molecule type: DNA  
 A/Residues: 223-357 <COO>  
 R/Brown, T.A.; Bouchard, T.; St. John, T.; Wayner, E.; Carter, W.G.  
 J. Cell Biol. 113, 207-221, 1991  
 A/Title: Human Keratinocytes express a new CD44 core protein (CD44E) as a heparan-sulfat  
 A/Reference number: A39209; MUID:91177958; PMID:2007624  
 A/Accession: A39209  
 A/Molecule type: mRNA  
 A/Residues: 184-376 <BRO>  
 A/Cross-references: GB:X55938; NID:G29802; PIDN:CAA39404.1; PID:9930047  
 R/Jackson, D.G.; Buckley, J.; Bell, J.I.  
 J. Biol. Chem. 267, 4732-4739, 1992  
 A/Title: Multiple variants of the human lymphocyte homing receptor CD44 generated by ins  
 A/Reference number: A42402; MUID:92165834; PMID:1537855  
 A/Accession: A42402  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 217-320 <JA2>  
 A/Note: sequence extracted from NCBI backbone (NCBIN:83964, NCBIP:83965)  
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 A/Accession: C42402  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 217-320 <JA2>  
 A/Note: sequence extracted from NCBI backbone (NCBIN:83968, NCBIP:83969)  
 A/Note: variant D  
 R/Shepley, M.P.; Racanietello, V.R.  
 J. Virol. 68, 1301-1308, 1994  
 A/Title: A monoclonal antibody that blocks poliovirus attachment recognizes the lymphocy  
 A/Reference number: A53029; MUID:94149816; PMID:7508992  
 A/Accession: A53029  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 67-76, 'X', '78-89 <SHE>  
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 A/Gene: GDB:CD44; MDU2; MDU3; MI  
 A/Cross-references: GDB:120739; OMIM:107269  
 A/Map position: 11pter-11p13  
 A/Introns: 35/1; 65/1; 133/1  
 C/Superfamily: human cell adhesion protein CD44  
 C/Keywords: alternative splicing; cell adhesion; chondroitin sulfate proteoglycan; glyco  
 F:1-426/Product: lymphocyte homing receptor CD44, splice form CD44R1 #status predicted  
 F:1-223, 288-426/Product: lymphocyte homing receptor CD44, splice form CD44R2 #status pr  
 F:259/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:354/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted

Alignment Scores:



Pred. No.:	1-75e-09	Length:	426
Score:	202.50	Matches:	92
Percent Similarity:	34.11%	Conservative:	54
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Query Match:	5.62%	Indels:	129
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Db	37	GluLysAsnGlyArgTyrSerIleSerArgThrGluAlaAlaAspLeuCysLysAlaPhe	56
QY	375	GGACTAAGTTTGGCGGCAAGGACCAAGTTGAAACAGCCCTCAAGAGCTAGCTTTGAAACT	434
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Db	135	LeuProAsnAlaPheAspGlyProIleThrIleValAsnArgAspGlyThrArg	154
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QY	672	-----GTCAGTGAC	680
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Db	215	SerThrAspArgIleProAlaThrAsnMetAspSerSerHisSerThrThrLeuGlnPro	234
QY	726	ACTACTACTCTCTCTCTCCAGCTTCCACTTCTATTCCACGAGAGAAAATTTGATTGT	785
Db	235	ThrAlaAsnProAsnThrGlyLeuValGluAspLeuAspArgThrGlyProLeuSerMet	254
QY	786	GTCACAGAGTTTTATGGAACACTAGCACCATGTCTACAGAAACTGAACCATTTGTTGA	845
Db	255	ThrThrGlnGln---SerAsnSerGlnSerPheSerThrSerHisGluGlyLeuGlu	273
QY	846	AATAA-----GCAGCATTCAGAAATGAAGCTGCTGGG	878
Db	274	AspLysAspHisProThrThrSerThrLeuThrSerSerAsnArgAsnValThrGly	293
QY	879	TTTGGAGGTGTCCTCC-----ACGGCTCTGCTAGTGTCTCTCTCTC	920
Db	294	GlyArgArgAspProAsnHisSerGluGlySerThrThrLeuLeu-----	308
QY	921	TTCTTTGGTGTGCAGCTGGCTTGGATTTTCTATGTCAAAAGGTATGTGAAGCCCTTC	980
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QY	981	CCTTTTACAAACAGATCAGCAGAGGAATGATCGAAACCAAGTA-----	1028
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QY	1086	AAAAACCCAGAGAGTCCAAGAGTCCAAGCAAACTACCGTCCGATGCTCGAAGCTGAA	1145
Db	349	ValAsn--ArgSerLeuSerGlyAspGlnAspThrPheHisProSerGlyGlySerHisT	368
QY	1146	GTTTAGATGACAGACAAATAGGAGACACACCTGAGGCTGGTTCTTTCATCTCTCTAC	1205
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QY	1206	CCTGCCCCAGCTGGGGAATCAAAAGGCGCAAGAACCAAGAAAGTCCA-----	1258
Db	378	-----SerHisGlySerGlnGluGlyGlyAlaAsnThrThrSerGlyProIleArgT	395
QY	1259	--CCCTTGGTCTCAACTGG	1276
Db	395	hrProGlnIleProGluTyr	401
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C:Species: Homo sapiens (man)			
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jul-2000			
C:Accession: I77371			
R:Tanabe, K.K.; Nishi, T.; Sava, H.			
Mol. Carcinog. 7, 212-220, 1993			
A>Title: Novel variants of CD44 arising from alternative splicing: changes in the CD44 a			
A:Reference number: 157483; MUID:93356912; PMID:8352881			
A:Accession: I77371			
A>Status: preliminary; translated from GB/EMBL/DBJ			
A:Molecule type: mRNA			
A:Residues: 1-395 <RES>			
A:Cross-references: GB:S66400; NID:g435697; PIDN:AAB27919.1; PID:g435700			
C:Genetics:			
A:Gene: GDB:CD44			
A:Cross-references: GDB:120739; OMIM:107269			
A:Map position: 11pter-11p13			
A:Introns: 257/1			
C:Superfamily: human cell adhesion protein CD44			
Alignment Scores:			
Pred. No.:	4-34e-09	Length:	395
Score:	198.00	Matches:	85
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Best Local Similarity:	23.04%	Mismatches:	145
Query Match:	5.49%	Indels:	90
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US-10-079-111-2 (1-2029) x I77371 (1-395)			
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Db 345 Asp 345  
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chondroitin sulfate proteoglycan PG-M core protein - chicken  
C:Species: Gallus gallus (chicken)  
C>Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jul-2000  
C:Accession: A47171  
R:Shinomura, T.; Nishida, Y.; Ito, K.; Kimata, K.  
J. Biol. Chem. 268, 14461-14469, 1993  
A:Title: cDNA cloning of PG-M, a large chondroitin sulfate proteoglycan expressed during  
A:Reference number: A47171; PMID:93300846; PMID:8314802  
A:Accession: A47171  
A>Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-3562 <SH1>  
A:Cross-references: GB:DI13542; NID:g991643; PIDN:BA02742.1; PID:g991644  
A:Experimental source: stage 22-23 developing limb buds  
A>Note: sequence extracted from NCBI backbone (NCBIN:134456, NCBIIP:134457)  
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F:264-345/Domain: link protein repeat homology <LNK2>  
F:3258-3289/Domain: EGF homology <EGF1>  
F:3296-3327/Domain: EGF homology <EGF>  
F:3334-3454/Domain: C-type lectin homology <LCH>  
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Db 181 -----ProGlu---GlnLeuLysAlaAlaTyrGluAspGlyPheGluGlnCysasp 196  
QY 138 AGTGGCCATCTCAGG-----TGT 155  
Db 197 AlaGlyTrpLeuSerAspGlnThrValArgTyrProIleArgHisProArgIleGlyCys 216  
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Db 232 -----ArgPhePro 234  
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Db 295 TyrGlyTrpLeuAlaAspGlySerValArgTyrProAlaSerValAlaArgProGlnCys 314  
QY 501 GGGAAAAATGGGGTGGGTGCTCGATT-----TGAAG 533  
Db 315 GlyGlyGlyLeuLeuGlyValArgThrLeuTyrArgTyrGluAsnGlnThrGlyPhePro 334  
QY 534 GTTCCAGTTCAGCGACAGTTTCAGCCTATTGTTACAACTCATCTCATATCTTCGACTAAC 593  
Db 335 TyrProAspSerLys---PheAspAlaTyrCysTyrGluArgLysLysIleValSerGlu 353  
QY 594 TCGTGCATTCAGAAATTATCACACC-----AAAGATCCCATATTCACACACTCAAACT 647  
Db 354 ProThrThrValLysLeuValThrThrLeuLysThrAspSerValGluLeuSerSerAla 373  
QY 648 GCNACACAAACACAGAAATTTATGTCAGTACAGTACCTACTCCGGTGGCATCCCTTAC 707  
Db 374 LysValThrLeuLysProSerValPheGluSerSerValThrGluValAlaValThrLys 393  
QY 708 TCTACATACTCT-----GCCCTACTACTACTCTCTCTCTCTCTCTCTCTCTCTCT 755  
Db 394 ThrLysValProAlaTrpGluGluAlaThrLeuGluThrGluAspThrLysMetThrThr 413  
QY 756 TCTATTCACGGAGAAAAAATTTGTTGTGCACAGAAATTTTATGGAACCT----- 809  
Db 414 GluValAlaGluLysArgGluMet-----GluValLeuMetGluAsnIleLys 430  
QY 810 ---AGCACCATGCTACAGAAACTGAACCATTTGTTGAAAAATAAGACAGATTCAGAAAT 866  
Db 431 LeuThrThrLeuLeuProGlnThrValThrAspGlyGlu-IleSerProTyrAspThrLe 450  
QY 867 GAAAGCTGCTGGTGTTCGAGGTGTCGCCACGGCTGCTGCTAGTGTCTCTCTCTCTCTCT 926  
Db 450 uGlyArgThrGluTyrAspValSerProArgLeu-----ThrGluSerThrSerAl 467  
QY 927 GGTGTGTCAGCTGCTGTGATTTTCTATGTCAAAAGGTATGTGAAGGCTTCCCTTTT 986  
Db 467 aAlaLeuGluValGluHisThrTyrSerGluAla-GluLeuSerGluGluGlnGly---- 485  
QY 987 ACAACACAGAACTCAGCAGAGGAATGATCGAAACCAAAAGTAGTAAGAGAGAGAAAG--- 1043  
Db 486 ---ArgSerGluSerThrGlu-AspAlaPheLeuThrSerValPheGlnAspSerThr 504  
QY 1044 -----GCCAATGATAGCAACCTTAATGAGGAATCAAGAAACTCATAAACCCAGAA 1097  
Db 505 AlaValAlaLysSerSerThrGlySerTrpGluAspIleGluThrGly-AspThrGlnLy 524  
QY 1098 GAGTCCAAAGTCCAAAGCAAAACTACCGTGCATGCTGGAAGCTGAAGTTAGATGAGA 1157  
Db 524 shisasp-----G1 527  
QY 1158 CAGAAATGAGGAGACACACCTGAGGCTGGTTCTTTCATGCTCTTACCTGCCCGCAGCT 1217  
Db 527 yAspAsnGlnThrGluGlnIleGluValGlyProValMetThrAlaThr----- 543  
QY 1218 GGGGAAATCAAAAGGGCCAAAGAACCAAGAGAAAGTCCACCTTGTGTCTCTAATCGA 1277  
Db 544 -----AspSerLeuValProAlaSerGlnArgGluLeuProArgThrGlySer----- 559  
QY 1278 ATCAGCTCAGGACTGCCATTCGACTATGAGTGCACCAAGAGAAATGCCCTTCTCTTAT 1337  
Db 560 -----SerValSerLeuThrLysGluAsnLeuTyrLeu----- 570  
QY 1338 TGTAACCTCTGCTGATCTCTAT-----CCTCTTACTCCAAAGCTTCCCGGCT 1388

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Db 571 -----GlySerHisSerThrLysGluProThrLysLysSerMetGluAlaLys 586
QY 1389 TTCTAGCCTGGCTATGTCCTAATAATATCCACTGGGAGAAAGAGATTTTGCAAAGTGCA 1448
Db 586 sSerAsp-----LysLysLeuThrThrValVa 595
QY 1449 AGGACCTAAACA-----TCTCATCAGTATCCAGTGGTAAAGGCCCTCCTGGCTGTCT 1502
Db 595 lIleProLysAlaLeuPheThrAspGlnTyrAsp-----Le 607
QY 1503 GAGGCTAGGTGGGTTGAAAGCCCAAGGAGTCACTG 1536
Db 607 uThrThrGlyGly---GluGlyArgGluSerMet 617

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Search completed: September 13, 2004, 10:25:30  
Job time : 97.5 secs

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 13, 2004, 10:03:01; Search time 40.5 Seconds  
(without alignments)  
5217.301 Million cell updates/sec

Title: US-10-079-111-2

Perfect score: 3604

Sequence: 1 cctgacagtcagagctt.....aaacatttaaaaaaaaaa 2029

Scoring table:

BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 283362

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame\_n2p.model -DEV=xlp  
-Q/cgn2\_1/USPTO\_spool\_p/US10079111/runat\_13092004\_102125\_1816/app.query.fasta\_1.2183  
-DB=SwissProt 42 -QFMT=fastan -SUFFIX=xsp -MINMATCH=0.1 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10079111\_@CGN\_1\_1\_56\_@runat\_13092004\_102125\_1816 -NCPUS=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOB=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	233.5	6.5	362	1 CD44_CRIGR	P20944 cricetus
2	228.5	6.3	503	1 CD44_RAT	P26051 rattus norv
3	222.5	6.2	362	1 CD44_FAPHA	P14745 papio hamad
4	221	6.1	742	1 CD44_HUMAN	P16070 h cd44 anti
5	212.5	5.9	431	1 CD44_MESAU	Q60522 m cd44 anti
6	211	5.9	778	1 CD44_MOUSE	P15379 mus musculu
7	208.5	5.8	366	1 CD44_BOVIN	Q29423 bos taurus
8	202.5	5.6	351	1 CD44_CANFA	Q28284 canis faml
9	186	5.2	359	1 CD44_HORSE	Q05078 equus cabal
10	152.5	4.2	3562	1 PGCV_CHICK	Q90953 gallus gall
11	150	4.2	537	1 PGCA_PIG	Q29011 sus scrofa
12	148.5	4.1	2109	1 PGCA_CHICK	P07898 gallus gall
13	145	4.0	277	1 TS66_HUMAN	P98066 homo sapien
14	144	4.0	275	1 TS66_MOUSE	O08859 mus musculu
15	143	4.0	2364	1 PGCA_BOVIN	P13608 bos taurus
16	139.5	3.9	2333	1 PGCA_CANFA	Q28343 canis faml
17	138.5	3.8	2415	1 PGCA_HUMAN	P16112 homo sapien
18	137	3.8	276	1 TS66_RABIT	P98065 oryctolagus

19	136.5	3.8	2124	1 PGCA_RAT	P07897 rattus norv
20	132.5	3.7	2132	1 PGCA_MOUSE	Q61282 mus musculu
21	131.5	3.6	912	1 PGCB_BOVIN	Q28062 bos taurus
22	131.5	3.6	883	1 PGCB_MOUSE	Q61361 mus musculu
23	130.5	3.6	883	1 PGCB_RAT	P55068 rattus norv
24	128	3.6	2738	1 PGCV_RAT	Q9erb4 rattus norv
25	127.5	3.5	1321	1 PGCN_HUMAN	O14594 homo sapien
26	127.5	3.5	3358	1 PGCV_MOUSE	Q62059 mus musculu
27	126	3.5	1257	1 PGCN_RAT	P55067 rattus norv
28	122	3.4	394	1 PGCA_RABIT	Q28670 oryctolagus
29	120	3.3	3396	1 PGCV_HUMAN	P13611 homo sapien
30	118	3.3	341	1 BRA1_MOUSE	Q9esm3 mus musculu
31	117	3.2	340	1 BRA1_HUMAN	Q9gav7 homo sapien
32	115	3.2	3381	1 PGCV_BOVIN	P81282 bos taurus
33	113	3.1	341	1 BRA1_RAT	Q9esm2 rattus norv
34	113	3.1	892	1 LDL2_XENLA	Q99088 xenopus lae
35	112.5	3.1	417	1 PGCB_FELCA	P41725 felis silve
36	112	3.1	390	1 VGL1_HSV11	P06487 herpes simp
37	112	3.1	1268	1 PGON_MOUSE	P55066 mus musculu
38	111.5	3.1	402	1 ODP2_MYCPN	P75392 mycoplasma
39	110	3.1	354	1 PLK_HUMAN	P10915 homo sapien
40	109.5	3.0	355	1 PLK_CHICK	P07354 gallus gall
41	109	3.0	354	1 PLK_RAT	P03994 rattus norv
42	109	3.0	356	1 PLK_MOUSE	Q9qup5 mus musculu
43	109	3.0	1609	1 FIG2_YEAST	P25653 saccharomyc
44	107	3.0	354	1 PLK_BOVIN	P5252 bos taurus
45	106.5	3.0	1169	1 YK82_YEAST	P36170 saccharomyc

## ALIGNMENTS

### RESULT 1

CD44\_CRIGR  
ID CD44\_CRIGR STANDARD; PRT; 362 AA.  
AC P20944;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE CD44 antigen precursor (phagocytic glycoprotein I) (PGP-1) (HUTCH-I)  
DE (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte  
DE homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor).  
GN CD44.  
OS Cricetulus griseus (Chinese hamster).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
OC Cricetulus.  
OX NCBI\_TaxID=10029;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90304889; PubMed=1694723;  
RA Aruffo A., Stamenkovic I., Melnick M., Underhill C.B., Seed B.;  
RT "CD44 is the principal cell surface receptor for hyaluronate.";  
RL Cell 61:1303-1313(1990).  
CC !- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to  
CC mucosal high endothelial venule and to types I and VI collagen.  
CC Probably involved in matrix adhesion, lymphocyte activation and  
CC lymph node homing.  
CC !- SUBCELLULAR LOCATION: Type I membrane protein.  
CC !- INDUCTION: By EBV.  
CC !- PTM: Extensively modified including N- and O-linked glycosylation,  
CC addition of the glycosaminoglycan chondroitin sulfate, of sulfate,  
CC of phosphate to cytoplasmic domain serine residues.  
CC !- SIMILARITY: Contains 1 link domain.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC or send an email to license@isb-sib.ch).  
CC  
CC EMBL; M33827; AAA36967.1; -.









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QY 360 GCGTGTAGCTGCTGGGACTAAGTTTGGCGGCAAGGACCAAGCTTGARACAGCCTTGAAA 419
Db      |||:::      |||:::      |||:::      |||:::      |||:::
QY 52  LeuCysLysAlaPheAsnSerThrLeuProThrMetAlaGlnMetGlnLysAlaLeuSer 71
Db      |||:::      |||:::      |||:::      |||:::      |||:::
QY 420 GCTAGCTTTGAACTTGCAGCTATGCTGGTGGTGGAGATGGATTCGTGCTATCTCTACG 479
Db      |||:::      |||:::      |||:::      |||:::      |||:::
QY 72  IleGlyPheGluThrCysArgTyrGlyPheIle---GluGlyHisValValIleProArg 90
Db      |||:::      |||:::      |||:::      |||:::      |||:::
QY 480 ATTAGCCCAACCCCAAGTGTGGGAAAAATGGGTGGTCTGATTTGGGAAGGTTCCA 539
Db      |||:::      |||:::      |||:::      |||:::      |||:::
QY 91  IleHisProAsnSerIleCysAlaAlaAsnAsnThrGlyValTyrIleLeuThrSerAsn 110
Db      |||:::      |||:::      |||:::      |||:::      |||:::
QY 540 GTGAGCCGACAGTTTCAGCCTATTCTTACAACTCATCTGATACCTTGGACTAACTCGTC 599
Db      |||:::      |||:::      |||:::      |||:::      |||:::
QY 111 ThrSer---GlnTyrAspThrTyrCysPheAsnAlaSerAlaProProGlyGluAspCys 129
Db      |||:::      |||:::      |||:::      |||:::      |||:::
QY 600 ATTCCAGAAATTTATCACCAACCAAGATCCATATTCACAACTCAAACTGCACACAAACA 659
Db      |||:::      |||:::      |||:::      |||:::      |||:::
QY 130 -----ThrSerValThrAspLeuProAsnAlaPheAspGlyProIleThr 144
Db      |||:::      |||:::      |||:::      |||:::      |||:::
QY 660 ACAGAAATTTATGTAGTCAGTCAGTACC---TACTCGGTGGCATCCCTTACTCTCAATA 716
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QY 145 IleThrIleValAsnArgAspGlyThrArgTyrValLysLysGlyGluTyrArgThrAsn 164
Db      |||:::      |||:::      |||:::      |||:::      |||:::
QY 717 CCT-----GCCCTACT----- 728
Db      |||:::      |||:::      |||:::      |||:::      |||:::
QY 165 ProGluAspIleAsnProSerSerProThrAspAspValSerSerGlySerSerSer 184
Db      |||:::      |||:::      |||:::      |||:::      |||:::
QY 729 -----ACTACTCTCTCT 740
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QY 185 GluArgSerSerThrLeuGlyGlyTyrIlePheTyrAsnHisPheSerThrSerProPro 204
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QY 741 GCTCCAGCTTCACCTTCTATTCACGGAGAAATAATGATTGTGTACAGAAGTTTT 800
Db      |||:::      |||:::      |||:::      |||:::      |||:::
QY 205 IleProAspGluAspGly----- 210
Db      |||:::      |||:::      |||:::      |||:::      |||:::
QY 801 ATGAAACTAGCACCATGTCTACAGAACTGAACCATTTGTTGAAATAAAGCAGCANTC 860
Db      |||:::      |||:::      |||:::      |||:::      |||:::
QY 211 ---ProTyrIleThrAspSerThrAspArgThrProAlaThrArgAspGlnGlyAlaPhe 229
Db      |||:::      |||:::      |||:::      |||:::      |||:::
QY 861 AAG-----AATGAAGCTGCTGGGTTT----- 881
Db      |||:::      |||:::      |||:::      |||:::      |||:::
QY 230 AspProSerGlyGlySerHisThrThrHisGlySerGluSerAlaGlyHisSerHisGly 249
Db      |||:::      |||:::      |||:::      |||:::      |||:::
QY 882 -----GGAGG-----GTCCCCAGC 896
Db      |||:::      |||:::      |||:::      |||:::      |||:::
QY 250 SerArgGluGlyGlyAlaAsnThrThrSerGlyProLeuArgThrProGlnIleProGlu 269
Db      |||:::      |||:::      |||:::      |||:::      |||:::
QY 897 GCTCTGTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTAT 956
Db      |||:::      |||:::      |||:::      |||:::      |||:::
QY 270 TrpLeuIleIleLeuAlaSerLeu---LeuAlaLeuAlaLeuIleLeuAlaValCys--- 287
Db      |||:::      |||:::      |||:::      |||:::      |||:::
QY 957 GTCAAAGGTATGTGAAGCCTTCCCTTTTACAAACAAGATTCACAGAGGAATGATC 1016
Db      |||:::      |||:::      |||:::      |||:::      |||:::
QY 288 -----IleAlaValAsnSerArgArgCysGlyGlnLysLysLysLeuVal 303
Db      |||:::      |||:::      |||:::      |||:::      |||:::
QY 1017 GAAACCAAA-----GTAGTAAGGAGGAGAGGCCAATGATAGCAACCTTAATCAG 1067
Db      |||:::      |||:::      |||:::      |||:::      |||:::
QY 304 IleAsnAsnGlyAsnGlyAlaValGluAspArgLysSerSerGlyLeuAsn---GlyGlu 322
Db      |||:::      |||:::      |||:::      |||:::      |||:::
QY 1068 GAATCAAGAAACCTGATAAA-----AACCCAGGAAGAGTCCCAAGAGTCCAAGC 1115
Db      |||:::      |||:::      |||:::      |||:::      |||:::
QY 323 AlaSerLysSerGlnGluMetValHisLeuValAsnLysGluSerSerGluThrProAsp 342
Db      |||:::      |||:::      |||:::      |||:::      |||:::
QY 1116 AAA 1118
Db      |||:::      |||:::      |||:::      |||:::      |||:::
QY 343 Gln 343
Db      |||:::      |||:::      |||:::      |||:::      |||:::

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Q16208; Q16522; Q96J24;  
 01-APR-1990 (Rel. 14, Created)  
 01-NOV-1997 (Rel. 35, Last sequence update)  
 15-MAR-2004 (Rel. 43, Last annotation update)  
 CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I)  
 (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte  
 homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor)  
 (Heparan sulfate proteoglycan) (Epican) (CDw44).  
 CD44 OR LHR.  
 GN  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RC TISSUE=Lymphoblast;  
 RX MEDLINE=93101687; PubMed=1465456;  
 RA Sreaton G.R., Bell M.V., Jackson D.G., Cornelis F.B., Gerth U.,  
 RA Bell J.I.;  
 RT "Genomic structure of DNA encoding the lymphocyte homing receptor  
 CD44 reveals at least 12 alternatively spliced exons.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:12160-12164(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM EPIDERMAL).  
 RC TISSUE=Keratinocytes;  
 RA Kugelman L.C., Ganguly S., Haggerty J.G., Weissman S.M.,  
 RA Milstone L.M.;  
 RT "The core protein of epican, a heparan sulfate proteoglycan on  
 keratinocytes, is an alternative form of CD44.";  
 RL J. Invest. Dermatol. 99:381-385(1992).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM EPITHELIAL CD44E).  
 RX MEDLINE=91122041; PubMed=1991450;  
 RA Stamenkovic I., Aruffo A., Amiot M., Seed B.;  
 RT "The hematopoietic and epithelial forms of CD44 are distinct  
 polypeptides with different adhesion potentials for  
 hyaluronate-bearing cells.";  
 RL EMBO J. 10:343-348(1991).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORMS CD44R1 AND CD44R2).  
 RC TISSUE=Myeloid leukemia cells;  
 RX MEDLINE=91277598; PubMed=2056274;  
 RA Dougherty G.J., Lanadorp P.M., Cooper D.L., Humphries R.K.;  
 RT "Molecular cloning of CD44R1 and CD44R2, two novel isoforms of the  
 human CD44 lymphocyte 'homing' receptor expressed by hemopoietic  
 cells.";  
 RL J. Exp. Med. 174:1-5(1991).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORMS CD44SP; CD44R4 AND CD44R5).  
 RC TISSUE=Breast carcinoma;  
 RX MEDLINE=93356912; PubMed=8352881;  
 RA Tanabe K.K., Nishi T., Saya H.;  
 RT "Novel variants of CD44 arising from alternative splicing: changes in  
 the CD44 alternative splicing pattern of MCF-7 breast carcinoma cells  
 treated with hyaluronidase";  
 RL Mol. Carcinog. 7:212-220(1993).  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM RETICULOCYTE).  
 RC TISSUE=Reticulocytes;  
 RX MEDLINE=91337049; PubMed=1840487;  
 RA Harn H.J., Isola N., Cooper D.L.;  
 RT "The multispecific cell adhesion molecule CD44 is represented in  
 reticulocyte cDNA.";  
 RL Biochem. Biophys. Res. Commun. 178:1127-1134(1991).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89168434; PubMed=2466575;  
 RA Stamenkovic I., Amiot M., Pesando J.M., Seed B.;  
 RT "A lymphocyte molecule implicated in lymph node homing is a member of  
 the cartilage link protein family.";  
 RL Cell 56:1057-1062(1989).  
 RN [8]  
 RP SEQUENCE FROM N.A. (ISOFORMS SHORT-TAILED HEMATOPOIETIC AND CD44H).

RESULT 4  
 CD44 HUMAN

ID CD44 HUMAN STANDARD; PRT; 742 AA.  
 AC P16070; P22511; Q04958; Q13419; Q13957; Q13958; Q13959; Q13960;  
 AC Q13961; Q13967; Q13968; Q13980; Q15861; Q16064; Q16065; Q16066;

RX MEDLINE=89168435; PubMed=2466576;  
 RA Goldstein L.A., Zhou D.F.H., Picker L.J., Minty C.N., Bargatzse R.F.,  
 RA Ding J.F., Butcher E.C.;  
 RT "A human lymphocyte homing receptor, the hermes antigen, is related  
 RT to cartilage proteoglycan core and link proteins.";  
 RL Cell 56:1063-1072(1989).  
 RN [9]  
 RP SEQUENCE FROM N.A. (ISOFORM WITHOUT EXON 6).  
 RC TISSUE=Pancreas;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klautner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., McQuellian N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [10]  
 RP SEQUENCE OF 184-222 AND 473-625 FROM N.A. (ISOFORM KERATINOCYTE).  
 RC TISSUE=Foreskin;  
 RX MEDLINE=91177958; PubMed=2007624;  
 RA Brown T.A., Bouchard T., St John T., Wayner E., Carter W.G.;  
 RT "Human keratinocytes express a new CD44 core protein (CD44E) as a  
 RT heparan-sulfate intrinsic membrane proteoglycan with additional  
 RT exons.";  
 RL J. Cell Biol. 113:207-221(1991).  
 RN [11]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Articular cartilage;  
 RA Bosch P.P., Stevens J.W., Buckwalter J.A., Midura R.J.;  
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.  
 RN [12]  
 RP SEQUENCE OF 267-603 FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=92005448; PubMed=1717145;  
 RA Hofmann M., Rudy W., Zoeller M., Toelg C., Ponta H., Herrlich P.,  
 RA Guenther U.;  
 RT "CD44 splice variants confer metastatic behavior in rats: homologous  
 RT sequences are expressed in human tumor cell lines.";  
 RL Cancer Res. 51:5292-5297(1991).  
 RN [13]  
 RP SEQUENCE OF 223-265 FROM N.A.  
 RX MEDLINE=94198700; PubMed=8148709;  
 RA Matsumura Y., Hanbury D., Smith J., Tarin D.;  
 RT "Non-invasive detection of malignancy by identification of unusual  
 RT CD44 gene activity in exfoliated cancer cells.";  
 RL BMJ 308:619-624(1994).  
 RN [14]  
 RP SEQUENCE OF 1-22 FROM N.A.  
 RC TISSUE=Lymphoblast;  
 RX MEDLINE=92017823; PubMed=1922057;  
 RA Shivelman E., Bishop J.W.;  
 RT "Expression of CD44 is repressed in neuroblastoma cells.";  
 RL Mol. Cell. Biol. 11:5446-5453(1991).  
 RN [15]  
 RP REVIEW ON FUNCTION AND POST-TRANSLATIONAL MODIFICATIONS.  
 RX MEDLINE=22399881; PubMed=12511867;  
 RA Ponta H., Sherman L., Herrlich P.A.;  
 RT "CD44: from adhesion molecules to signalling regulators.";  
 RL Nat. Rev. Mol. Cell Biol. 4:33-45(2003).

RN [16]  
 RP PHOSPHORYLATION OF SER-706.  
 RX MEDLINE=98248445; PubMed=9580567;  
 RA Peck D., Isaacke C.M.;  
 RT "Hyaluronan-dependent cell migration can be blocked by a CD44  
 RT cytoplasmic domain peptide containing a phosphoserine at position  
 RT 325.";  
 RL J. Cell Sci. 111:1595-1601(1998).  
 RN [17]  
 RP PHOSPHORYLATION OF SER-672.  
 RX MEDLINE=22038351; PubMed=12032545;  
 RA Legg J.W., Lewis C.A., Parsons M., Ng T., Isaacke C.M.;  
 RT "A novel PKC-regulated mechanism controls CD44 ezrin association and  
 RT directional cell motility.";  
 RL Nat. Cell Biol. 4:399-407(2002).  
 RN [18]  
 RP GLYCOSYLATION AND PROCESSING.  
 RX MEDLINE=22766015; PubMed=12883358;  
 RA Bartolazzi A.;  
 RT "CD44s adhesive function spontaneous and PMA-inducible CD44 cleavage  
 RT are regulated at post-translational level in cells of melanocytic  
 RT lineage.";  
 RL Melanoma Res. 13:325-337(2003).  
 RN [19]  
 RP VARIANT BLOOD GROUP INDIAN PRO-46.  
 RX MEDLINE=96215152; PubMed=8636151;  
 RA Telen M.J., Udani M., Washington M.K., Levesque M.C., Lloyd E.,  
 RA Rao N.;  
 RT "A blood group-related polymorphism of CD44 abolishes a hyaluronan-  
 RT binding consensus sequence without preventing hyaluronan binding.";  
 RL J. Biol. Chem. 271:7147-7153(1996).  
 CC -!- FUNCTION: Receptor for hyaluronic acid (HA). Mediates cell-cell  
 CC and cell-matrix interactions through its affinity for HA, and  
 CC possibly also through its affinity for other ligands such as  
 CC osteopontin, collagens, and matrix metalloproteinases (MMPs).  
 CC Adhesion with HA plays an important role in cell migration, tumor  
 CC growth and progression. Also involved in lymphocyte activation,  
 CC recirculation and homing, and in hematopoiesis. Altered expression  
 CC or dysfunction causes numerous pathogenic phenotypes. Great  
 CC protein heterogeneity due to numerous alternative splicing and  
 CC post-translational modification events.  
 CC -!- SUBUNIT: Interacts with HA, as well as other glycosaminoglycans,  
 CC collagen, laminin, and fibronectin via its N-terminal segment.  
 CC Interacts with ANK, the ERM proteins (VIL2, RDX and  
 CC MSN), and NF2 via its C-terminal segment.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Comment=Additional isoforms seem to exist. Additional isoforms  
 CC are produced by alternative splicing of 10 out of 19 exons  
 CC within the extracellular domain. Additional diversity is

Alignment Scores:  
 Pred. No.: 4.45e-11 Length: 742  
 Score: 221.00 Matches: 116  
 Percent Similarity: 32.08% Conservative: 63  
 Best Local Similarity: 20.79% Mismatches: 176  
 Query Match: 6.13% Indels: 203  
 DB: 23 Gaps: 23

US-10-079-111-2 (1-2029) x CD44\_HUMAN (1-742)  
 QY 255 TTGCGTGACAGAGCTTCCATCCAGGTGTCATGCAGAAATATGGGATCATCCCTGTGG 314  
 Db 17 LeuSerLeuAlaGlnIleAspLeuAenIleThrCysArgPheAlaGlyValPheHisVal 36  
 QY 315 AGCAAAAGCGCAACAGCAGCTGAATTTTCACAGAGCTTAAGAGCGCTGTAGCTGCTG 374  
 Db 37 GluLysAsnGlyArgTyrSerIleSerArgThrGluAlaAspLeuLysAlaPhe 56  
 QY 375 GGAATAAGTTTGGCCGGCAGACCAAGTTGAACAGCCTTGAAGCTAGCTTTGAAGT 434  
 Db 57 AsnSerThrLeuProThrMetAlaGlnMetGluLysAlaLeuSerIleGlyPheGluThr 76



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[illegible]

Db 78 ThrCysArgTyrGlyPheIle---GluGlyHisValValIleProArgIleGlnProAsn 96  
 Qy 492 CCCAAGTGTGGGAAAATGGGTGGGTGCTCTGATTGGAAAGTTCACAGTGAGCCGACAG 551  
 Db 97 AlaIleCysAlaIleAsnHisThrGlyValTyrIleLeuThrSerIleThrSer 115  
 Qy 552 TTTCGACGCCATTGTTTACAACTCATCTGACTACTTGGACTAACTCGTCGTCATTCGACAAATT 611  
 Db 116 TyrAspThrTyrCysPheAsnAlaSerAlaProLeuGluGluAspCys----- 131  
 Qy 612 ATCACCACCAAGAGTCCCATTTCAACACTCAACTCAACGTCACACAAACACACAGAAATTATT 671  
 Db 132 ---ThrSerValThrAspLeuProAsnSerPheGluGlyProValThrIleThrIleVal 150  
 Qy 672 GTCAGTCACAGTACC---TACTCGGTGGCATCCCTTACTCTACA-----ATA 716  
 Db 151 AsnArgAspGlyThrArgTyrSerLysLysGlyGluTyrArgThrHisGlnGluAspIle 170  
 Qy 717 CCTGCCCTACTACTCTCTCTCTGCTCCAGCTTCC----- 752  
 Db 171 AspAlaSerAsnThrThrAspAspValSerSerGlySerSerGlyLysSerThr 190  
 Qy 753 -----ACTCTATTCCACGGAGAAAATAATGATTTGTGTACACA 791  
 Db 191 SerGlyGlyTyrValPheHisThrTyrLeuProThrIleHisSerThrAlaAspGlnAsp 210  
 Qy 792 GAAGTTTTTATGAAACTACACACCATGCTCACAGAAACTGAACCAATTTGTTGAAATATAA 851  
 Db 211 AspProTyrPheIleGlySerThrMetAlaThr-----ThrArg 223  
 Qy 852 GCAGCAATTCAGAAATGAAGTGTGGTGGTGGAGGTCTCCACCGGCTCTGCTAGTGTCTT 911  
 Db 224 SerGlyGlyLysAspGlyArgArgGly--GlyGlyLeuProLys----- 237  
 Qy 912 GCTCTCCTCTTCTTGTGTGTGTCGACGTGGTCTTGGATTTTGCTATGCTCAAAAGGTATGTG 971  
 Db 238 -----AspAlaThrThrSerLeu-----GluGlyTyrThr 247  
 Qy 972 AAGGCCTTCCTTTTACAAACAGAAATCAGCAGAAGGAATGATC----- 1016  
 Db 248 ThrHisTyrProGluThrMetGluAsnGlyThrLeuThrProValThrProAlaLysThr 267  
 Qy 1017 -----GAAACCAAAGTAGTAAAGGAGGAGGAGCCCAAT-----GAT 1052  
 Db 268 GlyValPheGlyGluThrGluValThrValAlaGluAspSerAsnPheAsnValAspGly 287  
 Qy 1053 AGCAACCTTAATGAGGAATCAAGAAACTGAT 1085  
 Db 288 SerLeuProGlyAspGlnAspSerSerMetAsp 298  
 RESULT 6  
 CD44\_MOUSE  
 ID CD44\_MOUSE STANDARD; PRT; 778 AA.  
 AC P15379; Q05732; Q61395; Q62060; Q62061; Q62062; Q62063; Q62408;  
 AC Q62409; Q64296; Q99J14; Q9QYX8;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE CD44 antigen precursor (phagocytic glycoprotein I) (PGP-1) (HUTCH-I)  
 DE (extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte  
 DE homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor)  
 DE (LY-24).  
 GN CD44  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 4; 6; 7 AND 12).  
 RC STRAIN=DBA/2, TISSUE=Lung;  
 RX MEDLINE=93107170; PubMed=1469058;  
 RA He Q., Lesley J., Hyman R., Ishihara K., Kincade P.W.;  
 RT "Molecular isoforms of murine CD44 and evidence that the membrane

RT proximal domain is not critical for hyaluronate recognition.";

RL J. Cell Biol. 119:1711-1719(1992).

[2]

RP SEQUENCE FROM N.A. (ISOFORM 13).

RA MEDLINE=90038499; PubMed=2681416;

RX Zhou D.F.H., Ding J.F., Picker L.J., Bargatzke R.F., Butcher E.C., Goedel D.V.;

RA "Molecular cloning and expression of Pgp-1. The mouse homolog of the human H-CAM (Hermes) lymphocyte homing receptor.";

RT J. Immunol. 143:3390-3395 (1989).

[3]

RP SEQUENCE FROM N.A. (ISOFORM 13).

RX MEDLINE=90046829; PubMed=2682651;

RA Nottenburg C., Rees G., St John T.;

RA "Isolation of mouse CD44 cDNA: structural features are distinct from the primate cDNA.";

RT Proc. Natl. Acad. Sci. U.S.A. 86:8521-8525(1989).

[4]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RX MEDLINE=20318634; PubMed=10859330;

RA Wittig B.M., Johansson B., Zoeller M., Schwaerzler C., Guenther U.;

RA "Abrogation of experimental colitis correlates with increased apoptosis in mice deficient for CD44 variant exon 7 (CD44v7).";

RL J. Exp. Med. 191:2053-2064(2000).

[5]

RP SEQUENCE FROM N.A. (ISOFORM 13).

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Fellgold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Schmen C.M., Schuler G.D., Altschul S.F., Zelling B., Buettow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J.J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[6]

RP SEQUENCE FROM N.A. (ISOFORM 13).

RC STRAIN=C57BL/6J; TISSUE=Embryo;

RX MEDLINE=22354683; PubMed=12466851;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaudo I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sanderlin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

RA Hara A., Hashizume W., Imotani K., Iehi Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;

RA "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

[7]

RP SEQUENCE OF 8-778 FROM N.A. (ISOFORM 13).

RX MEDLINE=90094420; PubMed=2403559;

RA Wolffe E.J., Gause W.C., Pelfrey C.M., Holland S.M., Steinberg A.D., August J.T.;

RA "The cDNA sequence of mouse Pgp-1 and homology to human CD44 cell surface antigen and proteoglycan core/link proteins.";

RT J. Biol. Chem. 265:341-347(1990).

[8]

RP SEQUENCE OF 224-637 FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6; 7 AND 8).

RC STRAIN=GR;

RX MEDLINE=93219085; PubMed=8464707;

RA Toelig C., Hofmann M., Herrlich P., Ponta H.;

RA "Splicing choice from ten variant exons establishes CD44 variability.";

RT Nucleic Acids Res. 21:1225-1229(1993).

[9]

RP SEQUENCE OF 224-637 FROM N.A. (ISOFORM 9).

RC STRAIN=BALB/c;

RX MEDLINE=93286043; PubMed=8509359;

RA Screation G.R., Bell M.V., Bell J.I., Jackson D.G.;

RA "The identification of a new alternative exon with highly restricted tissue expression in transcripts encoding the mouse Pgp-1 (CD44) homing receptor. Comparison of all 10 variable exons between mouse, human, and rat.";

RT J. Biol. Chem. 268:12235-12238(1993).

[10]

RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS 10 AND 11).

RC STRAIN=Swiss Webster;

RX MEDLINE=96355396; PubMed=8702806;

RA Yu Q., Toole B.P.;

RA "A new alternatively spliced exon between v9 and v10 provides a molecular basis for synthesis of soluble CD44.";

RL J. Biol. Chem. 271:20603-20607(1996).

CC -!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to mucosal high endothelial venule and to types I and VI collagen. Probably involved in matrix adhesion, lymphocyte activation and lymph node homing.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=13;

CC Name=1;

CC IsoId=P15379-14; Sequence=Displayed;

CC Name=2;

CC IsoId=P15379-7; Sequence=VSP\_007329;

CC Name=3;

CC IsoId=P15379-8; Sequence=VSP\_007330;

CC Name=4; Synonyms=M2;

CC IsoId=P15379-4; Sequence=VSP\_007331;

CC Name=5;

CC IsoId=P15379-9; Sequence=VSP\_007332;

CC Name=6; Synonyms=M3;

CC IsoId=P15379-5; Sequence=VSP\_005326;

CC Name=7; Synonyms=M4;

CC IsoId=P15379-6; Sequence=VSP\_005327;

CC Name=8;

CC IsoId=P15379-10; Sequence=VSP\_007330, VSP\_007334;

CC Name=9;

CC IsoId=P15379-11; Sequence=VSP\_007332, VSP\_007335;

CC Name=10;

CC IsoId=P15379-12; Sequence=VSP\_007336, VSP\_007337;

CC Name=11;

CC IsoId=P15379-13; Sequence=VSP\_007338, VSP\_007339;

CC Name=12; Synonyms=M1;

CC IsoId=P15379-3; Sequence=VSP\_005328;

CC Name=13; Synonyms=M0;





OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Beagle; TISSUE=Thymus;  
 RA MEDLINE=94250687; PubMed=7514890;  
 RX Milde K.F., Alejandro R., Mintz D.H., Pastori R.L.;  
 RL "Molecular cloning of the canine CD44 antigen cDNA";  
 RT Biochim Biophys. Acta 1218:112-114(1994).  
 CC -!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to  
 CC mucosal high endothelial venule and to types I and VI collagen.  
 CC Probably involved in matrix adhesion, lymphocyte activation and  
 CC lymph node homing.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- TISSUE SPECIFICITY: Lymph nodes.  
 CC -!- FTM: Extensively modified including N- and O-linked glycosylation,  
 CC addition of the glycosaminoglycan chondroitin sulfate, of sulfate,  
 CC of phosphate to cytoplasmic domain serine residues (By  
 CC similarity).  
 CC -!- SIMILARITY: Contains 1 link domain.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; Z27115; CAAB1630.1; -;  
 DR PIR; S45305; S45305.  
 DR HSP; P98066; ITSG.  
 DR InterPro; IPR001231; CD44 antigen.  
 DR InterPro; IPR000538; Link.  
 DR Pfam; PF00193; Xlink; 1.  
 DR PRINTS; PR00658; CD44.  
 DR PRINTS; PR01265; LINKMODULE.  
 DR ProDom; PD000918; Link; 1.  
 DR SMART; SM00445; LINK; 1.  
 DR PROSITE; PS01241; LINK; 1.  
 DR Cell adhesion; Transmembrane; Glycoprotein; Phosphorylation; Receptor;  
 KW Proteoglycan; Signal; Alternative splicing;  
 KW Pyrolicidone carboxylic acid.  
 FT NON\_TER 1 1  
 FT SIGNAL <1 13 POTENTIAL.  
 FT CHAIN 14 >351 CD44 ANTIGEN.  
 FT DOMAIN 14 263 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 264 284 POTENTIAL.  
 FT DOMAIN 285 >351 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 41 112 LINK.  
 FT DOMAIN 143 151 ARG/LYS-RICH (BASIC).  
 FT DOMAIN 218 263 STEM.  
 FT MOD\_RES 14 14 PYROLIDONE CARBOXYLIC ACID (BY  
 FT SIMILARITY).  
 FT DISULFID 46 111 BY SIMILARITY.  
 FT DISULFID 70 90 BY SIMILARITY.  
 FT MOD\_RES 286 286 PHOSPHORYLATION (BY PKC) (PARTIAL) (BY  
 FT SIMILARITY).  
 FT MOD\_RES 320 320 PHOSPHORYLATION (PARTIAL) (BY  
 FT SIMILARITY).  
 FT CARBOHYD 18 18 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 50 50 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 250 250 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT NON\_TER 351 351  
 SQ SEQUENCE 351 AA; 38066 MW; E73387E70E20C0E0 CRC64;

## Alignment Scores:

Pred. No.: 1,51e-09 Length: 351  
 Score: 202.50 Matches: 84  
 Percent Similarity: 23.05% Conservative: 49  
 Best Local Similarity: 27.40% Mismatches: 145

Query Match:	5.62%	Indels:	81
DB:	1	Gaps:	15
US-10-079-111-2 (1-2029) x CD44_CANFA (1-351)			
QY 225 TGGACACGAGGCTCTGGTCCAGAGGCTTTTCGTCGTCAGAACGAGCTTTCATCCAGGTG 284			
Db 3 TrpGlyLeuCysLeuLeu-----ArgLeuSerLeuAlaGlnIleAspLeuAsnIle 19			
QY 285 TCATGCAGAAATTATGGGATCACCTTGTGAGCAAAAGCGCAACGACGAGCTGAAATTC 344			
Db 20 ThrCysArgTyrAlaGlyValPheHisValGluLysAsnGlyArgTyrSerIleSerArg 39			
QY 345 ACAGAACTAAGGAGCCCTGTAGGCTGTGGGACTAAGTTTGGCCGCGAAGGACCAAGTT 404			
Db 40 ThrAlaAlaAlaAspLeuCysLysAlaPheAsnSerThrLeuProThrMetAlaGlnMet 59			
QY 405 GAAACAGCCTTGAAGCTAGCTTTGAACTTGACGCTATGGCTGTGGGTGGAGATGGATTC 464			
Db 60 GluArgAlaLeuSerValGlyPheGluThrCysArgTyrGlyPheIle-----GluGlyHis 78			
QY 465 GTGGTCATCTCTAGGATTAGCCCAACCCCAAGTGTGGGAAAATAATGGGTGGGTGCTCTG 524			
Db 79 ValValIleProArgIleGlnProAsnAlaIleCysAlaAlaAsnHisThrGlyValTyr 98			
QY 525 ATTTGGAAGTTCCAGTGGAGCCGACAGTTTGCAGCCTATTGTACAACTCATCTGATCTACT 584			
Db 99 Ile---LeuIleSerAsnThrSerGlnTyrAspThrTyrCysPheAsnAlaSerAlaPro 117			
QY 585 TGGACTAACTCGTGCATTCCAGAAATTATCACCAACCAAGATCCCATATATTCAACACTCAA 644			
Db 118 ProGluGluAspCys-----ThrSerValThrHisLeuProAsnAlaPhe 132			
QY 645 ACTGCAACACAAACACAGAAATTTATGTGACGTGACAGTACC---TACTCGTGGGATCC 701			
Db 133 AspGlyProIleThrIleThrIleValAsnArgAspGlyThrArgTyrSerGlnLysGly 152			
QY 702 CCTTACTCTACATACTCTGCC-----CCTACTACTCTCTCTCTCTCTCTCTCTCTCT 752			
Db 153 GluTyrArgThrAsnProGluAspIleAsnProSerAsnProThrAspAspValSer 172			
QY 753 ACTTCTATTCCACGGAGAAAAAATGATTGTGTGCACAGAGTCTTT-----800			
Db 173 SerGlySerSerSerGluArgSerThrSerAlaGlyTyrAsnIlePheHisThrHisLeu 192			
QY 801 -----ATGGAACTAGCACCATCTGTCTACAGAACTGAA---833			
Db 193 ProThrAlaTyrProThrGluAspGlnAspSerSerArgValSerSerAsnSerAspHis 212			
QY 834 -----CCATTCTTGTGAAAATAAAGCAGCA 857			
Db 213 ThrProIleThrLysAspHisAspSerSerValHisProSerGluArgSerHisThrThr 232			
QY 858 TTCAAGATGAAGCTCTGGTCTT-----GGAGGT-----887			
Db 233 HisGlySerGluSerAlaGlyHisSerSerGlySerGlnGluGlyGlyAlaAsnThrThr 252			
QY 888 -----GTCCACGGCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 923			
Db 253 SerGlyProMetArgLysProGlnIleProGluTyrPheIleIleLeuAlaSerLeu--- 271			
QY 924 TTTGGTCTGCAGCTGGTCTTGGATTTCCTATGTCTCAAAAGGTATGTGAAGGCCCTTCCCT 983			
Db 272 LeuAlaLeuAlaLeuIleLeuAlaValCysIleAla-----283			
QY 984 TTTCAACAAGAATCAGCAGAGGAAATGATCGAAACCAAGTAGTAAGGAGGAGAAG 1043			
Db 284 -----ValAsnSerArgArgArgCysGlyGlnLysLysLysLeuValIleAsnAsn 300			
QY 1044 GCCAAT-----CATAGCAACCT-----AATCAGGAATCAAGAAACT 1082			
Db 301 GlyAsnGlyAlaValGlyAspArgLysProSerGlyIleAsnGlyGluAlaSerLysSer 320			



QY 1083 GATAAA-----RACCAGAGAGTCCAGAGTCCAGCAAACTACC 1124  
 Db 321 GlnGluMetValHisLeuValAsnLysGluProSerGluThrProAspGlnTyrThr 339  
 RESULT 9  
 CD44\_HORSE  
 ID CD44\_HORSE STANDARD; PRT; 359 AA.  
 AC Q05078; 1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE CD44 antigen precursor (phagocytic glycoprotein I) (PGP-1) (HUTCH-I)  
 DE (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte  
 DE homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor).  
 GN CD44.  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93170897; PubMed=8436424;  
 RA Tavernor A.S., Deverson E.V., Coadwell W.J., Lunn D.P., Zhang C.,  
 RA Davis W., Butcher G.W.;  
 RT "Molecular cloning of equine CD44 cDNA by a COS cell expression  
 RT system";  
 RL Immunogenetics 37:474-477(1993).  
 CC -!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to  
 CC mucosal high endothelial venule and to types I and VI collagen.  
 CC Probably involved in matrix adhesion, lymphocyte activation and  
 CC lymph node homing.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- PTM: Extensively modified including N- and O-linked glycosylation,  
 CC addition of the glycosaminoglycan chondroitin sulfate, of sulfate,  
 CC of phosphate to cytoplasmic domain serine residues.  
 CC -!- SIMILARITY: Contains 1 link domain.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; X66862; CAA47331.1; -.  
 DR FIR; I46245; S24240.  
 DR HSSP; P98066; ITSG.  
 DR InterPro; IPR001231; CD44\_antigen.  
 DR InterPro; IPR000538; Link.  
 DR Pfam; PF00193; Xlink; 1.  
 DR PRINTS; PR00659; CD44.  
 DR PRINTS; PR01265; LINKMODULE.  
 DR ProDom; PD000918; Link; 1.  
 DR SMART; SM00445; LINK; 1.  
 DR PROSITE; PS01241; LINK; 1.  
 DR Cell adhesion; Transmembrane; Glycoprotein; Phosphorylation; Receptor;  
 KW Proteoglycan; Signal; Alternative splicing;  
 KW Pyrolysine carboxylic acid.  
 FT SIGNAL 1 20  
 FT CHAIN 21 359  
 FT DOMAIN 21 266  
 FT EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 267 287  
 FT DOMAIN 288 359  
 FT CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 48 119  
 FT LINK.  
 FT DOMAIN 150 158  
 FT ARG/LYS-RICH (BASIC).  
 FT DOMAIN 225 266  
 FT STEM.  
 FT MOD\_RES 21 21  
 FT PHOSPHOLIPID CARBOXYLIC ACID (BY  
 FT SIMILARITY).  
 FT DISULFID 53 118  
 FT BY SIMILARITY.  
 FT DISULFID 77 97  
 FT BY SIMILARITY.  
 FT MOD\_RES 289 289  
 FT PHOSPHORYLATION (BY PKC) (PARTIAL) (BY  
 FT SIMILARITY).

FT MOD\_RES 323 323 PHOSPHORYLATION (PARTIAL) (BY  
 FT SIMILARITY).  
 FT CARBOHYD 25 25 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 359 AA; 38990 MW; BE20461C587AA34B CRC64;  
 Alignment Scores:  
 Pred. No.: 4,21e-08 Length: 359  
 Score: 186.00 Matches: 84  
 Percent Similarity: 36.95% Conservative: 42  
 Best Local Similarity: 24.63% Mismatches: 159  
 Query Match: 5.16% Indels: 56  
 DB: 1 Gaps: 11  
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 QY 255 TTGCGTGCAAGAGAGCTTTCATCCAGGTGTCATGAGAAATTATGGGGATCACCTTGTG 314  
 Db 17 LeuSerLeuAlaGlnIleAspLeuAsnIleThrCysArgTyrAlaGlyValPheHisVal 36  
 QY 315 AGCAAAAGGCGAACCCAGCAGCTGAATTTACAGAGAGCTAAGAGGCGCTGTAGCTGCTG 374  
 Db 37 GluLysAsnGlyArgTyrSerIleSerArgThrGluAlaAspLeuCysLysAlaPhe 56  
 QY 375 GGACTAAGTTTGGCGGCAAGGACCAAGTTGAAACAGCCTTGAAGCTAGCTTTGAAACT 434  
 Db 57 AsnSerThrLeuProThrMetAlaGlnMetGlnLysAlaLeuAsnIleGlyPheGluThr 76  
 QY 435 TCAGCTATGCTGGTGGAGATGAGATTCGTGGTTCATCTCTAGGATAGCCCAACCC 494  
 Db 77 CysArgIleGlyPheIle---GluGlyHisValIleProProIleHisProAsnSer 95  
 QY 495 AAGTGTGGGAAATAATGGGTGGTGTCTGCTGCTGTTTGGAGGTTCCAGTGGCCGACAGTTT 554  
 Db 96 IleCysAlaAlaAsnAsnThrGlyValTyrIleLeuThrSerAsnThrSer---GlnTyr 114  
 QY 555 GCAGCCTATTGTACAACTCATCTGATCTATCTGGACTAATCTCGTGCTT----- 602  
 Db 115 AspThrTyrCysPheAsnAlaSerAlaProGluGluAspCysThrSerValThrAsp 134  
 QY 603 -----CCAGAAATTATCACC----- 617  
 Db 135 LeuProAsnAlaPheGluGlyProIleThrIleThrIleValAsnArgAspGlyThrArg 154  
 QY 618 -----ACCAAGATCCCATATTCAACACTCAAACTCAAACTGCAACA 653  
 Db 155 TyrThrLysLysGlyGluTyrArgThrAsnProGluAspIleAsnProSerThrProAla 174  
 QY 654 CAAACACAGAAATTTATTCAGTGACAGTACTCTCGTGGCAGTCCCTACTCTACTCTACA 713  
 Db 175 AspAspValSerSerGlySerSerGluAspSerThrSerGlyGlyTyrSerIle 194  
 QY 714 ATACCTGCC-----CCTACTACTCTCTCT----- 737  
 Db 195 PheHisThrHisLeuProThrArgProThrGlnAspGlnSerProTrpValSer 214  
 QY 738 -----CCTGCTCCAGCTTCCACTTCTATTCCACGAGAGAAAAAATTGATTGTGTGCA 791  
 Db 215 AspSerProGluLysThrProThrThrLysAspArgAlaSerGlyGlyArgAlaGlnThr 234  
 QY 792 GAAGTTTTTATGGAACACTAGCACCATGTCTACAGAAACTGAACCACTTTGTTGAAATAAA 851  
 Db 235 ThrHisGlySerGluThrSerGlyHisSerThrGlySerGln-----GluGlyGly 251  
 QY 852 GCAGATTCGAAGATGAAGCTCTGGTGGTGGAGGTGTCGCCACGGCTCTGCTAGTCTT 911  
 Db 252 AlaSerThrThrSerGlyProIleArgArgProGlnIleProGluTrpLeuIleLeu 271  
 QY 912 GCTCTCTCTCTCTTGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 971  
 Db 912 GCTCTCTCTCTCTTGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 971

Db 272 AlaSerLeu---LeuAlaLeuAlaLeuIleLeuAlaValCys-----Ile 285  
 QY 972 AAGCGCTTCCTTTTACAAACAGATCAGCAGAGGAATGATCGAAACCAA----- 1025  
 Db 286 AlaValAsnSerArgArgCysGlyGlnLysLysLeuValIleAsnAsnGlyAsn 305  
 QY 1026 ---GTAGTAAGCAGGAGAGGCAATGATAGCAACCTAATGAGGAATCAAGAAACT 1082  
 Db 306 GlyAlaValAspAspArgLysAlaSerGlyLeuAsn---GlyGluAlaSerArgSerGln 324  
 QY 1083 GATAAAACCCAGAGAGTCCCAAGAGTCCCAAGCAAACTACCTGCGATCCCTCGAAGCT 1142  
 Db 325 GluMetValHisLeuValAsnLysGluSerSerGluThrGlnAspGlnPheMetThrAla 344  
 QY 1143 GAA 1145  
 Db 345 Asp 345  
 RESULT 10  
 PGCV\_CHICK STANDARD; PRT; 3562 AA.  
 AC Q90953; Q90945;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Versican core protein precursor (Large fibroblast proteoglycan)  
 DE (Chondroitin sulfate proteoglycan core protein 2) (PG-M).  
 GN CPG2.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 [1]  
 SEQUENCE FROM N.A. (ISOFORMS V0 AND V1).  
 RP STRAIN=White leghorn; TISSUE=Limb bud;  
 RC MEDLINE=93300846; PubMed=8314802;  
 RA Shinomura T., Nishida Y., Ito K., Kimata K.;  
 RT "cDNA cloning of PG-M, a large chondroitin sulfate proteoglycan  
 expressed during chondrogenesis in chick limb buds. Alternative  
 RT spliced multiforms of PG-M and their relationships to versican.";  
 RL J. Biol. Chem. 268:14461-14469(1993).  
 CC -!- FUNCTION: May play a role in intercellular signaling and in  
 CC connecting cells with the extracellular matrix. May take part in  
 CC the regulation of cell motility, growth and differentiation. Binds  
 CC hyaluronic acid.  
 CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Comment=Additional isoforms seem to exist;  
 CC Name=V0;  
 CC IsoId=Q90953-1; Sequence=Displayed;  
 CC Name=V1;  
 CC IsoId=Q90953-2; Sequence=VSP\_003093;  
 CC -!- TISSUE SPECIFICITY: Prechondrogenic condensation area of  
 CC developing limb buds.  
 CC -!- DEVELOPMENTAL STAGE: Disappears after the cartilage development  
 CC (By similarity).  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.  
 CC -!- SIMILARITY: Contains 2 link domains.  
 CC -!- SIMILARITY: Contains 2 EGF-like domains.  
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.  
 CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; X60226; CAA42787.1; -.

DR EMBL; D13542; BAA02742.1; -.  
 DR PIR; A47171; A47171.  
 DR HSP; P00740; 1EDM.  
 DR InterPro; IPR000152; Asx\_hydroxyl\_s.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF\_like.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR001304; Lectin\_C.  
 DR InterPro; IPR000538; Link.  
 DR InterPro; IPR004336; Sushi\_SCR\_CCP.  
 DR Pfam; PF00008; EGF; 2.  
 DR Pfam; PF00047; ig; 1.  
 DR Pfam; PF00059; lectin\_c; 1.  
 DR Pfam; PF00084; sushi; 1.  
 DR Pfam; PF00193; Xlink; 2.  
 DR PRINTS; PR01265; LINKMODULE.  
 DR ProDom; PD000918; Link; 2.  
 DR SMART; SM00032; CCP; 1.  
 DR SMART; SM00034; CLECT; 1.  
 DR SMART; SM00179; EGF\_CA; 1.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00445; LINK; 2.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE; PS00615; C-TYPE\_LECTIN\_1; 1.  
 DR PROSITE; PS00041; C-TYPE\_LECTIN\_2; 1.  
 DR PROSITE; PS00022; EGF\_1; 2.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR PROSITE; PS00026; EGF\_3; 2.  
 DR PROSITE; PS01187; EGF\_CA; 1.  
 DR PROSITE; PS00835; IG\_LINK; 1.  
 DR PROSITE; PS01241; LINK; 2.  
 KW Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi;  
 KW Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain;  
 FT HYALURONIC ACID; Alternative splicing.  
 FT SIGNAL 1 26 POTENTIAL.  
 FT CHAIN 27 3562 VERSICAN CORE PROTEIN.  
 FT DOMAIN 27 143 IG-LIKE V-TYPE.  
 FT DOMAIN 166 243 LINK 1.  
 FT DOMAIN 264 345 LINK 2.  
 FT DOMAIN 3254 3290 EGF-LIKE 1.  
 FT DOMAIN 3292 3328 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 3341 3455 C-TYPE LECTIN.  
 FT DOMAIN 3460 3518 SUSHI.  
 FT DISULFID 44 129 BY SIMILARITY.  
 FT DISULFID 171 242 BY SIMILARITY.  
 FT DISULFID 195 216 BY SIMILARITY.  
 FT DISULFID 269 344 BY SIMILARITY.  
 FT DISULFID 293 314 BY SIMILARITY.  
 FT DISULFID 3258 3269 BY SIMILARITY.  
 FT DISULFID 3263 3278 BY SIMILARITY.  
 FT DISULFID 3280 3289 BY SIMILARITY.  
 FT DISULFID 3296 3307 BY SIMILARITY.  
 FT DISULFID 3301 3316 BY SIMILARITY.  
 FT DISULFID 3318 3327 BY SIMILARITY.  
 FT DISULFID 3334 3345 BY SIMILARITY.  
 FT DISULFID 3362 3454 BY SIMILARITY.  
 FT DISULFID 3430 3446 BY SIMILARITY.  
 FT DISULFID 3461 3504 BY SIMILARITY.  
 FT DISULFID 3490 3517 BY SIMILARITY.  
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 235 235 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 329 329 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 529 529 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 709 709 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 948 948 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1409 1409 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1479 1479 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1523 1523 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1530 1530 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1625 1625 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 1751 1751 N-LINKED (GLCNAC. .) (POTENTIAL).

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FT CARBOHYD 1988 1988 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 2088 2088 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 2089 2089 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 2507 2507 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 2642 2642 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 2679 2679 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 2748 2748 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 2762 2762 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 3069 3069 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 3194 3194 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 3232 3232 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 3545 3545 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT VARSPLIC 485 1411 Missing (in isoform V1) .
SQ SEQUENCE 3562 AA; 388078 MW; 98C56E88C1602D2 CRC64;

Alignment Scores:
Pred. No.: 6.62e-05 Length: 3562
Score: 152.50 Matches: 126
Percent Similarity: 35.02% Conservative: 68
Best Local Similarity: 22.74% Mismatches: 217
Query Match: 4.23% Indels: 143
DB: 1 Gaps: 24

US-10-079-111-2 (1-2029) x PGCV_CHICK (1-3562)
QY 18 CTTGAAGCAGGGAATCCGGATGCTCGGTATGAAGTGGAGCAGTGTGAGCCTC 77
Db 162 LeuAsnPheThrGlnAlaGlnInThrCysLeuAspAsnGlyAlaValIleAlaSer--- 180
QY 78 AACATAGTCCAGAACTCTCCATCCGACTAGTATTGACCACTGCCTCTCATATCACC 137
Db 181 -----ProGlu-----GlnLeuLysAlaAlaTyrGluAspGlyPheGluGlnCysAsp 196
QY 138 AGTGGCCATCTGAGG-----TGT 155
Db 197 AlaGlyTriPheSerAspGlnThrValArgTyrProIleArgHisProArgIleGlyCys 216
QY 156 TTC-----CCTGGCTCTGAAGGGTAGGCAGCATGCCAGGTGCTTACGCTGGTG 206
Db 217 PheGlyAspLysMetGlyLysLysGlyValArgThrTyrGlyArg----- 231
QY 207 TTGCTTCTCACTTCCATCTCGGACCAGCAGGCTCCTGGTCCAGGCTCTTGGCTGCAGAA 266
Db 232 -----ArgPhePro 234
QY 267 GAGCTTTCCATCCAGCTGTTCATGCAGAAATT-----ATGGGGATCACCTTGTGAGCAAA 320
Db 235 AsnGluThrTyrAspValTyrCysTyrValGluHisMetGlnAspGluValValHisVal 254
QY 321 AAGCGCAACAGCAGCTGAATTTTCAGAAAGCTTAAGAGCCCTGTAGGCTGTGGGACTA 380
Db 255 SerValProGluLysLeuThrPheGluGluAlaLysGluLeuCysArgLysArgAspGly 274
QY 381 AGTTTCGGCGGCAAGCAGCAAGTTGAAACAGCTTGAAGCTAGCTTGAACCTGCAGC 440
Db 275 valLeuAlaSerValGlyAsnMetTyrValAlaTrpArgAsnGlyPheAspGlnCysAsp 294
QY 441 TATGGCTGGGTGGAGATGCTGGTCTATCTCTAGGATTAGCCCAACCCCAAGTGT 500
Db 295 TyrGlyTriPheLeuAlaAspGlySerValArgTyrProAlaSerValAlaArgProGlnCys 314
QY 501 GGGAAAAATGGGTGGTGCCTGATT-----TGAAG 533
Db 315 GlyGlyGlyLeuLeuGlyValArgThrLeuTyrArgTyrGluAsnGlnInThrGlyPhePro 334
QY 534 GTTCCAGTGAAGCCGACAGTTTTCAGAGCTATTGTTAGAACTCATCTGATCTTGCAGCTAAC 593
Db 335 TyrProAspSerLys----PheAspAlaTyrCysTyrGluArgLysLysIleValSerGlu 353
QY 594 TCGTGCATTCAGAAAATTATCACCACC-----AAAGATCCCATATTCACACTCAAACT 647
Db 354 ProThrThrValLysLeuValThrThrLeuLysThrAspSerValGluLeuSerSerAla 373
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QY 648 GCAACACAAACACAGAAATTTATGTCAAGTACAGTACCTACTCGGTGGCAATCCCTTAC 707
Db 374 LysValThrLeuLysProSerValPheGluSerSerValThrGluValAlaValThrLys 393
QY 708 TCTACATACCT-----GCCCTACTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCT 755
Db 394 ThrLysValProAlaTrpGluAlaThrLeuGluThrGluAspThrLysMetThrThr 413
QY 756 TCTATTCCACGGGAAAAAATTTGTTGTGTGCACAGAAAGTTTATGGAAGT----- 809
Db 414 GluValAlaGluLysArgGluMet-----GluValLeuMetGluAsnIleLys 430
QY 810 ---AGCACCATGTCTACAGAACTGAACATTTGTTGAAATAAAGACAGCATTCAGAAAT 866
Db 431 LeuThrThrLeuLeuProGlnThrValThrAspGlyGlu-IleSerProTyrAspThrLe 450
QY 867 GAAGCTGCTGGTTCGAGGTGTCCTCCACGGCTCTGCTAGTGTCTCTCTCTCTCTCTTT 926
Db 450 uGlyArgThrGluTyrAspValSerProArgLeu-----ThrGluSerThrSerAl 467
QY 927 GGTGCTGCAGCTGCTTGGATTTCCTATGTCAAAAGGTATGTGAAGGCTTCCCTTTT 986
Db 467 aAlaLeuGluValGluHisThrTyrSerGluAla-GluLeuSerGluGluGlnGly--- 485
QY 987 ACMAACAAGATCAGCAGAGGAATGATCGAAACCAAGTAGTAGTAAGAGGAGAGAG--- 1043
Db 486 --ArgSerGluSerThrGlu-AspAlaPheLeuThrSerValValPheGlnAspSerThr 504
QY 1044 -----GCCAATGATAGCAACCTAATAGGAATCAAGAAAGTATGATAAAACCCAGAA 1097
Db 505 AlaValAlaLysSerSerThrGlySerTrpGluAspIleGluThrGly-AspThrGlnLy 524
QY 1098 GAGTCCAGAGTCCAAACAACTACCGTCGATGCTCGAAGCTGAAAGTTAGATGAGA 1157
Db 524 bHisAsp-----G1 527
QY 1158 CAGAAATGAGAGACACACTGAGGCTGGTTCTTTTCATGCTCTTACCTGCCCGCAGCT 1217
Db 527 yAspAsnGlnInThrGluGlnIleGluValGlyProValMetThrAlaThr----- 543
QY 1218 GGGGAATCAAAAGGGCCAAAGAACCAAGAGAGAGAGTCCACCTTGGTTCCTAACTGGA 1277
Db 544 ---AspSerLeuValProAlaSerGlnArgGluLeuProArgThrGlySer----- 559
QY 1278 ATCAGCTCAGGACTGCGATTGGACTATGGAGTGCACCAAGAGATGCCCTTCTCTTAT 1337
Db 560 -----SerValSerLeuThrLysGluAsnLeuTyrLeu----- 570
QY 1338 TGTAACCTCTGTGGATCTCTAT-----CCTCTACTCTCAAGCTTCCACCGGCT 1388
Db 571 -----GlySerHisSerThrLysGluProThrLysLysSerMetGluAlaLy 586
QY 1389 TTCTAGCTGGCTATGCTCTAATAATATCCACTGGGAGAGAGAGTTCGCAAGTGA 1448
Db 586 sSerAsp-----LysLysLeuThrThrValVa 595
QY 1449 AGGACCTAAACA-----TCTCATCAGTATCCAGTGGTAAAGAGCCCTCTGGCTGTCT 1502
Db 595 lIleProLysAlaLeuPheThrAspGlnTyrAsp-----Le 607
QY 1503 GAGGCTAGTGGTGGTGAAGCCCAAGAGTCACTG 1536
Db 607 uThrThrGlyGly---GluGlyArgGluSerMet 617

RESULT 11
PGCA_PIG
ID PGCA_PIG STANDARD; PRT; 537 AA.
AC Q29011; O18833;
DT 01-NOV-1997 (Rel. 35, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Aggrecan core protein (Cartilage-specific proteoglycan core protein)
```



```

Db      443 PheThrSerGluAspLeuValGlnValThrSerAlaAlaThrGluGluGlyThrGlu 462
QY      807 -----ACTAGCACATGCTCTACAGAACTGAACATTTGTTGAAATAAA 851
Db      463 GlyProSerAlaThrGluAlaProSerThrSerGluGluProPheProSerGluLys 481
RESULT 12
PGCA CHICK
ID PGCA_CHICK STANDARD; PRT; 2109 AA.
AC P07898; Q90810; Q90820; Q90991; Q91047;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Aggrecan core protein precursor (Cartilage-specific proteoglycan core
DE protein) (CSFPCP).
GN AGC1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn; TISSUE=Embryo;
RX MEDLINE=94043149; PubMed=8226878;
RA Li H., Schwartz N.B., Vertel B.M.;
RT "cDNA cloning of chick cartilage chondroitin sulfate (aggrecan) core
RT protein and identification of a stop codon in the aggrecan gene
RT associated with the chondrodystrophy, nanomelia.";
RL J. Biol. Chem. 268:23504-23511(1993).
RN [2]
RP SEQUENCE OF 1042-1559 FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=90307744; PubMed=1694853;
RA Krueger R.C. Jr., Fields T.A., Mensch J.R. Jr., Schwartz N.B.;
RT "Chick cartilage chondroitin sulfate proteoglycan core protein. II.
RT Nucleotide sequence of cDNA clone and localization of the S103L
RT epitope.";
RL J. Biol. Chem. 265:12088-12097(1990).
RN [3]
RP SEQUENCE OF 1-1855 AND 1893-2109 FROM N.A.
RC TISSUE=Cartilage;
RX MEDLINE=93111968; PubMed=1339285;
RA Chandrasekaran L., Tanzer M.L.;
RT "Molecular cloning of chicken aggrecan. Structural analyses.";
RL Biochem. J. 288:903-910(1992).
RN [4]
RP ERRATUM.
RX MEDLINE=94107258; PubMed=8280087;
RA Chandrasekaran L., Tanzer M.L.;
RL Biochem. J. 296:885-887(1993).
RN [5]
RP SEQUENCE OF 1492-1610 FROM N.A.
RC STRAIN=White leghorn; TISSUE=Chondrocytes;
RX MEDLINE=95128519; PubMed=7827752;
RA Primorac D., Stover M.L., Clark S.H., Rowe D.W.;
RT "Molecular basis of nanomelia, a heritable chondrodystrophy of
RT chicken.";
RL Matrix Biol. 14:297-305(1994).
RN [6]
RP SEQUENCE OF 1894-2109 FROM N.A.
RX MEDLINE=89008500; PubMed=3170613;
RA Tanaka T., Har-El R., Tanzer M.L.;
RT "Partial structure of the gene for chicken cartilage proteoglycan
RT core protein.";
RL J. Biol. Chem. 263:15831-15835(1988).
RN [7]
RP SEQUENCE OF 1693-1855 AND 1893-2109 FROM N.A.
RX MEDLINE=86259736; PubMed=3460082;
RA Sai S., Tanaka T., Koshner R.A., Tanzer M.L.;
RT "Cloning and sequence analysis of a partial cDNA for chicken
RT cartilage proteoglycan core protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:5081-5085(1986).

```

CC CC

-!- FUNCTION: This proteoglycan is a major component of extracellular matrix of cartilaginous tissues. A major function of this protein is to resist compression in cartilage. It binds avidly to hyaluronic acid via an amino-terminal globular region. May play a regulatory role in the matrix assembly of the cartilage.

CC CC

-!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By similarity).

CC CC

-!- ALTERNATIVE PRODUCTS:

CC CC

Event=Alternative splicing; Named isoforms=2;

CC CC

Name=1;

CC CC

Isoid=P07898-1; Sequence=Displayed;

CC CC

Name=2;

CC CC

Isoid=P07898-2; Sequence=VSP\_003073;

CC CC

-!- DOMAIN: Two globular domains, G1 and G2, comprise the amino terminus of the proteoglycan, while another globular region, G3, makes up the COOH terminus. G1 contains link domains and thus consists of three disulfide-bonded loop structures designated as the A, B, B' motifs. G2 is similar to G1. The keratan sulfate (KS) and the chondroitin sulfate (CS) attachment domains lie between G2 and G3.

CC CC

-!- PTM: Contains mostly chondroitin sulfate, but also keratan sulfate chains, N-linked and O-linked oligosaccharides.

CC CC

-!- DISEASE: DEFECTS IN AGC1 ARE THE CAUSE OF NANOMELIA, A LETHAL CONNECTIVE TISSUE DISORDER AFFECTING CARTILAGE DEVELOPMENT (CHONDRODYSTROPHY) CHARACTERIZED BY SHORTENED AND MALFORMED LIMBS. AGGREGAN IS TRUNCATED AT ITS C-TERMINAL IN THE CS-2 BINDING DOMAIN AND IS NOT ANYMORE SECRETED FROM THE CHONDROCYTES.

CC CC

-!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.

CC CC

-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

CC CC

-!- SIMILARITY: Contains 4 link domains.

CC CC

-!- SIMILARITY: Contains 1 EGF-like domain.

CC CC

-!- SIMILARITY: Contains 1 C-type lectin family domain.

CC CC

-!- SIMILARITY: Contains 1 Sushi (SCR) domain.

CC CC

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CC CC

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CC CC

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DR EMBL; L21913; AAB19128.1; -;

DR EMBL; M38187; AAA48731.1; -;

DR EMBL; M88101; -; NOT ANNOTATED CDS.

DR EMBL; S74657; AAC60751.1; -;

DR EMBL; S74656; AAC60751.1; JOINED.

DR EMBL; J04028; AAA48719.1; -;

DR EMBL; M13993; AAA48720.1; -;

DR PIR; I50421; I50421.

DR HSSP; P08709; IBF9.

DR InterPro; IPR002353; Antifreeze1.

DR InterPro; IPR000152; Asx hydroxyl\_s.

DR InterPro; IPR000742; EGF\_2.

DR InterPro; IPR001881; EGF\_Ca.

DR InterPro; IPR006209; EGF\_like.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR001304; Lectin\_C.

DR InterPro; IPR000538; Link\_.

DR InterPro; IPR003324; SGXSG.

DR InterPro; IPR000436; Sushi\_SCR\_CCP.

DR Pfam; PF00008; EGF; 1.

DR Pfam; PF00059; lectin\_c; 1.

DR Pfam; PF00047; Ig; 1.

DR Pfam; PF00059; SGXSG; 56.

DR Pfam; PF00084; sushi; 1.

DR Pfam; PF00193; Xlink; 4.

DR PRINTS; PR00356; ANTIFREEZE1.

DR PRINTS; PR01265; LINKMODULE.

DR ProDom; PD000918; Link; 4.

DR SMART; SM00032; CCP; 1.

DR SMART; SM00034; CLECT; 1.





DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor-inducible protein TSG-6 precursor (TNF-  
 stimulated gene 6 protein).  
 GN TNFAIP6 OR TNFIP6 OR TSG6.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND DEVELOPMENTAL STAGE.  
 RC STRAIN=CD-1; TISSUE=Cumulus cell, Embryo, and Oocyte;  
 RX MEDLINE=98087423; PubMed=9427551;  
 RA Fuelcep C., Kamath R.V., Li Y., Otto J.M., Salustri A., Olsen B.R.,  
 RA Glant T.T., Hascall V.C.;  
 RT "Coding sequence, exon-intron structure and chromosomal localization  
 of murine TNF-stimulated gene 6 that is specifically expressed by  
 expanding cumulus cell-oocyte complexes.";  
 RL Gene 202:95-102(1997).  
 CC -1- FUNCTION: Possibly involved in cell-cell and cell-matrix  
 interactions during inflammation and tumorigenesis (By  
 similarity).  
 CC -1- DEVELOPMENTAL STAGE: Expressed in cumulus cell-oocyte complexes  
 during expansion in vivo.  
 CC -1- SIMILARITY: Contains 1 link domain.  
 CC -1- SIMILARITY: Contains 1 CUB domain.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: U83903; AAC53527.1; --  
 DR PIR: JC6506; JC6506.  
 DR HSP: P98066; ITSG.  
 DR MGD: MGI:1195266; Tnfalp6.  
 DR InterPro: IPR000859; CUB.  
 DR InterPro: IPR000538; Link.  
 DR Pfam: PF00431; CUB; 1.  
 DR Pfam: PF00193; Xlink; 1.  
 DR PRINTS: PR01265; LINKMODULE.  
 DR ProDom: PD000918; Link; 1.  
 DR SMART: SM00042; CUB; 1.  
 DR SMART: SM00445; LINK; 1.  
 DR PROSITE: PS01180; CUB; 1.  
 DR PROSITE: PS01241; LINK; 1.  
 KM Cell adhesion; Signal; Glycoprotein.  
 FT SIGNAL 1 17  
 FT CHAIN 18 275  
 FT POTENTIAL.  
 FT TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN  
 FT TSG-6.  
 FT LINK.  
 FT CUB.  
 FT BY SIMILARITY.  
 FT BY SIMILARITY.  
 FT BY SIMILARITY.  
 FT BY SIMILARITY.  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 275 AA; 30924 MW; 1CD247228260B8F9 CRC64;  
 Alignment Scores:  
 Pred. No.: 0.000184 Length: 275  
 Score: 144.00 Matches: 29  
 Percent Similarity: 51.14% Conservative: 16  
 Best Local Similarity: 32.95% Mismatches: 41  
 Query Match: 4.00% Indels: 2  
 DB: 1 Gaps: 1

US-10-079-111-2 (1-2029) x TSG6\_MOUSE (1-275)

QY 315 AGCAAAAGCGGACGAGCTGAATTTACAGAGCTAAGGAGGCTCTAGGCTGCTG 374  
 Db 42 AlaAGAlaGlyArgTyrLysLeuThrTyrAlaGluAlaLysAlaValCysGluPheGlu 61  
 QY 375 GGACTAAGTTTGGCCGCGCAAGGACCAAGTTGAAACAGCCTTGAAGCTAGCTTTGAAACT 434  
 Db 62 GlyGlyArgLeuAlaThrTyrLysGlnLeuGluAlaAlaArgLysIleGlyPheHisVal 81  
 QY 435 TGCAGCTATGCTGGGTTGGAGATGGATTCTGTGTCATCTCTAGGATTACCCAAACCCC 494  
 Db 82 CysAlaAlaGlyTyrMetAlaLysGlyArgValGlyTyrProIleValLysProGlyPro 101  
 QY 495 AAGTGTGGGAAATGGGTGGCTGCTCTGATTTGGAAGCTTCAGTGAGCCGA----- 548  
 Db 102 AsnCysGlyPheGlyLysThrGlyIleAspIleAspIleAspIleAspIleAspIleAspIle 121  
 QY 549 CAGTTTGCAGCCTATTGTTACAAC 572  
 Db 122 ArgTyrAspAlaTyrCysTyrAsn 129  
 RESULT 15  
 PGCA\_BOVIN  
 ID PGCA\_BOVIN STANDARD; PRT; 2364 AA.  
 AC P13608; P79117; Q28159;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE AggreCan core protein precursor (Cartilage-specific proteoglycan core  
 protein) (CSPCP).  
 GN AGC1.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hering T.M., Kollar J., Huynh T.D.;  
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 563-1056 FROM N.A.  
 RX MEDLINE=89380219; PubMed=2528543;  
 RA Antonsson P., Heinegaard D., Oldberg A.;  
 RT "The keratan sulfate-enriched region of bovine cartilage proteoglycan  
 consists of a consecutively repeated hexapeptide motif.";  
 RL J. Biol. Chem. 264:16170-16173(1989).  
 RN [3]  
 RP SEQUENCE OF 1609-2113 AND 2151-2364 FROM N.A.  
 RX MEDLINE=87270630; PubMed=3111460;  
 RA Oldberg A., Antonsson P., Heinegaard D.;  
 RT "The partial amino acid sequence of bovine cartilage proteoglycan,  
 deduced from a cDNA clone, contains numerous Ser-Gly sequences  
 arranged in homologous repeats.";  
 RL Biochem. J. 243:255-259(1987).  
 RN [4]  
 RP SEQUENCE OF 2114-2150 FROM N.A.  
 RX TISSUE=Cartilage; PubMed=8349621;  
 RA MEDLINE=9352525; PubMed=8349621;  
 RX Fueleop C., Walcz E., Valyon M., Glant T.T.;  
 RA "Expression of alternatively spliced epidermal growth factor-like  
 domains in aggregates of different species. Evidence for a novel  
 module.";  
 RL J. Biol. Chem. 268:17377-17383(1993).  
 RN [5]  
 RP PARTIAL SEQUENCE.  
 RX MEDLINE=85027710; PubMed=6489519;  
 RA Perin J.-P., Bonnet F., Jolles J., Jolles P.;  
 RT "Sequence data concerning the protein core of the cartilage  
 proteoglycan monomers. Characterization of a sequence allowing the  
 synthesis of an oligonucleotide probe.";  
 RL FEBS Lett. 176:37-42(1984).  
 RN [6]



```

RP PARTIAL SEQUENCE.
RX MEDLINE=87005253; PubMed=3530809;
RA Perin J.P.; Bonnet F.; Jolles P.;
RT "Structural relationship between link proteins and proteoglycan
RL monomers.";
RL FEBS Lett. 206:73-77(1986).
CC -!- FUNCTION: This proteoglycan is a major component of extracellular
CC matrix of cartilagenous tissues. A major function of this protein
CC is to resist compression in cartilage. It binds avidly to
CC hyaluronic acid via an amino-terminal globular region. May play a
CC regulatory role in the matrix assembly of the cartilage.
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
CC similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P13608-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P13608-2; Sequence=VSP_003072;
CC -!- DOMAIN: Two globular domains, G1 and G2, comprise the amino
CC terminus of the proteoglycan, while another globular region, G3,
CC makes up the C-terminus. G1 contains link domains and thus
CC consists of three disulfide-bonded loop structures designated as
CC the A, B, B' motifs. G2 is similar to G1. The keratan sulfate (KS)
CC and the chondroitin sulfate (CS) attachment domains lie between G2
CC and G3.
CC -!- CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO N-LINKED AND O-
CC LINKED (ABOUT 40%) OLIGOSACCHARIDES.
CC -!- PTM: THE KERATAN SULFATE CONTENTS DIFFER CONSIDERABLY BETWEEN
CC ADULT AND FETAL BOVINE PROTEOGLYCANS.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 4 link domains.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC -----
DR EMBL; U76615; AAB38524.1; -;
DR EMBL; L07053; -; NOT_ANNOTATED_CDS.
DR PIR; A34234; A39808.
DR PIR; T42630; T42630.
DR HSSP; P08709; 1BF9.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR000538; Link.
DR InterPro; IPR003324; SGXXSG.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00059; lectin_c; 1.
DR Pfam; PF02339; SGXXSG; 61.
DR Pfam; PF00084; sushi; 1.
DR Pfam; PF00193; Xlink; 4.
DR PRINTS; PR00356; ANTIFREEZEII.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 4.
DR SMART; SM00032; CCP; 1.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00179; EGF_CA; 1.

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DR SMART; SM00445; LINK; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; FALSE_NEG.
DR PROSITE; PS01241; LINK; 4.
KW Glycoprotein; Proteoglycan; Lectin; Signal; Sushi; EGF-like domain;
KW Calcium; Alternative splicing; Repeat; Immunoglobulin domain.
FT SIGNAL 1 16
FT CHAIN 17 2364
FT DOMAIN 25 147
FT DOMAIN 170 247
FT DOMAIN 268 349
FT DOMAIN 504 581
FT DOMAIN 602 683
FT DOMAIN 774 907
FT DOMAIN 1433 2112
FT DOMAIN 2113 2149
FT DOMAIN 2114 2364
FT DOMAIN 2161 2276
FT DOMAIN 2280 2338
FT DISULFID 51 133
FT DISULFID 175 246
FT DISULFID 199 220
FT DISULFID 273 348
FT DISULFID 297 318
FT DISULFID 509 580
FT DISULFID 533 554
FT DISULFID 607 682
FT DISULFID 631 652
FT DISULFID 2117 2128
FT DISULFID 2182 2274
FT DISULFID 2250 2266
FT DISULFID 2281 2324
FT DISULFID 2310 2337
FT CARBOHYD 126 126
FT CARBOHYD 239 239
FT CARBOHYD 333 333
FT CARBOHYD 387 387
FT CARBOHYD 611 611
FT CARBOHYD 667 667
FT VARSPPLIC 2114 2150
FT SEQUENCE 2364 AA; 246359 MW; 6FF83763420C3D4C CRC64;

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Alignment Scores:
Pred. No.: 0.000401 Length: 2364
Score: 143.00 Matches: 67
Percent Similarity: 36.80% Conservative: 18
Best Local Similarity: 29.00% Mismatches: 100
Query Match: 3.97% Indels: 46
DB: 1 Gaps: 11
US-10-079-111-2 (1-2029) x PGCA_BOVIN (1-2364)
QY 330 CAGCAGCTGAATTTCACAGAAGCTAGGAGGCTGTAGGCTGTGGACTAGTTGGCC 389
Db 262 GIULysPheThrPheGlnGluAlaAenGluCysArgGluGlyAlaArgLeuAla 281
QY 390 GGCAAGGAGCAAGTTGAAACAGCAGCTTGAAGAGCTAGCTTTGAAACTTGCAGCTATGGCTGG 449
Db 282 ThrThrGlyGlnLeuTyrlleuAlaTrpGlnGlyGlyMetAspMetCysSerAlaGlyTrp 301
QY 450 GTTGGAGATGGATTGGTGTG-----GTCACTCTAGATTAGCCAAACCCCAAGTGTGG 503
Db 302 LeuAlaAspArgSerValArgTyrProIleSerLysAlaArgProAsn-----CysGly 319
QY 504 AAAATGGGGTGGGTGCTCTCTGATT-----TGGAAAGTT 536

```



GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: September 13, 2004, 10:01:56 ; Search time 235.5 Seconds  
(without alignments)  
5436.827 Million cell updates/sec

Title: US-10-079-111-2

Perfect score: 3604

Sequence: 1 cctgacaagtcagaagctt.....aaacatttaaaaaaaaaa 2029

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2034082

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlsp  
-Q=/cgn2.1/USPTO.spool.p/US10079111/runat\_13092004\_102126\_1826/app.query.fasta\_1.2183  
-DB=SPTREMBL 25 -QFMT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pct -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10079111@cgn 1.1.344 @runat\_13092004\_102126\_1826 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SPTREMBL\_25.\*

1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phase.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_xvirus.\*  
16: sp\_bacteriaph.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1657	46.0	322	4 Q9UNF4	Q9unf4 homo sapien

ID	Q9UNF4	PRELIMINARY;	PRT;	322 AA.
AC	Q9UNF4;			
DT	01-MAY-2000 (Tremblrel. 13, Created)			
DT	01-MAR-2001 (Tremblrel. 16, Last sequence update)			
DE	01-OCT-2003 (Tremblrel. 25, Last annotation update)			
DE	Hyaluronic acid receptor.			
GN	HAR.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RA	Winkelman J.C., Basu S., Ozdemir E., Blough R.I.;			
RT	"HAR: a novel homolog of CD44 and putative hyaluronidic acid receptor encoded by a gene on human chromosome 11p15.1";			
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF127670; RAD49220.2; -			
DR	HSSP; P98066; ITSG.			
DR	GO; GO:0005540; F:hyaluronidic acid binding; IEA.			
DR	GO; GO:0004872; F:receptor activity; IEA.			
DR	GO; GO:0007155; P:cell adhesion; IEA.			
DR	InterPro; IPR000538; Link.			

#### ALIGNMENTS

RESULT 1

ID	Q9UNF4	PRELIMINARY;	PRT;	322 AA.
AC	Q9UNF4;			
DT	01-MAY-2000 (Tremblrel. 13, Created)			
DT	01-MAR-2001 (Tremblrel. 16, Last sequence update)			
DE	01-OCT-2003 (Tremblrel. 25, Last annotation update)			
DE	Hyaluronic acid receptor.			
GN	HAR.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RA	Winkelman J.C., Basu S., Ozdemir E., Blough R.I.;			
RT	"HAR: a novel homolog of CD44 and putative hyaluronidic acid receptor encoded by a gene on human chromosome 11p15.1";			
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF127670; RAD49220.2; -			
DR	HSSP; P98066; ITSG.			
DR	GO; GO:0005540; F:hyaluronidic acid binding; IEA.			
DR	GO; GO:0004872; F:receptor activity; IEA.			
DR	GO; GO:0007155; P:cell adhesion; IEA.			
DR	InterPro; IPR000538; Link.			

DR Pfam; PF00193; Xlink; 1.  
DR PRINTS; PR01265; LINKMODULE.  
DR ProDom; PD000918; Link; 1.  
DR SMART; SM00445; LINK; 1.  
DR KW Receptor.  
SQ SEQUENCE 322 AA; 35213 MW; 8B4D6D623F52D559 CRC64;  
  
Alignment Scores:  
Pred. No.: 9.12e-156 Length: 322  
Score: 1657.00 Matches: 322  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 45.98% Indels: 0  
DB: 4 Gaps: 0  
  
US-10-079-111-2 (1-2029) x Q9UNF4 (1-322)  
  
QY 183 ATGGCCAGGTGCTTCAGCCCTGGTGTGCTTCTCATTCTCCATCTGGACCAAGAGGCTCCTG 242  
Db 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20  
  
QY 243 GTCCAAAGGCTCTTGGTGCAGAAAGCTTTCATCCAGGTGTCATGCAGAAATTATGGGG 302  
Db 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
  
QY 303 ATCACCCCTTGTGAGCAAAAGGCGAACCAAGCAGCTGAATTTCCAGAACTAAGGAGGCC 362  
Db 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
  
QY 363 TGTAGCTCTGGGACTAAGTTTGGCCGCGCAAGCAAGTTCGAAACAGCTTTGAAAGCT 422  
Db 61 CysArgLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
  
QY 423 AGCTTTGAACTTGCAGCTATGCTGCTGGTGGAGATGGAATTCGTGTCATCTAGGATT 482  
Db 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100  
  
QY 483 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCTGATTTGGAAAGGTTCCAGTG 542  
Db 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
  
QY 543 AGCCGACAGTTGACGCTATTGTTTAACTATCTGATCTGACTTGGACTAAGTCTGTCATT 602  
Db 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
  
QY 603 CCAGAAATATACACCAAAAGTCCCATATTCAACACTCAACTCAACTCAACAAACA 662  
Db 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
  
QY 663 GAATTTATTGTCAAGTACAGTACCTACTCGGTGGCATCCCTTACTCTCAATACCTGCC 722  
Db 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
  
QY 723 CTTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 782  
Db 181 ProThrThrThrProAlaProAlaSerThrSerIleProArgLysLysLeuIle 200  
  
QY 783 TGTGTCACAGAGTTTTATGAACTAGCACCATGCTTACAGAACTCAACCATTTGTT 842  
Db 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
  
QY 843 GAAATAAAGCAGCATTCAAGAAATGAAGCTGCTGGGTGGAGGTGTCCTCCACGGCTCG 902  
Db 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
  
QY 903 CTAGTGTCTGCTCTCTCTCTTGTGGTGTGAGTGTGGATTTGCTATGTCAAA 962  
Db 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
  
QY 963 AGGTATGTCAAGGCTTCCTCTTTTACAAACAGAAATCAGCAAGGAATGATCGAACC 1022  
Db 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280

QY 1023 AAAGTAGTAAGGAGGAGGCAATGATAGCAACCTAATGAGGAATCAAGAAAACT 1082  
Db 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
  
QY 1083 GATAAAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGGATGCTTGGAAAGCT 1142  
Db 301 AspLysAsnProGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
  
QY 1143 GAAGTT 1148  
Db 321 GluVal 322  
  
RESULT 2  
Q8TC18 PRELIMINARY; PRT; 322 AA.  
AC Q8TC18;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Extracellular link domain-containing 1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RA Strausberg R.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC026231; AAH26231.1; -  
DR Genew; HGNC:14687; XKDL.  
DR GO; GO:0005540; F-hyaluronic acid binding; IEA.  
DR GO; GO:0007155; P-cell adhesion; IEA.  
DR InterPro; IPR000538; Link.  
DR Pfam; PF00193; Xlink; 1.  
DR PRINTS; PR01265; LINKMODULE.  
DR ProDom; PD000918; Link; 1.  
DR SMART; SM00445; LINK; 1.  
SQ SEQUENCE 322 AA; 35183 MW; 0B1EDBD76CE4610A CRC64;  
  
Alignment Scores:  
Pred. No.: 2.26e-154 Length: 322  
Score: 1643.00 Matches: 321  
Percent Similarity: 99.69% Conservative: 0  
Best Local Similarity: 99.69% Mismatches: 1  
Query Match: 45.59% Indels: 0  
DB: 4 Gaps: 0  
  
US-10-079-111-2 (1-2029) x Q8TC18 (1-322)  
  
QY 183 ATGGCCAGGTGCTTCAGCCCTGGTGTGCTTCTCATTCTGGACCAAGAGGCTCCTG 242  
Db 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrThrArgLeuLeu 20  
  
QY 243 GTCCAAAGGCTCTTGGTGCAGAAAGCTTTCATCCAGGTGTCATGCAGAAATTATGGGG 302  
Db 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
  
QY 303 ATCACCCCTTGTGAGCAAAAGGCGAACCAAGCAGCTGAATTTCCAGAACTAAGGAGGCC 362  
Db 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
  
QY 363 TGTAGGCTCTGGGACTAAGTTTGGCCGCGCAAGCAAGTTCGAAACAGCTTTGAAAGCT 422  
Db 61 CysArgLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
  
QY 423 AGCTTTGAACTTGCAGCTATGCTGCTGGTGGAGATGGAATTCGTGTCATCTAGGATT 482  
Db 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100  
  
QY 483 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCTGATTTGGAAAGGTTCCAGTG 542  
Db 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120

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QY 543 AGCCGACAGTTTGGAGCCTATTGTTACAACTCATCTGATACTTGACTGAACCTCGTGCAATT 602
Db SerArgGlnPheAlaAlaIaIyrCysYrAsnSerSerAspThrTrpThrAsnSerCysIle 140
QY 603 CCAGAAATATCACACCAAGATCCCATATTCAACACTCAAACTGCAACACAAACAACA 662
Db ProGluIleIleThrThrLysAspProllePheAsnThrGlnThrAlaThrGlnThrThr 160
QY 663 GAATTTATTGTGTCAGTACAGTACCTACTCGTGGCATCCCTTACTCTACAATACCTGCC 722
Db GluPheIleValSerAspSerThrThrYrSerValAlaSerProTyRSerThrIleProAla 180
QY 723 CCTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 782
Db ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
QY 783 TGTGTGCACAGAAGTTTATGGAACCTAGCACCATGTCTACAGAACTCAACCATTTGTT 842
Db CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
QY 843 GAAATAAAGCAGCATTCAGATCAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 902
Db GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
QY 903 CTAGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 962
Db LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysYrValLys 260
QY 963 AGGTATGTGAAGCCTCTCCCTTTTACAAACAAGATCAGCAGAAGGAAATGATCGAAACC 1022
Db ArgTyRValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
QY 1023 AAAGTAGTAAAGGAGAGAGAGCCCAATGATGACCAACCCCTTAATGAGGAATCAAGAAACT 1082
Db LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
QY 1083 GATAAAACCCAGAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGT 1142
Db AspLysAsnProGluGluSerLysSerProSerLysThrValArgCysLeuGluAla 320
QY 1143 GAAGTT 1148
Db 321 GluVal 322

RESULT 3
Q9Y5Y7
ID Q9Y5Y7 PRELIMINARY; PRT; 322 AA.
AC Q9Y5Y7;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lymphatic endothelium-specific hyaluronan receptor LYVE-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99156989; PubMed=10037799;
RA Banerji S., Ni J., Wang S.X., Clasper S., Su J., Tammi R., Jones M.,
RA Jackson D.G.;
RT "LYVE-1, a new homologue of the CD44 glycoprotein, is a lymph-specific
RT receptor for hyaluronan.";
RL J. Cell Biol. 144:789-801(1999).
DR EMBL; AF118108; AAD42764.1; -.
DR HSSP; P98066; 1TSG
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005624; C:membrane fraction; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0006928; P:cell motility; TAS.
DR GO; GO:0007160; P:cell-matrix adhesion; TAS.
DR GO; GO:0007345; P:embryogenesis and morphogenesis; TAS.
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DR GO; GO:0009611; P:response to wounding; TAS.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PRO1265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; Link; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 35238 MW; 0EBEA56729CEFF7 CRC64;
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Alignment Scores:
Pred. No.: 7,12e-154 Length: 322
Score: 1638.00 Matches: 319
Percent Similarity: 99.38% Conservative: 1
Best Local Similarity: 99.07% Mismatches: 2
Query Match: 45.45% Indels: 0
DB: 4 Gaps: 0
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US-10-079-111-2 (1-2029) x Q9Y5Y7 (1-322)

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QY 183 ATGGCCAGGTGCTTTCAGCTGCTGTTGCTTCTCACTTCCATCTGCACGAGGCTCCTG 242
Db 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTrpThrArgLeuLeu 20
QY 243 GTCCAAAGGCTCTTTCGCTGCAGACAGCTTTCATCCAGGTGTCATGCAGAAATTATGGG 302
Db 21 ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly 40
QY 303 ATCACCTTGTGAGCAAAAGCGCAACACAGCTGAATTTCAAGAACTAAGAGGCC 362
Db 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60
QY 363 TGTAGCTGCTGGGACTAAGTTTGGCCGCGCAGGACCAAGTTGNAACACCCCTGGAAGCT 422
Db 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValAspThrAlaLeuLysAla 80
QY 423 AGCTTTGAAACTTGCAGCTATGCTGGGTGGGTGGAGATGATTCGTGTCTATCTTAGGATT 482
Db 81 SerPheGluThrCysSerTyRValGlyValGlyValGlyValValIleSerArgIle 100
QY 483 AGCCCAAAACCCCAAGTGTGGGAAATAATGGGTGGGTGCTCTGATTTGGAGGTTCCAGTG 542
Db 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120
QY 543 AGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGATCTTGACTGAACCTCGTGCAATT 602
Db 121 SerArgGlnPheGlyAlaIaIyrCysYrAsnSerSerAspThrTrpThrAsnSerArgIle 140
QY 603 CCAGAAATATCACACCAAGATCCCATATTCAACACTCAAACTCAACACCAACAACA 662
Db 141 ProGluIleIleThrThrLysAspProllePheAsnThrGlnThrAlaThrGlnThrThr 160
QY 663 GAATTTATTGTGTCAGTACAGTACCTACTCGTGGGATCCCTTACTCTACAATACCTGCC 722
Db 161 GluPheIleValSerAspSerThrThrYrSerValAlaSerProTyRSerThrIleProAla 180
QY 723 CCTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 782
Db 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
QY 783 TGTGTGCACAGAAGTTTATGGAACCTAGCACCATGTCTACAGAACTCAACCATTTGTT 842
Db 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
QY 843 GAAATAAAGCAGCATTCAGATCAAGCTGCTGGGTTTGGAGGTGTCCTCCACGGCTCTG 902
Db 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
QY 903 CTAGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 962
Db 241 LeuValLeuAlaLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysYrValLys 260
QY 963 AGGTATGTGAAGCCTCTCCCTTTTACAAACAAGATCAGCAGAAGGAAATGATCGAAACC 1022
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Db 261 ArgTyrVallysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
 QY 1023 AAGTAGTAAAGAGAGAGAGCAATGATAGCAACCTAATGAGGAATCAAGAAACT 1082  
 Db 281 LybValVallysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysThr 300  
 QY 1083 GATAAAACCCAGAGAGTCCAAAGAGTCCAAAGCAAAACTACCGTGGATGCCCTGGAGCT 1142  
 Db 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
 QY 1143 GAAGTT 1148  
 Db 321 GluVal 322

## RESULT 4

## Q8BHC0

ID Q8BHC0 PRELIMINARY; PRT; 318 AA.  
 AC Q8BHC0;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Extra cellular link domain-containing 1.  
 GN XLKDL.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CZECH II; TISSUE=Lung, and Mammary gland;  
 RA Strausberg R.;  
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/60; TISSUE=Lung;  
 RX MEDLINE=22354693; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573 (2002).  
 DR EMBL; BC038653; AAH38653.1; -  
 DR EMBL; BC038892; AAH38892.1; -  
 DR EMBL; AK004726; BAC25094.1; -  
 DR MGD; MGI:2136348; Xlkd1.  
 DR GO; GO:0005886; C:plasma membrane; IDA.  
 DR GO; GO:0005540; F:hyaluronic acid binding; IDA.  
 DR GO; GO:0004888; F:transmembrane receptor activity; IDA.  
 DR GO; GO:0006027; P:glycosaminoglycan catabolism; IDA.  
 DR InterPro; IPR000538; Link.  
 DR Pfam; PF00193; Xlink; 1.  
 DR ProDom; PD000918; Link; 1.  
 DR SMART; SM00445; LINK; 1.  
 DR PROSITE; PS01241; LINK; 1.  
 SQ SEQUENCE 318 AA; 34573 MW; 34AA31AEF5430B08 CRC64;

## Alignment Scores:

Pred. No.: 1 4e-100 Length: 318  
 Score: 1103.00 Matches: 221  
 Percent Similarity: 79.18% Conservative: 60  
 Best Local Similarity: 69.72% Mismatches: 62  
 Query Match: 30.60% Indels: 3  
 DB: 11 Gaps: 3

US-10-079-111-2 (1-2029) x Q8BHC0 (1-318)

QY 198 AGCTGGTGTCTCTCACTTCCATCTGACACAGAGCTCCTGGTCCAAAGGCTTTTG 257  
 Db 6 SerLeuValLeuLeuAlaSerIleTrpThrArgHisProValGlnGlyAlaAsp 25  
 QY 258 CTGCAGAGAGCTTCCATCCAGGTGTCATCAGAAATATGCGATCACCCCTTGTGAGC 317  
 Db 26 LeuValGlnAspSerIleSer---ThrCysA-rgileMetGlyValAlaLeuValGly 44

QY 318 AAAAAAGCGCAACACGAGCGTGAATTTACAGAAAGCTAAGAGCGCTGTAGCTGCTGGGA 377  
 Db 45 ArgAsnLysAsnProGlnMetAsnPheThrGluAlaAsnGluAlaCysLysMetLeuGly 64  
 QY 378 CTAAGTTTCGCCGCGCAAGGACCAAGTTGAAACAGCCTTGAAGAGCTAGCTTTGAACCTGC 437  
 Db 65 LeuThrLeuAlaSerArgAspGlnValGluSerAlaGlnLysSerGlyPheGluThrCys 84  
 QY 438 AGCTATCGGTGGGTTCGAGATGATTCGTGGTTCATCTCTAGGATTAGCCCAACCCCAAG 497  
 Db 85 SerTyrGlyTrpValGluGlnPheSerValIleProArgIlePheSerAsnProArg 104  
 QY 498 TGTGGGAAAAATGGGGTGGGTCTCTGATTTGAAAGGTTCCAGTGGAGCCGACAGTTTGCA 557  
 Db 105 CysGlyLysAsnGlyLysGlyValLeuIleTrpAsnAlaProSerSerGlnLysPheLys 124  
 QY 558 GCCTATTGTTACAACCTCATCTGACTTCTGACTTAACCTCGTCGATTCAGAAATATATCACC 617  
 Db 125 AlaTyrCysHisAsnSerSerAspThrTrpValAsnSerCysIleProGluIleValThr 144  
 QY 618 ACCAAAGATCCCATATTCAACACTCAAACTGCAACACACAAACACAGAAATTTATTGTCACT 677  
 Db 145 ThrPheTyrProValLeuAspThrGln-----ThrProAlaThrGluPheSerValSer 162  
 QY 678 GACAGTACCTACTCGGTGGCATCCCTTACTCTTACAAATACCTGCCCTCTACTACTCTCT 737  
 Db 163 SerSerAlaTyrLeuAlaSerSerProAspSerThrThrProValSerAlaThrThr--- 181  
 QY 738 CTGTCTCCAGCTTCCACTTCTATTCCACGAGAGAAAAAATTTGATTTGTCTCAGAGATT 797  
 Db 182 ArgAlaProLeuThrSerMetAlaArgLysThrLysLysIleCysIleThrGluVal 201  
 QY 798 TTTATGGAACACTAGCACCATGTCTACAGAAACTGAAACCACTTTGTTGAAATATAAGCAGA 857  
 Db 202 TyrThrGluProIleThrMetAlaThrGluThrGluAlaPheValAlaSerGlyAlaAla 221  
 QY 858 TTCAGAAATGAAGCTGCTGGTGTGGAGGTGTCGCCACGGCTCTGCTAGTGTGCTCTC 917  
 Db 222 PheLysAsnGluAlaGlyPheGlyGlyValProThrAlaLeuLeuValLeuAlaLeu 241  
 QY 918 CTCTCTTTTGGTGTGCAGCTGGTCTTGGATTTTGTATGTCAAAGAGTATGTGAAGGCC 977  
 Db 242 LeuPhePheGlyAlaAlaAlaValLeuAlaValCysTyrValLysArgTyrValLysAla 261  
 QY 978 TTCCCTTTTACAAACAGAAATCAGCAGAGAGAAATGATCCAAACCAAAAGTAGTAAGGAG 1037  
 Db 262 PheProPheThrThrLysAsnGlnGlnLysGluMetIleGluThrLysValLysGlu 281  
 QY 1038 GAGAGGCCAATGATAGCACCCCTAATGAGGAATCAAGGAATCAAGAAACTGATAAAACCCAGAA 1097  
 Db 282 GluLysAlaAspValAsnAlaAsnGluGluSerLysLysThrIleLysAsnProGlu 301  
 QY 1098 GAGTCCCAAGAGTCCCAAGCAAAACTACCGTCCGATGCTCGGAAGCTGAAGTT 1148  
 Db 302 GluAlaLysSerProProLysThrThrValArgCysLeuGluAlaGluVal 318

## RESULT 5

## Q99NE4

ID Q99NE4 PRELIMINARY; PRT; 318 AA.  
 AC Q99NE4;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hyaluronan receptor precursor.  
 GN XLKDL OR LYVE-1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Balb/c; TISSUE=Digestive tract;

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RX MEDLINE=99156989; PubMed=100377799;
RA Banerji S.;
RT "LYVE-1, a new homologue of the CD44 glycoprotein is a lymph-specific
RT receptor for hyaluronan.";
RL J. Cell Biol. 144:789-801(1999).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=Balb/c; TISSUE=Digestive tract;
RX MEDLINE=21276443; PubMed=11278811;
RA Prevo R., Banerji S., Ferguson D.J.P., Clasper S., Jackson D.G.;
RT "Mouse LYVE-1 is an endocytic receptor for hyaluronan in lymphatic
RT endothelium.";
RL J. Biol. Chem. 276:19420-19430(2001).
DR EMBL; AJ311501; CAC33082.1; -.
DR HSSP; P98066; ITSG.
DR MGD; MGI:2136348; Xikd1.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR GO; GO:0005540; F:hyaluronic acid binding; IDA.
DR GO; GO:0004888; F:transmembrane receptor activity; IDA.
DR GO; GO:0006027; P:glycosaminoglycan catabolism; IDA.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS01241; LINK; 1.
KW Receptor; Signal.
FT SIGNAL 1 23
FT CHAIN 24 318
FT SEQUENCE 318 AA; 34641 MW; 1248974A16113330 CRC64;
SQ
Alignment Scores:
Pred. No.: 8 8e-100 Length: 318
Score: 1095.00 Matches: 219
Percent Similarity: 78.55% Conservative: 30
Best Local Similarity: 69.09% Mismatches: 64
Query Match: 30.38% Indels: 4
DB: 11 Gaps: 3
US-10-079-111-2 (1-2029) x Q99NE4 (1-318)
QY 198 AGCTGTGGTGTGCTTCTCACTCGACAGGCTCTCGTCCAAAGGCTCTTG 257
DB 6 SerLeuValPhePheLeuAlaSerIleTyrThrArgHisProValGlnGlyAlaAsp 25
QY 258 CGTGCGAGAGAGCTTTCATCCAGGTGTCATGAGAGATTCACCTTGTGAGC 317
DB 26 LeuValGlnAspLeuSerIleSer---ThrCysArgIleMetGlyValAlaLeuValGly 44
QY 318 AAAAGGCGCAACAGCAGCTGAATTCACAGAGCTTAAGGAGCGCTGAGCTGGGA 377
DB 45 ArgAsnLysAsnProGlnMetAsnPheThrGluAlaAsnGluAlaCysLysMetLeuGly 64
QY 378 CTAAGTTTGGCGGCAAGGACCAAGTTGAACAGCCTTGAAGCTAGCTTTGAACTTGC 437
DB 65 LeuThrLeuAlaSerArgAspGlnValGluSerAlaGlnLysSerGlyPheGluThrCys 84
QY 438 AGCTATGCTGGTGGATGATGATCGGTGCTCATCTAGGATAGCCCAACCCCAAG 497
DB 85 SerTyrGlyTrpValGlyGluGlnPheSerValIleProArgIlePheSerAsnProArg 104
QY 498 TGTGGGAAAAATGGGTGGGTGCTTCCTGATTTTGAAGGTTCCAGTGAGCGACAGTTTGA 557
DB 105 CysGlyLysAsnGlyLysGlyValValIleLeuTrpAsnAlaProSerSerGlnLysPheLys 124
QY 558 GCCTATGTTTACAACTCATCTGATCTAGTCTGACTTAACCTCGTGCTATCCAGAAATATCAC 617
DB 125 AlaTyrCysHisAsnSerSerAspThrTyrValAsnSerCysIleProGluIleValThr 144
QY 618 ACCAAGATCCCATATTCACACTCAACTCAACTGCAACCAACCAAGAAATTTATGTCAGT 677
DB 145 ThrPheTyrProValLeuAspThrGln-----ThrProAlaThrGluPheSerValSer 162
QY 678 GACAGTACCTACTCTCGGTGGGCTCCCTTACTCTCAATACTACCTGCCCTACTACTCTCT 737

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Db 163 SerSerAlaTyrLeuAlaSerSerProAspSerThrThrProValSerAlaThrThr--- 181
QY 738 CTGTCTCCAGCTTTCACCTTCTATTCCACGAGAGAAAAAATTGATTTGTGTACAGAGATT 797
Db 182 ArgAlaProProLeuThrSerMetAlaArgLysThrLysLysIleCysIleThrGluVal 201
QY 798 TTTATCGAAACTAGCACCATGTCTACAGAACTGAACCATTTCTTGAATAATAAGCAGCA 857
Db 202 TyrThrGluProIleThrMetAlaThrGluThrGluAlaPheValAlaSerGlyAlaAla 221
QY 858 TTCACAAATGAGCTGCTGGTTTGAGGTGTCCTCCACGCTCTGCTAGTGTGCTCTC 917
Db 222 PheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeuLeuValLeuAlaLeu 241
QY 918 CTCCTCTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 977
Db 242 LeuPhePheGlyAlaAlaAlaValLeuAlaValCysTyrValLysArgTyrValLysAla 261
QY 978 TTCCCTTTTACAAACAGAAATCGACAGAGGAAATGATCGAAACCAAGTAGTAAGGAG 1037
Db 262 PheProPheThrThrLysAsnGlnGlnLysGluMetIleGluThrLysValValLysGlu 281
QY 1038 GAGAGGCGCAATGATAGCAACCTTATGAGGAATCAAGAGAACTGATAAAACCCAGAA 1097
Db 282 GluLysAlaAspAspValAsnAlaAsnGluGluSerLysThrLysThrLysAsnProGlu 301
QY 1098 GAGTCCAGAGTCCAGCAAACTACCGTGCAGTGCCTGGAAGCTGAAAGTT 1148
Db 302 GluAlaLysSerProProLysThrThrValArgCysLeuGluAlaGluVal 318
RESULT 6
QY7522 PRELIMINARY; PRT; 201 AA.
ID AC QY7522;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Lymphatic endothelial hyaluronan receptor LYVE-1 (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Michael K.W., Xu S.-H., Voisine P., Khan T.A., Feng J., Li J.,
RA Sellke F.W., Bianchi C.;
RT "Identification of pig LYVE-1.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY304537; AAP69946.1; -.
KW Receptor.
FT NON TER 1 1
FT NON TER 201 201
SQ SEQUENCE 201 AA; 22219 MW; BAAF34E7EACBBAE3 CRC64;
Alignment Scores:
Pred. No.: 3.85e-63 Length: 201
Score: 726.50 Matches: 141
Percent Similarity: 80.60% Conservative: 21
Best Local Similarity: 70.15% Mismatches: 36
Query Match: 20.16% Indels: 3
DB: 6 Gaps: 2
US-10-079-111-2 (1-2029) x QY7522 (1-201)
QY 423 AGCTTTGAAACTTGACAGCTATCGGTGGGTGGAGATGGATTCGTGCTCATCTAGGATT 482
Db 1 SerPheGluThrCysSerIleThrValLysAspGlnPheLeuValIleProArgIle 20
QY 483 AGCCCAAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCTGATTTGGAAGTTCCAGTG 542
Db 21 TyrProAsnProLysCysGlyLysAsnGlyLysGlyValLeuValTrpArgHisSerLeu 40

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QY 543 AGCCGACAGTTGTCAGCCTATTGTTACAACTCATCTGATCTTGGACTACTCGTGCATT 602
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
41 SerGlnLysPheGluAlaThrCysHisAsnSerSerAspThrArgThrAsnSerCysile 60
QY 603 CCAGAAATATATACACCAAGATCCCATATTCACAACTCAAACTGCACACACAAACA 662
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
61 ProGluIleProThrAsnAspProThrPheAsnThrAsnThrAlaProTyrThrThr 80
QY 663 GAATTTATGTCAGTGACAGTACTACTCTCGTGGCATCC-----CCTTACTCTACAATA 716
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
81 GluMetThrValAsnAspArgThrSerSerSerThrAsnGlyProSerSerSerVal 100
QY 717 ---CCTGCCCTACTACTCTCTCCCTGCTCCAGCTTCCACTTCTATTCCACGAGAAA 773
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
101 MetProThrValValThrThrSerLeuProLeuAlaThrThrSerThrProArgLysArg 120
QY 774 AAATTGATTGTCACAGAGTTTATGGAACCTAGCACCATGTCTACAGAAACTGAA 833
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
121 LysLeuIleCysileThrGluAlaPheMetGluThrSerThrIleSerThrGluThrGlu 140
QY 834 CCATTGTTGAAATAAAGCAGCATTCAGAAATGAAGCTCTCGGTTTGAGGTGCCCC 893
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
141 LeuTyrIleGluAsnArgThrAlaPheLysAsnGluAlaIleGlyPheGlyGlyIlePro 160
QY 894 ACGGCTCTGCTAGTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 953
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
161 ThrAlaLeuLeuValLeuAlaLeuLeuPhePheAlaAlaAlaAlaGlyLeuAlaValCys 180
QY 954 TATGTCAAAGGATGTGAAGGCTTCCCTTTTACAAACAAGATCAGCAGAGGAAATG 1013
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
181 TyrValLysArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMet 200
QY 1014 ATC 1016
Db |||
201 Ile 201

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## RESULT 7

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O08779 PRELIMINARY; PRT; 780 AA.
ID O08779;
AC O08779;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CD44 protein.
GN CD44.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BDX; TISSUE=Pancreas;
RA Hofmann M.;
RT "Rattus norvegicus CD44 protein sequence.";
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U96138; AAB54002.1; -.
DR HSP; P98066; ITSG.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004895; F:cell adhesion receptor activity; IEA.
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR001231; CD44 antigen.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR00658; CD44.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS01241; LINK; 1.
SQ SEQUENCE 780 AA; 85917 MW; CC4D35AB1EA7377C CRC64;

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Alignment Scores:

Pred. No.: 1.26e-13 Length: 780

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Score: 231.50 Matches: 138
Percent Similarity: 34.29% Conservative: 77
Best Local Similarity: 22.01% Mismatches: 254
Query Match: 6.42% Indels: 160
DB: 11 Gaps: 23
US-10-079-111-2 (1-2029) x O08779 (1-780)
QY 225 TGAACACAGAGGCTCTGTGTCAGAGCTCTTTTCGTCGACAGAGCTTTCATCCAGGTG 284
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
10 TrpGlyLeuLeuCysLeuLeuGlnLeuSerLeuAlaGlnGlnGlnLeuAspLeuAsnile 29
QY 285 TCATGACAGATTATGGGATCACCTTGTGAGCAAAAGCGCAACACGACGCTGAATTTC 344
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
30 ThrCysArgTyrAlaGlyValPheHisValGluLysAsnGlyArgTyrSerIleSerArg 49
QY 345 ACAGAGACTAAGAGGCGCTGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTT 404
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
50 ThrGluAlaAlaAspLeuLeuCysGluAlaPheAsnThrThrLeuProThrMetAlaGlnMet 69
QY 405 GAAACAGCCTTGAAGCTAGCTTTGAACTTGACGCTATGGCTGGTGGGTGGAGATGGATT 464
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
70 GluLeuAlaLeuArgLysGlyPheGluThrCysArgTyrGlyPheile---GluGlyHis 88
QY 465 GTGCTCATCTCTAGGATTAGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGTCTCTG 524
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
89 ValValIleProArgIleHisProAsnAlaIleCysAlaAlaAsnAsnThrGlyValTyr 108
QY 525 ATTTGGAAGGTTCCAGTGACCGACAGCTTTTGCAGCCTATTGTTTCACTCATCTGATPACT 584
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
109 IleLeuLeuAlaSerAsnThrSerHisTyrAspThrTyrCysPheAsnAlaSerAlaPro 128
QY 585 TGGACTAATCTGTCGATTCCAGAAATATCACCAACCAAGATCCCATATTCACACTCAA 644
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
129 LeuGluAspCys-----ThrSerValThrAspLeuProAsnSerPhe 143
QY 645 ACTGCAACACAAACAGAAATTTATTGTGTCAGTGACAGTACC--TACTCGTGGCATCC 701
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
144 AspGlyProValThrIleThrIleValAsnArgAspGlyThrArgTyrSerLysLysGly 163
QY 702 CCTTACTCTACA-----ATACCTGCCCCCTACTACTACTCTCTCTCTCTCTCTCTCT 749
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
164 GluTyrArgThrHisGlnGluAspIleAspAlaSerAsnIleIleAspGluAspValSer 183
QY 750 TCCACTTCTATCCACGGAGAAAAAATTCATTGTGTACACAGAGTTTATGGAAGT 809
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
184 SerGlySerThrIleGluLysSer-----ThrProGluGlyTyrIleLeuHis 199
QY 810 AGCACCATGCTACAGAACTGAACCATTTGTTGAAAAATAAAGCAGCATTCAGAAGTAA 869
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
200 ThrAspLeuProThr---SerGlnProThrGlyAspArgAspAlaPhe----- 215
QY 870 GCTGCTGGGTTGGAGGTGTCGCCAGCTCTGCTAGTGTCTGCTGCTCTCTCTCTCTCT 929
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
216 -----PheIleGlySerThrLeuAlaThrIleAlaSerThrVal----- 228
QY 930 GCTGACAGCTGGTCTTGATTTGCTATGTCAAAAGGTATGTGAAGGCTTGAAGGCTTCC 983
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
229 -----TyrSerLysSerHisAlaThrAlaGlnLysGlnAsn 240
QY 984 -----TTTACAAACAAGAAATCAGCAGAGGAAATGATCGAAACCAAA 1025
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
241 AsnTrpIleTrpSerTrpPheGlyAsnSerGlnSerThrThrGlnThrGlnAspSerPro 260
QY 1026 GTAGTAAGAGAGAGAGGCAATGATAGCAACCTTAATGAGGAATCAAGAAACTGAT 1085
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
261 ThrThrThrAlaThrThrAlaLeuMetThrThrProGluThrProLysArgGlnGlu 280
QY 1086 AAA-----AACCCAGAGAGTCCCAAGAGTCCACGACCAAACT 1121
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
281 AlaGlnAsnTrpPheSerTrpPhePheGlnProSerGluSerLysHisLeuHisThr 300
QY 1122 ACCGTGCG-ATGCTGGAAGCTGAAGTTTAGATGAGACAGAAATGAGGACACACCTGA 1180

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Db 301 ThrThrLysMetProGly-|||||-----ThrGluSerAsnThrAsnProThr 314
QY 1181 GGCTGGTTCTTCATGCTCTTACCCCTGCCAGCTGGGGAATCAAAAGGCCCAAGA 1240
Db 315 GlyTrp-|||||-----LysProAsnGlu 320
QY 1241 ACCAAGAGAAAGTCCACCTTGGTTCCTTAACGTGGAATCAGCTCAGGACTG- 1292
Db 321 GluAsnGluAspGluThrAspLysTyrProAsnPheSer-GlySerGlyIleAspAs 340
QY 1293 -|||||-----CCATTGGACTATGTCAGCTGCACCAAG 1318
Db 340 pGluAspPheIleSerSerThrIleAlaThrPro-TripValSerAlaHisThrLysG 360
QY 1319 AGAAT-|||||-----GCCCTTCTCCTTA 1336
Db 360 InAsnGlnGluArgThrGlnTrpAsnProIleHisSerAsnProGluValLeuLeuGln 380
QY 1337 TTGTAACCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCACGGCTTCTAGCC 1396
Db 380 hrThrThrArgMetThrAspIleAspArgAsnSerThrSerAlaHisGlyGluAsnTrp 400
QY 1397 TGGCTATGTCCTAATAATATCCCACTGGGAGAAAGAGTTTGCAGAAAGTGCAGGACCTA 1456
Db 400 hrGln-|||||-----GluProGlnProProp 407
QY 1457 AAACATCTCATCATGATCCAGTGGTAAAGGCTCTCTGG-CTGCTCAGGCTAGTGGG 1515
Db 407 heAsnAsnHisGluTyrGlnAspGluGluThrProHisAlaThrSerThr-TripA 427
QY 1516 TTGAAAGCCAAAGGAGTCACTGAGCAACAGGCT-|||||-----TTCTCTACTG 1557
Db 427 laAspProAsnSerThrThrGluGluAlaAlaThrGlnLysGluLysTrpPheGluAsnG 447
QY 1558 ATTCCGAGCTCAGACCCCTTCTTCAGCTCTGAAGAGAAACACGATCCACCTGCACAT 1617
Db 447 luTrpGlnGlyLysAsnProProThrProSerGluAspSerHisValThrGluGlyThr 467
QY 1618 GTCCCTTCTGAGCCCGGTAG-AGCAAAAGATGGCAGAAAAG-|||||----- 1658
Db 467 hrAlaSerAlaHisAsnAsnHisProSerGlnArgMetThrThrGlnSerGlnGluAspV 487
QY 1659 -|||||-----TTTAGCCCTGAAGGCAT-|-CGAGTCTCTATACTTG 1695
Db 487 alSerTrpThrAspPheAsp-ProIleSerHisProMetGlyGlnGlyHis-|- 504
QY 1696 AGACCTAATCTCTGAAGCTAAATAAGAAATAGAACAAAGCTGAGGATACACAGTA 1755
Db 505 -|||||-----GlnThrGluSerLysAspThrGlySerSerHisSerThrThrLeu 519
QY 1756 -|||||-----CACTGTACAGGAGTGTAAACACACAGACAGGCTCA 1791
Db 520 GlnProThrAlaAlaProAsnThrHisLeuValGluAspLeu-|-AsnArgThrGlyPro 538
QY 1792 AAGTGTTTCTCTGAACATTCAGTGGATCAGTGTGGATCTGTTAGACACACACACTTACTT 1851
Db 539 -|||||-----LeuSerValThrThrProGlnSerHisSerGlnAsn 550
QY 1852 TTCTGTCTCTACCA 1866
Db 551 PheSerThrLeuPro 555
RESULT 8
O70509 PRELIMINARY; PRT; 364 AA.
AC O70509;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Glycoprotein CD44s.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Lumbar spine;
RA Stevens J.W.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065147; AAC17117.1; -.
DR HSSP; P98066; ITSQ.
DR GO; GO:0016020; C.membrane; IEA.
DR GO; GO:0004895; F.cell adhesion receptor activity; IEA.
DR GO; GO:0005540; F.hyaluronic acid binding; IEA.
DR GO; GO:0007155; P.cell adhesion; IEA.
DR InterPro; IPR001231; CD44 antigen.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR00658; CD44.
DR PRINTS; PR01265; LINKMODULE.
DR PRODOM; PD000918; Link; 1.
DR SMART; SM00445; Link; 1.
DR PROSITE; PS01241; Link; 1.
SQ SEQUENCE 364 AA; 39725 MW; BA249776C4419AA7 CRC64;
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Alignment Scores:

Pred. No.:	2,72e-13	Length:	364
Score:	227.00	Matches:	86
Percent Similarity:	39.83%	Conservative:	55
Best Local Similarity:	24.29%	Mismatches:	153
Query Match:	6.30%	Indels:	60
DB:	11	Gaps:	13

US-10-079-111-2 (1-2029) x O70509 (1-364)

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QY 225 TGGACCAAGAGGCTCTCTGTCAGAGAGCTTTGCGTGCAGAGAGCTTTCATCCAGTG 284
Db 10 TrpGlyLeuLeuCysLeuGlnLeuSerLeuAlaGlnGlnLeuAspLeuAsnIle 29
QY 285 TCATGAGAAATATGGGATTCACCCCTTGAGCAAAAAGCGCAACAGCAGCTGAATTC 344
Db 30 ThrCysArgTyrAlaGlyValPheHisValGluLysAsnGlyArgTyrSerIleSerArg 49
QY 345 ACAGAGCTTAAGGAGCGCTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTT 404
Db 50 ThrGluAlaAlaAspLeuCysGluAlaPheAsnThrLeuProThrMetAlaGlnMet 69
QY 405 GAAACAGCCTTGAAAGCTAGCTTTGAACTTGACGCTATGCGTGGGTGGAGATGGATTC 454
Db 70 GluLeuAlaLeuSerLysGlyPheGluThrCysArgTyrGlyPheIle---GluGlyHis 88
QY 465 GTGGTCATCTCTAGGATTCAGCCCAACCCCAAGTGGGAAAATAATGGGTGGGTGCTG 524
Db 89 ValValIleProArgIleHisProAsnAlaIleCysAlaAlaAsnAsnThrGlyValTyr 108
QY 525 ATTTGGAAGGTTCCAGTGAGCGCAGAGTTTGACGCTATTGTACACATCATCTGATACT 584
Db 109 IleLeuLeuAlaSerAsnThrSerHisTyrAspThrTyrCysPheAsnAlaSerAlaPro 128
QY 585 TGGACTTAACCTCGTGCATTCAGAAATATTATCACCACCAAGATCCCATATTACACTCAA 644
Db 129 LeuGluGluAspCys-----ThrSerValThrAspLeuProAsnSerPhe 143
QY 645 ACTGCAACACAAACACAGAAATTTATGTCAGTCAGCAGTACC---TACTCGGTGGCATCC 701
Db 144 AspGlyProValThrIleThrIleValAsnArgAspGlyThrArgTyrSerLysLysGly 163
QY 702 CCTTACTCTACA-----ATACCTGCCCTACT----- 728
Db 164 GluTyrArgThrHisGlnGluAspIleAspAlaSerAsnIleIleAspGluAspValSer 183
QY 729 -----ACTACTCTCTCTGCT---CCAGCTTCCACTTCTTCA 764
Db 184 SerGlySerThrIleGluLysSerThrProGluGlyTyrIleLeuHisThrAspLeuPro 203
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Db 272 leSerAlaGlyTrpGlu-ProAsnGluGluAsnGluAspGluArgAspArgHisLeuSer 291
QY 1079 -----
Db 292 PheSerGlySerGlyIleAspAspGluAspPheIleSerSerThrIleSerThrThr 311
QY 1080 -----
Db 312 ProArgAlaPheAspHisThrLysGlnAsnGlnAspTrpThrGlnTrpAsnProSerHis 331
QY 1101 TCAACAGAGCCCAAGC-----AAACCTACCGTCGATGCGCTGGAAGCTGAAGTTAG 1151
Db 332 Ser--AsnProGluValLeuLeuGlnThrThrArgMetThrAspValAsp----- 348
QY 1152 ATGAGACAGAAATAGAGACACACCTGAGGCTGTTCTTTCATGCTCCTTACCCCTGCC 1211
Db 349 -----ArgAsnGlyThrThrAlaTyrgluGlyAsnTrpAsn----- 360
QY 1212 CCAGCTGGGGAAATCAAAAGGCCAAAGAACCAAGAAAGTCCACCTTGGTTCCTA 1271
Db 361 -----ProGluAlaHisPro----- 365
QY 1272 ACTGGAATCAGCTCAGGACTGCGATTGGACTATGAGTGCACCAAGAGAATGCCCTTCT 1331
Db 366 -----ProLeuIleHisHisGluHisHisGluGluGluGluThr 378
QY 1332 CTTATTGTAACCTGCTGTGATCCCTACTCTCCAAAGCTTCCACGCGCTTTC 1391
Db 379 ProHisSer-----ThrSerThrIleGlnAlaThrProSer----- 390
QY 1392 TAGCTGGGTATGCTCCTAATAATATCCACTGGGAAAGGATTTGCAAGTCAAGG 1451
Db 390 ----- 390
QY 1452 ACTTAAACATCTCATCAGTATCCAGTGGTAAAGGCCCTCTCGGCTGCTGAGGCTAG 1511
Db 391 -----SerThrThrGluGluThrAlaThrGlnLysGluGlnTrpPheGlyAsn---Arg 407
QY 1512 TGGTTGAAAGCAAGAGTCACTGAGACCAAGGCTTCTCTACTGATCCCGAGCTCAG 1571
Db 408 TrpHisGlu-----GlyTyrglnThr-----ProArgGluAspSerHisSer 422
QY 1572 ACCCTTCTCAGCTCTGAAAGAGAACAGTATCCAC-----CTGACATGT 1619
Db 423 ThrThrGlyThrAlaAlaAlaSerAlaHisThrSerHisProMetGlnGlyArgThrThr 442
QY 1620 CCTTCTGAGCCCGGTAAAGACAAAGATGGCAGAAAGTTTAGCCCC 1667
Db 443 ProSerProGluAspSerSer-----TrpThrAspPheAsnPro 456

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RESULT 10  
Q98SR5

ID Q98SR5 PRELIMINARY; PRT; 265 AA.  
AC Q98SR5;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE T cell antigen CD44 isoform b.  
OS Anas platyrhynchos (Domestic duck).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.  
OX NCBI\_TaxID=8833;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=White Pekin.  
RA Chan S.W.S., Warr G.W., Middleton D.L., Higgins D.A.;  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF332869; AAK18277.1; -  
DR HSSP; P98066; 1TSG.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0004895; F:cell adhesion receptor activity; IEA.  
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.

GO; GO:0007155; P:cell adhesion; IEA.  
InterPro; IPR001231; CD44\_antigen.  
DR InterPro; IPR000538; Link.  
DR Pfam; PF00193; Xlink; 1.  
DR PRINTS; PR00658; CD44.  
DR PRINTS; PR01265; LINKMODULE.  
DR ProDom; PD000918; Link; 1.  
DR SMART; SM00445; LINK; 1.  
DR PROSITE; PS01241; LINK; 1.  
SQ SEQUENCE 265 AA; 29215 MW; 77C176E0A898D081 CRC64;  
Alignment Scores:  
Pred. No.: 1,53e-12 Length: 265  
Score: 219.00 Matches: 66  
Percent Similarity: 42.06% Conservative: 32  
Best Local Similarity: 28.33% Mismatches: 103  
Query Match: 6.08% Indels: 32  
DB: 13 Gaps: 5

US-10-079-111-2 (1-2029) x Q98SR5 (1-265)

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QY 222 ATCTGACCAAGGCTCCTGCTCCAAAGCTCTTTTCGTGCAGAAAGAGCTTTCCATCCAG 281
Db 6 ValTtpAlaThrPheGlyLeuLeuLysLeuLysLeuThrGlnPheAsn 25
QY 282 GTGTCTATGAGAATATATGGGATCACCTTGTGAGCAAAAGCGNACAGCAGCTGAAT 341
Db 26 ValSerCysArgTyrglyValPheHisValGluLysAsnGlyArgTyrglySerLeuThr 45
QY 342 TTCACAGAAGCTAAAGAGGCTGTAGGCTGCTGGGACTAAGTTTGGCCGCGAAGGACCAA 401
Db 46 ArgThrGluAlaAlaAspLeuLysCysArgAlaLeuAsnSerThrLeuSerThrLeuGluGln 65
QY 402 GTTGAACAGCTCTGAAAGCTAGCTTTGAACTTGCACTGATGCTGGTGGGAGATGGA 461
Db 66 LeuGluLysAlaHisGluLeuGlyPheGluThrCysArgTyrglyPheVal---ValGly 84
QY 462 TTCGTGGTCTATCTTAGGATTAGCCCAACCCCAAGTGTGGGAAATATGGTGGGTGTC 521
Db 85 TyrIleValIleProArgIleAsnProTyrglyHisLeuLysAlaAlaAsnHisThrGlyIle 104
QY 522 CTGATTGGAAGGTTCCAGTGAGCCGACAGTTTGACAGCTATTGTTACAACTCATCTGAT 581
Db 105 TyrLysLeuSerAlaAsnThrThrGlyArgTyrglyAspAlaTyrglySerThrAlaThrGlu 124
QY 582 ACTTGACTTAACCTCGTGCATTCCA----- 605
Db 125 ThrArgAspLysAlaCysGluProIleGluArgIleAspThrSerPheLeuSerAsnGln 144
QY 606 ---GAAATTCACCAACCAAGATCCC-----ATATTCACACTCAAACT 647
Db 145 GlyGluIleValIleAspAsnGluAspGlySerArgTyrglySerAlaAspGlyThrArgHis 164
QY 648 GCAACACAAACACAGAAATTTATTGTCACTGACAGTACCTACTCGGTGGCATCCCTTAC 707
Db 165 SerGlyAspSerSerThrSerGlyValAspAspGluAsnValGlySerGlySerHis 184
QY 708 TCTACAATACCTGCCCCCTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 752
Db 185 AspThrThrProValAspThrSerIleArgArgSerSerProSerTyrglySerVal 204
QY 753 ACTTCTATTCCAGG-----AGAAAAAATGATTGTGTC 788
Db 205 ThrProValProHisLeuSerAspHisSerGlyGlyGlyGluPheProVal 224
QY 789 ACAGAAAGTTTTTATGAAACTAGCACCATGCTTACAGAA 827
Db 225 ThrAsnSerAspAspGluLeuSerProThrSerThrAsp 237

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RESULT 11

Q90ZL8  
ID Q90ZL8 PRELIMINARY; PRT; 398 AA.  
AC Q90ZL8;

Db	165	SerGlyAspSerSerThrSerGlyValAspAspGluAsnValGlySerGlySerHis	18
Qy	708	TCTACAATACCTGCCCTACTACT	731
Db	185	AspThrThrProValAspThrSer	192
RESULT 12			
Q9H5A5			
ID	Q9H5A5	PRELIMINARY;	PRT; 719 AA.
AC	Q9H5A5		
DT	01-MAR-2001	(TrEMBLrel. 16, Created)	
DT	01-MAR-2001	(TrEMBLrel. 16, Last sequence update)	
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)	
DE	DJ68D18.2.3	(CD44 antigen (Homing function and indian blood group system)) (Fragment).	
DE			
GN	CD44.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
NCBI_TaxID=9606;			
EN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Cobley V.;		
RL	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.		
ENBL	AL133330; CAC10347.1; -		
DR	HSP; P98066; 1TSG.		
DR	GO; GO:0016020; C-membrane; IEA.		
DR	GO; GO:0004895; F:cell adhesion receptor activity; IEA.		
DR	GO; GO:0005540; F:hyaluronic acid binding; IEA.		
DR	GO; GO:0007155; P:cell adhesion; IEA.		
DR	InterPro; IPR001231; CD44 antigen.		
DR	InterPro; IPR000538; Link.		
DR	Pfam; PF00193; Xlink; 1.		
DR	PRINTS; PR00658; CD44.		
DR	PRINTS; PR01265; LINKMODULE.		
DR	ProDom; PD000918; Link; 1.		
DR	SMART; SM00445; LINK; 1.		
DR	PROSITE; PS01241; LINK; 1.		
FT	NON_TER	1	
SQ	SEQUENCE	719 AA; 78854 MW; 365747A896AD7380 CRC64;	
Alignment Scores:			
Pred. No.:	4.3e-12	Length:	719
Score:	216.00	Matches:	115
Percent Similarity:	31.94%	Conservative:	61
Best Local Similarity:	20.87%	Mismatches:	172
Query Match:	5.99%	Indels:	203
DB:	4	Gaps:	23
US-10-079-111-2 (1-2029) x Q9H5A5 (1-719)			
Qy	276	ATCCAGTGTCATGCAAGATTATGGGATACCCCTGTGAGCAAAAGGCAACCCAGCAG	335
Db	1	LeuAsnIleThrCysArgPheAlaGlyValPheHisValGluLysAsnGlyArgTyrSer	20
Qy	336	CTGAATTTACAGAGCTTAAGAGCCCTGTAGGCTGTGGACTATGGCGGCGAAG	395
Db	21	IleSerArgThrGluAlaAlaAspLeuCysLysAlaPheAsnSerThrLeuProThrMet	40
Qy	396	GACCAAGTTGAACAGCCTTCGAAGTAGCTTCGAACTTGCAGCTATGCTGGTTGGA	455
Db	41	AlaGlnMetGluLysAlaLeuSerIleGlyPheGluThrCysArgTyrGlyPheIle	-59
Qy	456	GATGATTGCGGTTCATCTCTAGGATTAGCCAAACCCCAAGTGTGGGAAAAATGGGGTG	515
Db	60	GluGlyHisValIleProArgIleHisProAsnSerIleCysAlaAlaAsnAsnThr	79
Qy	516	GTGTGCTGATTGGAAGGTTCCAGTGAGCCGACAGTTTCGACGCTATTGTTACA	575
Db	80	GlyValTyrIleLeuThrSerAsnThrSer---GlnTyrAspThrTyrCysPheAsnAla	98
Qy	576	TCTGACTACTTGACTAACTCGTGCAAT	-602





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Db      41 AlaGlnMetGluGlyAlaLeuSerIleGlyPheGluThrCysArgTyrGlyPheIle----- 59
QY      456 GATGATTCTGCTCATCTCTAGGATTACCCCAACCCCAAGTGTGGGAAAAATGGGGTG 515
Db      60 GluGlyHisValIleProArgIleHisProAsnSerIleCysAlaAlaAsnThr 79
QY      516 GTGTCCTGATTGGAGGTTCCAGTGAGCCGACAGTTTGGACCCCTATTGTTTACAACTCA 575
Db      80 GlyValTyrIleLeuThrSerAsnThrSer---GlnTyrAspThrTyrCysPheAsnAla 98
QY      576 TCTGATACTTGACAACTCGTGCAATT----- 602
Db      99 SerAlaProProGluGluAspCysThrSerValThrAspLeuProAsnAlaPheAspGly 118
QY      602 ----- 602
Db      119 ProIleThrIleThrIleValAsnArgAspGlyThrArgTyrValGlnLysGlyGluTyr 138
QY      603 -----CCAGAAATTATCCACCAAGATCCCATATTCAACACTCAAACTGCAACA 653
Db      139 ArgThrAsnProGluAspIleTyrProSerAsnProThrAspAspValSerSerGly 158
QY      654 CAAACACAGAAATTATTCTCAGTGACAGTACTCTCGTGGCATCCCTTACTCTACA 713
Db      159 SerSerSerGluArgSerThrSerGlyGlyTyr---IlePheTyrThrPheSerThr 177
QY      714 ATA---CCTGCCCTTACTACTCTCTCTCTCT-----GCTCCAGCTTCCACTTCTATTCCA 764
Db      178 ValHisProIleProAspGluAspSerProTyrIleThrAspSerThrAspArgIlePro 197
QY      765 CCGAGAAAAAATTGATTGTGTGCAGAGTTTATGGAACATAGCACCATGCTCTACA 824
Db      198 AlaThrSer-----ThrSerSerAsnThrIleSerAla 208
QY      825 GAACTGACCACTTTGTTGAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGTTTGA 884
Db      209 GlyTyrGluProAsnGluGluAsnGluAspGlu---ArgAspArgHisLeuSerPheSer 227
QY      885 GGTGTCCCAACGGCTCTGTAGTGTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 944
Db      228 Gly-----SerGlyIle 231
QY      945 GGATTTGCTATGTCAAAAGTATGTGAAGGCCTTCCTCTTTTACAAACAGATCAGCAG 1004
Db      232 -----AspAspAsp 234
QY      1005 AAGGAATGATCGAAACCAAGTAGTAAAGGAGGAGGAGCCCAATGATAGCAACCTAAT 1064
Db      235 GluAspPheIleSerThrIleSerThrThrProArgAlaPheAsp---HisThrLys 253
QY      1065 GAGGAATCAAGAAAACTGATAAAACCCAGAGAGTCCAAAGAGTCCCAAGC----- 1115
Db      254 GlnAsnGlnAspThrThrGlnTyrAsnProSerHisSer---AsnProGluValLeuLeu 272
QY      1116 AAACCTACCTGGTGCCTGGAGCTGAAGTGTAGATGAGACAGAAATGAGAGACACA 1175
Db      273 GlnThrThrThrArgMetThrAspValAsp-----ArgAsnGlyThrThr 287
QY      1176 CCTGAGGCTGTGTTCTTCTATGCTCTCTTACCTGCCCCAGCTGGGGAATCAAAAGGCC 1235
Db      288 AlaTyrGluGlyAsnThrAsn----- 294
QY      1236 AAAGAACCAAGAAAGATCCACCTTGTCTTCTTAATCGAATCAGCTCAGGACTGCCA 1295
Db      295 -----ProGluAlaHisPro-----Pro 300
QY      1296 TTGCACTATGAGTGACCAAAAGAGATGCCCTTCTCTTATTGTAACTCCTGTCTGATC 1355
Db      301 LeuIleHisHisGluHisGluGluGluGluThrProHisSer----- 315
QY      1356 CTATCCTCTCTACCTCCAAAGCTTCCACGGCCCTTCTAGCCTGGCTATGTCCTAATAATA 1415
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Db      316 ---ThrSerThrIleGlnAlaThrProSer----- 324
QY      1416 TCCCACTGGGAAAGAGGATTTTGGCAAGTGCAGAGCTAAACATCTCATCATGATCC 1475
Db      325 -----SerThrThrGluGluThr 330
QY      1476 AGTGTAAAAAGGCTCTCTGCTGCTGCTGAGGCTAGGTGGTTGAAAAGCCAGGAGTCACT 1535
Db      331 AlaThrGlnLysGluGlnTrpPheGlyAsn---ArgTrpHisGlu-----GlyTyrArg 347
QY      1536 GAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTTCAGCTCTGAAAGAG 1595
Db      348 GlnThr-----ProLysGluAspSerHisSerThrThrGlyThrAlaAlaAsn 364
QY      1596 AAACACGATATCCAC-----CTGACATCTCTTCTGAGCCCGGTAAAGAGCAA 1643
Db      365 AlaHisThrSerHisProMetGlnGlyArgThrThrProSerProGluAspSerSer--- 383
QY      1644 AGAATGGCAGAAAGTTTAGCCCC 1667
Db      384 ---TrpThrAspPheAsnPro 390

RESULT 15
Q90ZL6 PRELIMINARY; PRT; 168 AA.
AC Q90ZL6; 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE T-cell antigen CD44 isoform c.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP SEQUENCE FROM N.A.
RA Chan S.W.S., Middleton D.L., Lundqvist M., Warr G.W., Higgins D.A.;
RT 'Anas platyrhynchos T-cell antigens.';
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY032667; AAK52086.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004895; F:cell adhesion receptor activity; IEA.
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR001231; CD44_antigen.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR00658; CD44.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; Link; 1.
DR PROSITE; PS01241; Link; 1.
SQ SEQUENCE 168 AA; 18964 MW; 122EFE727977056E CRC64;

Alignment Scores:
Pred. No.: 2,29e-11 Length: 168
Score: 206.50 Matches: 45
Percent Similarity: 52.34% Conservative: 22
Best Local Similarity: 35.16% Mismatches: 60
Query Match: 5.73% Indels: 1
DB: 13 Gaps: 1

US-10-079-111-2 (1-2029) x Q90ZL6 (1-168)
QY 222 ATCTGACCAACAGGCTCTCTGTTCCAAAGGCTCTTTCGTCAGAGAGCTTTTCATCCAG 281
Db 6 ValTyrAlaThrPheGlyLeuCysLeuLeuLysLeuCysLeuThrLysThrGlnPheAsn 25
QY 282 GTGTCTATGAGAAATTATGGGATTCACCTTGTGAGCAAAAGCGCAACGACGCTGAAT 341
Db 26 ValSerCysLysTyrArgGlyValPheHisValGluLysAsnGlyArgTyrSerLeuThr 45
QY 342 TTCACAGAGCTAAGAGGCGCTGTAGGCTGCTGGGACTAAGTTTGGCGGAGGACCAA 401
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[illegible]

Search completed: September 13, 2004, 10:21:24  
Job time : 255.5 secs





Db 1 MetAlaArgCysPheSerLeuValLeuLeuThrSerIleTrpThrArgLeuLeu 20  
QY 243 GTCCAAAGCTCTTTCCGTCGACAGAGCTTTCCATCCAGGTGTATGCGAGAAATTATGGGG 302  
Db 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40  
QY 303 ATCCACCTGTGTGAGCAAAAGCGACACGAGCTGAATTTCCACAGAGCTTAAGGAGGCC 362  
Db 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
QY 363 TGTAGGCTGCTGGGACTAAGTTTGGCCGCAAGGACCAAGTTGAAACACAGCCTTGAAGCT 422  
Db 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
QY 423 AGCTTTGAAACTTGACGCTATCGCTGGGTGGAGATGGATTCTGGTGCATCTCTAGGATT 482  
Db 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValValIleSerArgIle 100  
QY 483 AGCCCAAAACCCAGCTGTGGGAAAATGGGTGGGTGCTCTGATTGGAAAGGTTCCAGTG 542  
Db 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
QY 543 AGCCACACAGTTTGACGCTATTGTTTACAACTCATCTGATCTTGGACTAACTCGTGCAAT 602  
Db 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle 140  
QY 603 CCAGAAATTTATCACCAACCAAGATCCCATATTCACTCAAACTGCAACACAAACAACA 662  
Db 141 ProGluIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
QY 663 GAATTTATTTGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACTGCTGC 722  
Db 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180  
QY 723 CCTACTACTACTCTCTCCCTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAATAATGTATT 782  
Db 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgLysLysLeuIle 200  
QY 783 TGTGTCACAGAAGTTTTATGGAAACTAGCACCATGTCTACAGAACTGAACCATTTGTT 842  
Db 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
QY 843 GAAATAAAGCAGCATTCAGAAATGAAGCTGCTGGTGGTGGAGGTGTCCTCCACGGCTCTG 902  
Db 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu 240  
QY 903 CTAGCTTGTGCTCTCTCTCTCTTTGGTGTGCTGAGCTGGTCTTGGATTTTGTATGTCAA 962  
Db 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260  
QY 963 AGGTATGTGAAGCCTTCCCTTTTACAAACAAGATCAGCAGAGGAATGATCGAACC 1022  
Db 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr 280  
QY 1023 AAAGTAGTAAGGAGAGAGCGCAATGATAGCAACCTTAATGAGGAATCAAGAGAAACT 1082  
Db 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
QY 1083 GATAAAACCCAGAGAGTCCAGAGTCCAAAGCAAACTACCGTGGGATGCTCTGGAAGCT 1142  
Db 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
QY 1143 GAAGTT 1148  
Db 321 GluVal 322

RESULT 2

US-09-907-794A-201  
; Sequence 201, Application US/09907794A  
; Patent No. 6635468  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/907,794A  
; CURRENT FILING DATE: 2001-07-17  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 201  
; LENGTH: 322  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic protein  
US-09-907-794A-201

Alignment Scores:

Pred. No.: 5.42e-174 Length: 322

Score: 1657.00 Matches: 322  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 45.98% Indels: 0  
DB: 4 Gaps: 0

US-10-079-111-2 (1-2029) x US-09-907-794A-201 (1-322)

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DB 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleThrThrArgLeuLeu 20  
QY 243 GTCCAAAGCTCTTTCGTCGACAGAGCTTCCATCCAGGTCATGACAGAAATTATGGG 302  
DB 21 ValGlnGlySerLeuArgAlaGluGluSerIleGlnValSerCysArgIleMetGly 40  
QY 303 ATCCCTTTGTGAGCAAAAGCGCAACAGCAGCTGAAATTTACAGAAAGCTTAAGAGGCC 362  
DB 41 IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla 60  
QY 363 TGTAGGCTGCTGGACTAAGTTTGGCCGCGAAGCAAGTTGAAACAGCCTTGAAGCT 422  
DB 61 CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80  
QY 423 AGCTTTGAACTTCAGCTATGGCTGGGTTCGAGATGGATTCTGTGTCATCTTAGGATT 482  
DB 81 SerPheGluThrCysSerTy-GlyTrpValGlyAspGlyPheValIleSerArgIle 100  
QY 483 AGCCCAAAACCCCAAGTGGGAAATAATGGGTGGGTGCTCTGATTGGAAAGTTCAGTG 542  
DB 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal 120  
QY 543 AGCGACAGTTTGGAGCTTATTTACAACTCATCTGATCTGACTGTAACCTGCTGCAAT 602  
DB 121 SerArgGlnPheAlaAlaTy-CysTy-AsnSerSerAspThrTrpThrAsnSerCysIle 140  
QY 603 CCAGAAATATCACACCAAGATCCCATATTTCAACACTCAACTCAACACCAACACACA 662  
DB 141 ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160  
QY 663 GAAATTTATGTACGTACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC 722  
DB 161 GluPheIleValSerAspSerThrTy-SerValAlaSerProTy-SerThrIleProAla 180  
QY 723 CCTACTACTCTCTCTCTCCAGCTTCCACTTCTATTCACGGAGAGAAAAATGTATT 782  
DB 181 ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200  
QY 783 TGTGTCACAGAAGTTTTTATGMAACTAGCACCATGCTCTACAGAACTGAACCATTTCTT 842  
DB 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220  
QY 843 GAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGAGGTTGTCCTCCACGCTCTG 902  
DB 221 GluAsnLysAlaAlaPheLysAsnGluAlaGlyPheGlyGlyValProThrAlaLeu 240  
QY 903 CTAGTGTGCT 962  
DB 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTy-ValLys 260  
QY 963 AGGTATGTGAAGGCTTCCCTTTTACAAACAGATCAGCAGAGGAATGATCGAACC 1022  
DB 261 ArgTy-ValLysAlaPheProPheThrAsnLysAenGlnGlnLysGluMetIleGluThr 280  
QY 1023 AAAGTAGTAAAGGAGAGGCCCAATGATGACCAACCTTAATGAGGAATCAAGAAAACT 1082  
DB 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300  
QY 1083 GATAAAACCCAGAGAGTCCAAAGAGTCCAAAGAACTACCGTCGATGCTGGAAGCT 1142  
DB 301 AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla 320  
QY 1143 GAAGTT 1148

Db 321 GluVal 322

RESULT 3

US-09-905-125A-201  
; Sequence 201, Application US/09905125A  
; Patent No. 6664376  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Macher, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: ROY, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tunas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/905,125A  
; CURRENT FILING DATE: 2001-07-12  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
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; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423

		; SEQ ID NO 201			
		; LENGTH: 322			
		; TYPE: PRT			
		; ORGANISM: Artificial sequence			
		; FEATURE:			
		; OTHER INFORMATION: Synthetic protein			
		US-09-905-125A-201			
		Alignment Scores:			
		Pred. No.:	5,42e-174	Length:	322
		Score:	1657.00	Matches:	322
		Percent Similarity:	100.00%	Conservative:	0
		Best Local Similarity:	100.00%	Mismatches:	0
		Query Match:	45.98%	Indels:	0
		DB:	4	Gaps:	0
		US-10-079-111-2 (1-2029) x US-09-905-125A-201 (1-322)			
QY	183	ATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCATCTCCATCTGCACACGAGGCTCCTG	242		
Db	1	MetAlaArgCysPheSerLeuValLeuLeuLeuLeuThrSerIleTrpThrArgLeuLeu	20		
QY	243	GTCCAAAGGCTCTTTGGTCGACAGAGCTTTCCATCCAGGTGTCTATGAGAAATTATGGG	302		
Db	21	ValGlnGlySerLeuArgAlaGluLeuSerIleGlnValSerCysArgIleMetGly	40		
QY	303	ATCACCTTGTGACGAAAAGCGAACACAGCAGCTGAATTTCCACAGAAGCTTAAGGAGCC	362		
Db	41	IleThrLeuValSerLysLysAlaAsnGlnGlnLeuAsnPheThrGluAlaLysGluAla	60		
QY	363	TGTAGCTGCTGGGACTAAGTTTGGCCGGCAGGACCAAGTTGAAACAGCCCTTCAAAAGCT	422		
Db	61	CysArgLeuLeuGlyLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla	80		
QY	423	AGCTTTGAAACTGCAGTATGCTGGTGGGTGGAGATGGAATTCGTGGTCACTCTAGGATT	482		
Db	81	SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle	100		
QY	483	AGCCCAACCCAGTGTGGGAAAATGGGTGGGTGCTCTGATTTGGAAGGTTCCACAGTG	542		
Db	101	SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTrpLysValProVal	120		
QY	543	AGCCGACAGTTTGACGCTATTGTTTACAACTCATCTGATCTTGCATTAACCTCGTGATT	602		
Db	121	SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTrpThrAsnSerCysIle	140		
QY	603	CCAGAAATATACCAACCAAGATCCCATATTCAACTCAACTCAAACTGCAACACAAACA	662		
Db	141	ProGluIleIleThrThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr	160		
QY	663	GAATTTATGTCAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCC	722		
Db	161	GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla	180		
QY	723	CCTACTACT	782		
Db	181	ProThrThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuLeu	200		
QY	783	TGTGTCCAGAAAGTTTATGAAACTAGCACCATGCTACAGAACTGAACACATTTGTT	842		
Db	201	CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal	220		
QY	843	GAATAATAAGCAGCATTCAGAATCAAGCTGCTGGTGGAGGTGTCGCCACGGCTCTG	902		
Db	221	GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyGlyValProThrAlaLeu	240		
QY	903	CTAGTGCTTGCT	962		
Db	241	LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys	260		
QY	963	AGGTATGTGAAGGCTTCCCTTTTCAACAACAGAAATCAGCAGAGGAATGATCGAACC	1022		
Db	261	ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnGlnLysGluMetIleGluThr	280		

QY	1023	AAAGTAGTAAAGGAGGAGGCCCAATGATGACCAACCTTAATAGGGAATCAAGAAAACT	1082
Db	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr	300
QY	1083	GATAAAACCCAGAGAGTCCAAAGAGTCCAAAGCAAACTACCGTCCGATGCCTGGAAGCT	1142
Db	301	AspLysAsnProGluGluSerLysSerProSerLysThrThrValArgCysLeuGluAla	320
QY	1143	GAAAGTT 1148	
Db	321	GluVal 322	
RESULT 4			
US-09-902-775A-201			
; Sequence 201, Application US/09902775A			
; Patent No. 6686451			
; GENERAL INFORMATION:			
; APPLICANT: Genentech, Inc.			
; APPLICANT: Ashkenazi, Avi			
; APPLICANT: Botstein, David			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Eaton, Dan L.			
; APPLICANT: Ferrara, Napoleone			
; APPLICANT: Filvaroff, Ellen			
; APPLICANT: Fong, Sherman			
; APPLICANT: Gao, Wei-Qiang			
; APPLICANT: Gerber, Hanspeter			
; APPLICANT: Gerritsen, Mary B.			
; APPLICANT: Goddard, A.			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Grimaldi, Christopher J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Hillan, Kenneth, J.			
; APPLICANT: Kijavini, Ivar J.			
; APPLICANT: Mather, Jennie P.			
; APPLICANT: Pan, James			
; APPLICANT: Paoni, Nicholas F.			
; APPLICANT: Roy, Margaret Ann			
; APPLICANT: Stewart, Timothy A.			
; APPLICANT: Tumas, Daniel			
; APPLICANT: Williams, P. Mickey			
; APPLICANT: Wood, William, I.			
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic			
; FILE REFERENCE: 10466-14			
; CURRENT APPLICATION NUMBER: US/09/902,775A			
; CURRENT FILING DATE: 2001-07-10			
; PRIOR APPLICATION NUMBER: PCT/US00/04414			
; PRIOR FILING DATE: 2000-02-22			
; PRIOR APPLICATION NUMBER: US 60/143,048			
; PRIOR FILING DATE: 1999-07-07			
; PRIOR APPLICATION NUMBER: US 60/145,698			
; PRIOR FILING DATE: 1999-07-26			
; PRIOR APPLICATION NUMBER: US 60/146,222			
; PRIOR FILING DATE: 1999-07-28			
; PRIOR APPLICATION NUMBER: PCT/US99/20594			
; PRIOR FILING DATE: 1999-09-08			
; PRIOR APPLICATION NUMBER: PCT/US99/20944			
; PRIOR FILING DATE: 1999-09-13			
; PRIOR APPLICATION NUMBER: PCT/US99/21090			
; PRIOR FILING DATE: 1999-09-15			
; PRIOR APPLICATION NUMBER: PCT/US99/21547			
; PRIOR FILING DATE: 1999-09-15			
; PRIOR APPLICATION NUMBER: PCT/US99/23089			
; PRIOR FILING DATE: 1999-10-05			
; PRIOR APPLICATION NUMBER: PCT/US99/28214			
; PRIOR FILING DATE: 1999-11-29			
; PRIOR APPLICATION NUMBER: PCT/US99/28313			
; PRIOR FILING DATE: 1999-11-30			
; PRIOR APPLICATION NUMBER: PCT/US99/28564			
; PRIOR FILING DATE: 1999-12-02			
; PRIOR APPLICATION NUMBER: PCT/US99/28565			

QY	1023	AAAGTAGTAAGCAGGAGAGCCCAATGATAGCAACCCCTAATGAGGAATCAAGAAACT	1082
Db	281	LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysThr	300
QY	1083	GATAAAACCCAGAGAGTCCAAGAGTCCAAGCAAAACTACCGTCGATGCCCTGGAAGCT	1142
Db	301	AspLysAsnProGluGluSerProSerLysThrValArgCysLeuGluAla	320
QY	1143	GAAATT 1148	
Db	321	GluVal 322	
RESULT 4			
US-09-902-775A-201			
; Sequence 201, Application US/09902775A			
; Patent No. 6686451			
; GENERAL INFORMATION:			
; APPLICANT: Genentech, Inc.			
; APPLICANT: Ashkenazi, Avi			
; APPLICANT: Botstein, David			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Eaton, Dan L.			
; APPLICANT: Ferrara, Napoleone			
; APPLICANT: Filvaroff, Ellen			
; APPLICANT: Fong, Sherman			
; APPLICANT: Gao, Wei-Qiang			
; APPLICANT: Gerber, Hanspeter			
; APPLICANT: Gerritsen, Mary E.			
; APPLICANT: Goddard, A.			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Grimaldi, Christopher J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Hillan, Kenneth, J.			
; APPLICANT: Kljavin, Ivar J.			
; APPLICANT: Mather, Jennie P.			
; APPLICANT: Pan, James			
; APPLICANT: Paoni, Nicholas F.			
; APPLICANT: Roy, Margaret Ann			
; APPLICANT: Stewart, Timothy A.			
; APPLICANT: Tumas, Daniel			
; APPLICANT: Williams, P. Mickey			
; APPLICANT: Wood, William, I.			
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic			
; TITLE OF INVENTION: Acids Encoding the Same			
; FILE REFERENCE: 10466-14			
; CURRENT APPLICATION NUMBER: US/09/902,775A			
; CURRENT FILING DATE: 2001-07-10			
; PRIOR APPLICATION NUMBER: PCT/US00/04414			
; PRIOR FILING DATE: 2000-02-22			
; PRIOR APPLICATION NUMBER: US 60/143,048			
; PRIOR FILING DATE: 1999-07-07			
; PRIOR APPLICATION NUMBER: US 60/145,698			
; PRIOR FILING DATE: 1999-07-26			
; PRIOR APPLICATION NUMBER: US 60/146,222			
; PRIOR FILING DATE: 1999-07-28			
; PRIOR APPLICATION NUMBER: PCT/US99/20594			
; PRIOR FILING DATE: 1999-09-08			
; PRIOR APPLICATION NUMBER: PCT/US99/20944			
; PRIOR FILING DATE: 1999-09-13			
; PRIOR APPLICATION NUMBER: PCT/US99/21090			
; PRIOR FILING DATE: 1999-09-15			
; PRIOR APPLICATION NUMBER: PCT/US99/21547			
; PRIOR FILING DATE: 1999-09-15			
; PRIOR APPLICATION NUMBER: PCT/US99/23089			
; PRIOR FILING DATE: 1999-10-05			
; PRIOR APPLICATION NUMBER: PCT/US99/28214			
; PRIOR FILING DATE: 1999-11-29			
; PRIOR APPLICATION NUMBER: PCT/US99/28313			
; PRIOR FILING DATE: 1999-11-30			
; PRIOR APPLICATION NUMBER: PCT/US99/28564			
; PRIOR FILING DATE: 1999-12-02			
; PRIOR APPLICATION NUMBER: PCT/US99/28565			

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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein
US-09-902-775A-201

Alignment Scores:
Pred. No.: 5 42e-174 Length: 322
Score: 1657.00 Matches: 322
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.98% Indels: 0
DB: 4 Gaps: 0

US-10-079-111-2 (1-2029) x US-09-902-775A-201 (1-322)
QY 183 ATGCCAGGTGCTTCAGCTGCTGTGTCTTCTCACTCGACACGAGGCTCCTG 242
DB 1 MetAlaArgCysPheSerLeuValLeuLeuLeuThrSerIleTyrThrArgLeuLeu 20
QY 243 GTCCAGGCTCTTCGTCGTCAGAGAGCTTCCATCCAGGTGTCATGAGATTTATGGG 302
DB 21 ValGlnGlySerLeuArgAlaGluGluLeuSerIleGlnValSerCysArgIleMetGly 40
QY 303 ATCACCCCTGTGAGCAAAAGCGAACCCAGCAGCTGAATTTACACAGAGCTAAAGGAGGCC 362
DB 41 IleThrLeuValSerLeuLysLysLysLysLysLysLysLysLysLysLysLysLys 60
QY 363 TGTAGGCTGCTGGGACTAAGTTTGGCCGCGAGGACCAAGTTGAAACAGCTTGAAGCT 422
DB 61 CysArgLeuLeuLeuLeuSerLeuAlaGlyLysAspGlnValGluThrAlaLeuLysAla 80
QY 423 AGCTTTGAACCTGCAGCTATGCTGGGTGGTGGATGATGATGCTGCTATCTCTAGGATT 482
DB 81 SerPheGluThrCysSerTyrGlyTrpValGlyAspGlyPheValIleSerArgIle 100
QY 483 AGCCCAAAACCCCAAGTGGGAAATAATGGGTGGGTGCTGATTGGGAAGTTCCAGTG 542
DB 101 SerProAsnProLysCysGlyLysAsnGlyValGlyValLeuIleTyrLysValProVal 120
QY 543 AGCCGACAGTTGACGCTATGTTTACAACTCATCTGATCTTGGACTAATCTGTCGATT 602
DB 121 SerArgGlnPheAlaAlaTyrCysTyrAsnSerSerAspThrTyrThrAsnSerCysIle 140
QY 603 CCAGAAATATCACCAACAGATCCCATATTCACACTCAAACTCAACAGCAACAACAACA 662
DB 141 ProGluIleIleThrLysAspProIlePheAsnThrGlnThrAlaThrGlnThrThr 160
QY 663 GAATTTATTTGTCAGTGACGTACTCTCGGTGGCATCCCTTACTCTACAACTACTGCC 722
DB 161 GluPheIleValSerAspSerThrTyrSerValAlaSerProTyrSerThrIleProAla 180
QY 723 CCTACTACTCTCTCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTTGATT 782
DB 181 ProThrThrProProAlaProAlaSerThrSerIleProArgArgLysLysLeuIle 200
QY 783 TGTGTACAGAGATTTTATGGAACACTAGCACCATCTCTACAGAACTGAACCATTTGTT 842
DB 201 CysValThrGluValPheMetGluThrSerThrMetSerThrGluThrGluProPheVal 220
QY 843 GAAATAAAGCAGCATTCAAGAATCAAGCTGCTGGGTTTGGAGGTTGTCCTCCACGCTCTG 902
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DB 221 GluAsnLysAlaAlaPheLysAsnGluAlaAlaGlyPheGlyValProThrAlaLeu 240
QY 903 CTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 962
DB 241 LeuValLeuAlaLeuLeuPhePheGlyAlaAlaAlaGlyLeuGlyPheCysTyrValLys 260
QY 963 AGTATGTGAAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1022
DB 261 ArgTyrValLysAlaPheProPheThrAsnLysAsnGlnLysGluMetIleGluThr 280
QY 1023 AAAGTAGTAAAGGAGGAGAGCCCAATGATGATAGCACCTTAATGAGGAATCAAAGAAACT 1082
DB 281 LysValValLysGluGluLysAlaAsnAspSerAsnProAsnGluGluSerLysLysThr 300
QY 1083 GATRAAAACCCAGAGAGTCCAAAGAGTCCAAAGAACTACCGTCGATGCTCGGAAGCT 1142
DB 301 AspLysAsnProGluGluSerLysSerProSerLysThrValArgCysLeuGluAla 320
QY 1143 GAAGTT 1148
DB 321 GluVal 322

RESULT 5
US-08-892-880-2
; Sequence 2, Application US/08892880
; Patent No. 5942417
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK J.
; TITLE OF INVENTION: CD44-LIKE PROTEIN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/892,880
; FILING DATE: HEREWITH
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/021,762
; FILING DATE: 15-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0490001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 322 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-892-880-2

Alignment Scores:
Pred. No.: 2.5e-173 Length: 322
Score: 1651.00 Matches: 321
Percent Similarity: 99.69% Conservative: 0
Best Local Similarity: 99.69% Mismatches: 1
Query Match: 45.81% Indels: 0
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APPLICATION NUMBER: US/07/946,497  
FILING DATE: 19921109  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 16915/145  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 503 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-946-497-2

## Alignment Scores:

Pred. No.: 4,64e-16 Length: 503  
Score: 228.50 Matches: 126  
Percent Similarity: 36.19% Conservative: 60  
Best Local Similarity: 24.51% Mismatches: 242  
Query Match: 6.34% Indels: 86  
DB: 1 Gaps: 21

US-10-079-111-2 (1-2029) x US-07-946-497-2 (1-503)

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Db 10 TrpGlyLeuLeuCysLeuGlnLeuSerLeuAlaGlnGlnLeuAsnLeu 29
QY 285 TCATCAGAAATTATGGGATACCTCTGTGAGCAAAAGCGCAACGACGAGCTGAAATTC 344
Db 30 ThrCysArgTyrAlaGlyValPheHisValGluLeuAsnGlyArgTyrSerIleSerArg 49
QY 345 ACAGAAGCTTAAGAGCGCTGTAGGCTGTGGGACTTAAGTTTGGCGGCAAGCAAGTT 404
Db 50 ThrGluAlaAlaAspLeuCysGluAlaPheAsnThrLeuLeuProThrMetAlaGlnMet 69
QY 405 GAAACAGCTTGAAGCTAGCTTTGAACTTCAGCTATGGCTGGGTGGAGATGGAATTC 464
Db 70 GluLeuAlaLeuArgLysGlyPheGluThrCysArgTyrGlyPheIle---GluGlyHis 88
QY 465 GTGCTCATCTTAGATTAGCCAAACCCCAAGTGTGGGAAATAATGGGTGGGTGCTCTG 524
Db 89 ValValIleProArgIleHisProAsnAlaIleCysAlaAlaAsnAsnThrGlyValTyr 108
QY 525 ATTTGGAAGTTCCAGTGGCGGACAGTTTGGAGCTATTGTACAACTCATCTGATACT 584
Db 109 IleLeuLeuAlaSerAsnThrSerHisTyrAspThrTyrCysPheAsnAlaSerAlaPro 128
QY 585 TGGACTAATCGTGCATCCAGAAATTATCACCAACCAAGATCCCATATTCACACTCAA 644
Db 129 LeuGluGluAspCys-----ThrSerValThrAspLeuProAsnSerPhe 143
QY 645 ACTGCAACAAACACAGAAATTTATGTGTCAGTGACAGTACC---TACTCGTGGCATCC 701
Db 144 AspGlyProValThrIleThrIleValAsnArgAspGlyThrArgTyrSerLysLysGly 163
QY 702 CTTTACTCTACAA-----ATACCTGCCCTTACT----- 728
Db 164 GluTyrArgThrHisGlnGluAspIleAspAlaSerAsnIleIleAspGluAspValSer 183
QY 729 -----ACTACTCTCTCTGCT---CCAGCTTCGACTTCTATTCCA 764
Db 184 SerGlySerThrIleGluLysSerThrProGluGlyTyrIleLeuHisThrAspLeuPro 203
QY 765 CGAGAAAAAATTGATTGTGTGCACAGAAAGTTTATGGAACCTAGACCATGCTACA 824
Db 204 ThrSerGlnProThrGlyAspArgAspAlaPheIleGlySerThrLeuAlaThr 223
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QY 825 ---GAAACTGAACCATTTTGTGAAATAAAGCAGCATTCAGAGATCAAGCTGCTGGTTT 881
Db 224 IleAlaThrThrProTyrValSerAlaHisThrLysGlnAsnGlnGluArgThrGlnTyr 243
QY 882 GGAGGTGTC-----CCACAGGCTCTGCTAGTGTGCTTGTCTCTCTCTCTTCTTGTGTC 932
Db 244 AsnProIleHisSerAsnProGluValLeuLeuGlnThrThrArgMetThrAspIle 263
QY 933 GCAGCTGGTCTTGGATTTTGTATGTCAAAGGTTATGTGAAG-----GCCTTCCTTTT 986
Db 264 AspArgAsnSerThrSerAlaHisGlyGluAsnTyrThrGlnGluProGlnProPhe 283
QY 987 ACAACAAGAATCAGCAGAGCAA-----ATGATC 1016
Db 284 AsnAsnHisGluTyrGlnAspGluGluThrProHisAlaThrSerThrThrTrpAla 303
QY 1017 GAAACCAAGTAGTAAAGGAGAGAGGCAATATAGCAACCTTAATGAGGAATCAAAAG 1076
Db 304 AspProAsnSerThrThrGluAlaAlaThrGlnLysGluLysTrpPheGluAsnGlu 323
QY 1077 AAAACTGATAAAACCCA-----GAAGAGTCCAAGAGTCCAAGCAAACTACC 1124
Db 324 TrpGlnGlyLysAsnProProThrProSerGluAspSerHisValThrGluGlyThrThr 343
QY 1125 GTGCGATGCTCGAAGCTGAAGTTTAGATGACA-----CAGAAATGAGGAGACACA 1175
Db 344 AlaSerAlaHisAsnAsnHisProSerGlnArgMetThrThrGlnSerGlnGluAspVal 363
QY 1176 CCTGAGGTGTTTCTTTCATCTCTTACCTGCCAGCTGGGGAATCAAAAGGGCC 1235
Db 364 SerTrpThrAspPheAsp---ProIleSerHisProMetGlyGln-----Gly 379
QY 1236 AAAGAACCAACAAAGAAAGTCCACCTGGTTCCTAACTGGAATCAGCTCAGACTGCCA 1295
Db 380 HisGlnThrGluSerLysGlyHis-----SerSerGly---Asn 391
QY 1296 TTGGACTATGAGTGCACCAAGAGAAATGCCCTTCT-----CCTTATTGTAACCTGTC 1349
Db 392 GlnAspSerGlyValThrThrThrSerGlyProAlaArgArgProGlnIle---ProGlu 410
QY 1350 TGGATCTTATCTCTCTTACCTCCAAAGTTCACCGCTTCTTAGCTGGCTATGCTTCA 1409
Db 411 TrpLeu---IleIleLeuAlaSerLeuLeuAlaLeuIleLeuAlaValCys--- 428
QY 1410 ATAATATCCACTGGGAGAAAGAGTTTTCAAAGTGCAGAGCACTTAAACATCTCATCA 1469
Db 429 -----IleAlaValAsnSerArgArgCysGlyGlnLysLysLeuVal- 444
QY 1470 GTATCCAGTGGTAAA-----AAGGCC 1490
Db 445 IleAsnSerGlyAsnGlyThrValGluAspArgLysProSerGluLeuAsnGlyGluAla 464
QY 1491 TCTCGGTGTCAGGCTAGTGGTTGAAAGCAAGAGTCACTGAGACC---AAGGCT 1547
Db 465 SerLysSerGlnGluMetValHisLeuValAsnLysGluProThrGluThrProAspGln 484
QY 1548 TTCTCTACTGATTCGCGAGCTCAGACCTTCTTCTCA 1583
Db 485 PheMetThrAlaAspGluThrArgAsnLeuGlnSer 496
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## RESULT 11

US-08-483-322-2

Sequence 2, Application US/08483322

Patent No. 5,760,178

GENERAL INFORMATION:

APPLICANT: HERRLICH, Peter

APPLICANT: PONTA, Helmut

APPLICANT: GUENTHER, Ursula

APPLICANT: MATZKU, Siegfried

APPLICANT: WENZL, Achim

TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA

TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,

TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY

645 ACTGCAACACAAACAAAGATTTATTGTCAGTACAGTACC---TACTCGGTGCATCC 701

144 AspGlyProValThrIleThrIleValAsnArgAspGlyThrArgTyrSerLysGly 163

702 CCTTACTTACA-----ATACCTGCCCTACT----- 728

164 GluTyrArgThrHisGlnGluAspIleAspAsnIleAspGluAspValSer 183

729 -----ACTACTCTCTCTGCT---CCAGCTTCACCTCTATTCCA 764

184 SerGlySerThrIleGluLysSerThrProGluGlyTyrIleLeuHisThrAspLeuPro 203

765 CGAGAGAAAAAATTGATTGTGTACAGCAAGCTTTTATGGAACCTAGCACCATGCTACA 824

204 ThrSerGlnProThrGlyAspArgAspAlaPhePheIleGlySerThrLeuAlaThr 223

825 ---GAACTGAACCATTTGTTTGAATAAAGACAGCATTCAGAATGAAGCTGCTGGGTT 881

224 IleAlaThrThrProTyrValSerAlaHisThrLysGlnAsnGlnGluArgThrGlnTyr 243

882 GGAGGTGTC-----CCACAGCTCTGCTAGTGTGCTCTCTCTCTCTCTTTGGTGCT 932

244 AsnProIleHisSerAsnProGluValLeuLeuGlnThrThrThrArgMetThrAspIle 263

933 GCAGCTGTCTTGGATTTTGCTATGTCAAAAGGTATGTGAAG-----GCCTTCCTCTTT 986

264 AspArgAsnSerThrSerAlaHisGlyGluAsnTyrThrGlnGluProGlnProPhe 283

987 ACAACAGAATCAGCAGAGGAA-----ATGATC 1016

284 AsnAsnHisGluTyrGlnAspGluGluThrProHisAlaThrSerThrThrTyrAla 303

1017 GAAACCAAGTAGTAAAGGAGGAAAGCCCAATCATACACACCTAATAGGAATCAAG 1076

304 AspProAsnSerThrThrGluGluAlaAlaThrGlnLysGluTyrTrpPheGluAsnGlu 323

1077 AAAACTGATAAAAACCCA-----GAAGAGTCCAAGAGTCCAAGCAAAACTACC 1124

324 TrpGlnGlyLysAsnProThrProSerGluAspSerHisValThrGluGlyThrThr 343

1125 GTGCGATGCTGGAAGCTGAAGTTTATGATGAGA-----CAGAAATCAGGAGACACA 1175

344 AlaSerAlaHisAsnAsnHisProSerGlnArgMetThrThrGlnSerGlnGluAspVal 363

1176 CCTCAGGCTGTTCTTTCTTCATGCTCCTTACCCTGCCAGCTGGGGAATCAAAAGGCC 1235

364 SerTrpThrAspPheAsp---ProIleSerHisProMetGlyGln-----Gly 379

1236 AAGAACAAGAGAAAGTCCACCTTGTGTTCTTAAGTCAAGTCAAGTCAAGTCAAGTCA 1295

380 HisGlnThrGluSerLysGlyHis-----SerSerGly---Asn 391

1296 TTGCACTATCGAGTGCACCAAGAGATGCCCTTCT---CCTTATTGTAACCTGTCT 1349

392 GlnAspSerGlyValThrThrThrSerGlyProAlaArgProGlnIle---ProGlu 410

1350 TGGATCTATCTCTCTACCTCCAAAGCTCCACGGCTTCTTACGCTGCTATGTCCTA 1409

411 TrpLeu---IleIleLeuAlaSerLeuLeuAlaLeuIleLeuAlaValCys--- 428

1410 ATAATATCCCACTGGGAGAAAGGAGTTTTCAAAGTCAAGGACCTCAAAACATCTCATCA 1469

429 -----IleAlaValAsnSerArgArgArgCysGlyGlnLysLysLeuVal- 444

1470 GTATCCAGTGTAAA-----AAGGCC 1490

445 IleAsnSerGlyAsnGlyThrValGluAspArgLysProSerGluLeuAsnGlyGluAla 464

1491 TCCTGGCTGCTCAGGCTAGGTGGTTGAAGCCAGGAGTCACTAGACC---AAGGCT 1547

465 SerLysSerGlnGluMetValHisLeuValAsnLysGluProThrGlnThrProAspGln 484

1548 TTCTCTACTGATTCCGAGCTCAGACCCCTTCTTCA 1583



Db 411 TrpLeu--IleIleLeuAlaSerLeuLeuAlaLeuAlaLeuAlaValCys---- 428  
 QY 1410 ATAATATCCCTGGAGAAAGGAGTTTGGAAAGTGAAGACCTAAACATCTCATCA 1469  
 Db 429 -----IleAlaValAsnSerArgArgCysGlyGlnLysLysLysLeuVal- 444  
 QY 1470 GTATCCAGTGGTAAA-----AAGGCC 1490  
 Db 445 IleAsnSerGlyAsnGlyThrValGluAspArgLysProSerGluLeuAsnGlyGluAla 464  
 QY 1491 TCCTGGCTGCTGAGGCTAGTGGTGGAAAGCAAGGAGTCACTGAGACC---AAGGCT 1547  
 Db 465 SerLysSerGlnGluMetValHisLeuValAsnLysGluProThrGluThrProAspGln 484  
 QY 1548 TTCTCTACTGATTCGCGAGCTCAGACCTTTCTTCA 1583  
 Db 485 PheMetThrAlaAspGluThrArgAsnLeuGlnSer 496

## RESULT 13

US-08-892-880-3  
 ; Sequence 3, Application US/08892880  
 ; Patent No. 5942417  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NI, JIAN  
 ; APPLICANT: GENTZ, REINER L.  
 ; APPLICANT: DILLON, PATRICK J.  
 ; TITLE OF INVENTION: CD44-LIKE PROTEIN  
 ; NUMBER OF SEQUENCES: 15  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 ; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600  
 ; CITY: WASHINGTON  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20005-3934

COMPUTER READABLE FORM: disk  
 ; MEDIUM TYPE: Floppy  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/892,880  
 ; FILING DATE: HEREWITH  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 60/021,762  
 ; FILING DATE: 15-JUL-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: STEFFE, ERIC K  
 ; REGISTRATION NUMBER: 36,688  
 ; REFERENCE/DOCKET NUMBER: 1488.0490001  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-371-2600  
 ; TELEFAX: 202-371-2540  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 339 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-08-892-880-3

Alignment Scores:  
 Pred. No.: 1,02e-15 Length: 339  
 Score: 224.50 Matches: 83  
 Percent Similarity: 41.39% Conservative: 54  
 Best Local Similarity: 25.08% Mismatches: 157  
 Query Match: 6.23% Indels: 37  
 DB: 2 Gaps: 11

US-10-079-111-2 (1-2029) x US-08-892-880-3 (1-339)

QY 225 TGGACACGAGGCTCTGCTCCAGGCTCTTTGGTGCAGAAAGAGCTTTTCATCCAGGTG 284  
 Db 10 TrpGlyLeuLeuCysLeuGlnLeuSerLeuAlaGlnGlnIleAspLeuAsnIle 29  
 QY 285 TCATGCAGAAATTATGGGATCACCTTGTGTAGCAAAAAGGCAACACGACGATGAATTC 344  
 Db 30 ThrCysArgTyrAlaGlyValPheHisValGluLysAsnGlyArgTyrSerIleSerArg 49  
 QY 345 ACAGAAGCTAAGGAGGCTGTAGGCTGTGGACTAAGTTTGGCCGGCAAGCAAGCAAGTT 404  
 Db 50 ThrGluAlaAlaAspLeuCysGluAlaPheAsnThrThrLeuProThrMetAlaGlnMet 69  
 QY 405 GAAACAGCCTTGAAGTAGCTTTGAAACTTGCAGCTATGCTGGTGGAGATGGATTC 464  
 Db 70 GluLeuAlaLeuArgLysGlyPheGluThrCysArgTyrGlyPheIle--GluGlyHis 88  
 QY 465 GTGTCATCTCTAGGATAGCCCAACCCCAAGGTGGGAAAAATGGGGTGGTGTCTCTG 524  
 Db 89 ValValIleProArgIleHisProAsnAlaIleCysAlaAlaAsnAsnThrGlyValTyr 108  
 QY 525 ATTTGGAAGGTTCAGTGAGCCGACAGCTTTGCAGCCTATTGTTACAACTCATCTGATCT 584  
 Db 109 IleLeuLeuAlaSerAsnThrSerHisTyrAspThrTyrCysPheAsnAlaSerAlaPro 128  
 QY 585 TGGACTAACTCGTGCAATTCAGAAATATCACCACCAAGATCCCATATTCACACTCAA 644  
 Db 129 LeuGluGluAspCys-----ThrSerValThrAspLeuProAsnSerPhe 143  
 QY 645 ACTGCACACAAACACAGCAATTTATGTCAGTGACAGTACC---TACTCGGTGGCATCC 701  
 Db 144 AspGlyProValThrIleThrIleValAsnArgAspGlyThrArgTyrSerLysLysGly 163  
 QY 702 CCTTACTCTACA-----ATACCTGCCCTACT----- 728  
 Db 164 GluTyrArgThrHisGlnGluAspIleAspAlaSerAsnIleAspGluAspValSer 183  
 QY 729 -----ACTACTCTCTCTGCT---CCAGCTTCCACTTCTATTCCTCA 764  
 Db 184 SerGlySerThrIleGluLysSerThrProGluGlyTyrIleLeuHisThrAspLeuPro 203  
 QY 765 CGAGAGAAAAATGATTTGTGTACAGAGATTTTATGAAACTAGCACCATGTCTACA 824  
 Db 204 ThrSerGlnProThrGlyAspArgAspAlaPhePheIleGlySerThrLeuAlaThr 223  
 QY 825 ---GAAACTGAACCATTTCTGAAATAAAGCAGCATTCAGAGATCAAGATCAACTGCTGGTTT 881  
 Db 224 GlyHisSerSerGlyAsnGlnAspSerGlyValThrThrSerGlyProAlaArgArg 243  
 QY 882 GGAGGTGTCCCGCGCTCTGCTAGTGTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 941  
 Db 244 ProGlnIleProGluTrpLeuIleIleLeuAlaSerLeu---LeuAlaLeuAlaLeuIle 262  
 QY 942 CTTGGATTTTGTATGTCAAAAGGTATGGAAGGCTTCCCTCTCTCTCTCTCTCTCTCTCT 1001  
 Db 263 LeuAlaValCys-----IleAlaValAsnSerArgArgCysGlyGln 277  
 QY 1002 CAGAAGGAAATGATCGAAACCAAAA-----GTAGTAAAGGAGGAGAGAGCCCAATGAT 1052  
 Db 278 LysLysLysLeuValIleAsnSerGlyAsnGlyThrValGluAspArgLysProSerGlu 297  
 QY 1053 AGCAACCTTAATGAGGAATCAAGAAAACTGATAAAAACCCAGAGAGCTCAAGAGTCCA 1112  
 Db 298 LeuAsn---GlyGluAlaSerLysSerGlnGluMetValHisLeuValAsnLysGluPro 316  
 QY 1113 AGCAAACTACCGTCGATGCTGGAAGCTGAA 1145  
 Db 317 ThrGluThrProAspGlnPheMetThrAlaAsp 327

## RESULT 14

5504194-2

; Patent No. 5504194

; APPLICANT: ST. JOHN, THOMAS P.; GALLATIN, W. MICHAEL; IDZERDA,

```
;REJEAN
; TITLE OF INVENTION: LYMPHOCYTE ADHESION RECEPTOR FOR HIGH
; ENDOTHELIUM, CD44
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/884,624
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 628,646
; FILING DATE: 12-DEC-1990
; APPLICATION NUMBER: 325,224
; FILING DATE: 17-MAR-1989
; SEQ ID NO:2:
; LENGTH: 362
5504194-2

Alignment Scores:
Pred. No.: 1,77e-15 Length: 362
Score: 222.50 Matches: 92
Percent Similarity: 37.40% Conservative: 43
Best Local Similarity: 25.48% Mismatches: 127
Query Match: 6.17% Indels: 99
DB: Gaps: 16

US-10-079-111-2 (1-2029) x 5504194-2 (1-362)

QY 240 CTGGTCCAGGCTCTTTGGTGCAGAGAGCTTTCATCCAGTGTCATGCAGAAATTATG 299
Db 14 LeuValGlnLeuSerLeu-----AlaGlnIleAspLeuAsnIleThrCysArgPheGlu 31
QY 300 GGATACACCTTTGTGAGCAAAAGGCGAACCCAGCAGCTGAATTTCCAGAGCTTAAGGAG 359
Db 32 GlyIleTyrHisValGluIleAsnGlyArgTyrSerIleSerArgThrGluAlaAlaAsp 51
QY 360 GCCTGTAGGCTGTGGGACTTAAGTTTGGCGGCAAGGAGCAAGTTGAAACAGCTTTGAAA 419
Db 52 LeuCysIleAlaPheAsnSerThrLeuProThrMetAlaGlnMetGluIleAlaLeuSer 71
QY 420 GCTAGCTTTGAAATTCAGCTATGGCTGGTGGAGATGGATTCGGTGGTCACTCTAGG 479
Db 72 IleGlyPheGluThrCysArgTyrGlyPheIle---GluGlyHisValIleProArg 90
QY 480 ATTAGCCAAACCCCAAGTGGGAAATGGGTGGTGGCTGCTGATTTGGAGGTTTCCA 539
Db 91 IleHisProAsnSerIleCysAlaAlaAsnAsnThrGlyValTyrIleLeuThrSerAsn 110
QY 540 GTGAGCCGACAGTTTGCAGCCTATTGTACAACTCATCTGATCTTGGACTTAACCTGTC 599
Db 111 ThrSer---GlnTyrAspThrTyrCysPheAsnAlaSerAlaProProGlyGluAspCys 129
QY 600 ATCCGAGAAATTATCACCAACAAAGATCCCATATTCAACATCAACTCAACACCAACA 659
Db 130 -----ThrSerValThrAspLeuProAsnAlaPheAspGlyProIleThr 144
QY 660 ACAGAAATTATTCAGTGACAGTACC---TACTCGGTGGCATCCCTTACTTACAAATA 716
Db 145 IleThrIleValAsnArgAspGlyThrArgTyrValIleGlyLysGlyGluTyrArgThrAsn 164
QY 717 CCT-----GCCCTACT----- 728
Db 165 ProGluAspIleAsnProSerSerProThrAspAspValSerSerGlySerSerSer 184
QY 729 -----ACTACTCCTCT 740
Db 185 GluArgSerSerThrLeuGlyGlyTyrIlePheTyrAsnHisPheSerThrSerProPro 204
QY 741 GCTCCAGCTTCCACTTATTCCACGGAGAAAAAATTGAATTTGTGTGCACAGAAATTTT 800
Db 205 IleProAspGluAspGly----- 210
QY 801 ATGGAACATAGCACCATGTCTACAGAAACTGAACCATTTGTTGAAAAATAAGCAGCATTC 860
Db 211 ---ProTyrIleThrAspSerThrAspArgThrProAlaThrArgAspGlnGlyAlaPhe 229
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QY 861 AAG-----AATGAAGCTGCTGGGTTT----- 881
Db 230 AspProSerGlyGlySerHisThrHisGlySerGluSerAlaGlyHisSerHisGly 249
QY 882 -----GGAGGT-----GTCCCCAGC 896
Db 250 SerArgGluGlyGlyAlaAsnThrThrSerGlyProLeuArgThrProGlnIleProGlu 269
QY 897 GCTCTGTAGTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTAT 956
Db 270 TrpLeuIleIleLeuAlaSerLeu---LeuAlaLeuAlaLeuIleLeuAlaValCys--- 287
QY 957 GTCAAAAGGTATGTGAAGGCCCTTCCCTTTTACAAACAAATCAGCAGAGGAATGATC 1016
Db 288 -----IleAlaValAsnSerArgArgGlyGlyGlnIleLysLysLeuVal 303
QY 1017 GAAACCAAA-----CTAGTAAAGGAGGAGGCAATGATAGCAACCTTAATGAG 1067
Db 304 IleAsnAsnGlyAsnGlyAlaValGluAspArgLysSerSerGlyLeuAsn---GlyGlu 322
QY 1068 GAATCAAGAAACTGATATA-----AACCCAGAGAGTCCAGAGTCCCAAGC 1115
Db 323 AlaSerLysSerGlnGluMetValHisLeuValAsnLysGluSerSerGluThrProAsp 342
QY 1116 AAA 1118
Db 343 Gln 343

RESULT 15
US-07-946-497-6
; Sequence 6, Application US/07946497
; Patent No. 5506119
; GENERAL INFORMATION:
; APPLICANT: HERRLICH, Peter
; APPLICANT: PONTA, Helmut
; APPLICANT: GUENTHERT, Ursula
; APPLICANT: MATZKU, Siegfried
; APPLICANT: WENZL, Achim
; TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
; TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
; TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,497
; FILING DATE: 19921109
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16915/145
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: hcd44
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US-07-946-497-6

## Alignment Scores:

Pred. No.:	9.1e-14	Length:	361
Score:	207.00	Matches:	83
Percent Similarity:	38.24%	Conservative:	47
Best Local Similarity:	24.41%	Mismatches:	144
Query Match:	5.74%	Indels:	66
DB:	1	Gaps:	14

US-10-079-111-2 (1-2029) x US-07-946-497-6 (1-361)

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QY 255 TTGCGTCAGAGAGCTTCCATCCAGGTGTCAGAGATTATGGGATCACCCCTTGTG 314
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 17 LeuSerLeuAlaGlnIleAspLeuAsnIleThrCysArgPheAlaGlyValPheHisVal 36

QY 315 AGCAAAAGCGAACACAGCAGCTGAATTTCACAGAGCTAAGGAGCGCTAGCGTCTG 374
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 37 GluLysAsnGlyArgTyrSerIleSerArgThrGluAlaAlaAspLeuCysLysAlaPhe 56

QY 375 GGACTAAGTTGGCCGCAAGGACCAAGTGAACAGCCCTGAAAGCTAGCTTTGAAACT 434
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 57 AsnSerThrLeuProThrMetAlaGlnMetGluLysAlaLeuSerIleGlyPheGluThr 76

QY 435 TGCAGCTATCGCTGGTGGAGATGGATTCTGTCATCTCTAGGATTAGCCCAACCCC 494
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 77 CysArgTyrGlyPheIle---GluGlyHisValIleProArgIleHisProAsnSer 95

QY 495 AAGTGTGGGAAATGGGTGGGTGCTCTGATTGGAAGGTTCCAGTAGCCGACAGATT 554
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 96 IleCysAlaAlaAsnAsnThrGlyValTyrIleLeuThrTyrAsnThrSer---GlnTyr 114

QY 555 GCAGCCTATTGTTACAACTCATCTGATCTACTTGACTTCCGCTGTCATCCAGAAATTATC 614
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 115 AspThrTyrCysPheAsnAlaSerAlaProProGluGluAspCys----- 129

QY 615 ACCACCAAGATCCCATATTCAACACTCAACTGCAACACAAACAGAAATTTATGTC 674
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 130 ThrSerValThrAspIleuProAsnAlaPheAspGlyProIleThrIleValAsn 149

QY 675 AGTGACAGTACC---TACTCGTGGCATCCCTTACTCTACAATACCTGCC----- 722
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 150 ArgAspGlyThrArgTyrValGlnLysGlyGluTyrArgThrAsnProGluAspIleTyr 169

QY 723 CCTACTACTACTCCTCTGCTCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATT 782
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 170 ProSerAsnProThrAspAspValSerSerGlySerSerSerSerGluArgSerThr 189

QY 783 TGTGTACAGAGTGTTTTATGGAACCTAGCACCATG----- 818
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 190 SerGlyGlyTyrIlePheTyrThrPheSerThrValHisProIleProAspGluAspSer 209

QY 819 -----TCTACAGAACTGAACCATTTGTTGAAATAATAAGCAGCATTC--- 860
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 210 ProTyrIleThrAspSerThrAspArgIleProAlaThrArgAspGlnAspThrPheHis 229

QY 861 -----AAGATCAAGCTCTGGT--- 881
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 230 ProSerGlySerHisThrThrHisGluSerGluSerAspGlyHisSerHisGlySer 249

QY 882 -----GGAGGT-----GTCCCCACCGCT 899
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 250 GlnGluGlyGlyAlaAsnThrThrSerGlyProIleArgThrProGlnIleProGluTyr 269

QY 900 CTGCTAGTGTCTCTCCCTCTTCTTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 959
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 270 LeuIleLeuAlaSerLeu---LeuAlaLeuAlaLeuIleLeuAlaValCys----- 286

QY 960 AAAGGTATGTGAAGCCCTTCCCTTTTACAAACAAGAAATCAGCAAGAAATGATCGAA 1019
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 287 -----IleAlaValAsnSerArgArgCysGlyGlnLysLysLysLeuValIle 303

QY 1020 ACCAAA-----GTAGTAAAGGAGGAGAGCCCAATCATAGCAACCTATGAGGAA 1070
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```
Db 304 AsnSerGlyAsnGlyAlaValGluAspArgLysProSerGlyLeuAsn---GlyGluAla 322
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1071 TCAAAGAAAACTGATAAA-----AACCCAGAGAGTCCAAAGAGTCCAAAGCAAA 1118
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 323 SerLysSerGlnGluMetValHisLeuValAsnLysGluSerSerGluThrProAspGln 342
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Search completed: September 13, 2004, 10:33:31
Job time : 53.5 secs
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